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TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, 8th Floor
San Francisco, California 94111-3834
(415) 576-0200

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By: John Fonteyn

Submitted herewith for filing under 37 CFR 1.53(b) is the

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☐ continuation patent application of
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Inventor(s)/Applicant Identifier: Alessandro Sette, John Sidney, Scott Southwood, Brian D. Livingston, Robert Chesnut, Denise Marie Baker, Esteban Celis, Ralph T. Kubo and Howard M. Grey

For: **INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS**

- [X] This application claims priority from each of the following Application Nos./filing dates:
CIP 09/189,702, filed November 10, 1998; which is a CIP of 08/205,713, filed March 4, 1994; which is a CIP of 08/159,184, filed November 29, 1993; which is a CIP of 08/073,205, filed June 4, 1993; which is a CIP of 08/027,146, filed March 5, 1993

the disclosure(s) of which is (are) incorporated by reference.

Please amend this application by adding the following before the first sentence: "This application is a [] continuation [] continuation-in-part of and claims the benefit of U.S. Application No. 60/_____, filed _____, the disclosure of which is incorporated by reference."

Enclosed are:

- [X] 429 page(s) of specification
[X] 6 page(s) of claims
[X] 1 page of Abstract
[X] 2 sheet(s) of [] formal [x] informal drawing(s).

An assignment of the invention to _____

A [] signed [] unsigned Declaration & Power of Attorney

A [] signed [] unsigned Declaration.

A Power of Attorney.

A verified statement to establish small entity status under 37 CFR 1.9 and 37 CFR 1.27 [] is enclosed [] was filed in the prior application and small entity status is still proper and desired.

A certified copy of a _____ application.

Information Disclosure Statement under 37 CFR 1.97.

A petition to extend time to respond in the parent application.

Notification of change of [] power of attorney [] correspondence address filed in prior application.

In view of the Unsigned Declaration as filed with this application and pursuant to 37 CFR §1.53(f), Applicant requests deferral of the filing fee until submission of the Missing Parts of Application.

DO NOT CHARGE THE FILING FEE AT THIS TIME.

Telephone:
(415) 576-0200

Facsimile:
(415) 576-0300

Jean M. Lockyer
Reg. No.: P-44,879
Attorneys for Applicant

PATENT APPLICATION

**INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN
IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID
COMPOSITIONS**

Inventor(s): Alessandro Sette, an Italian citizen, residing at
5551 Linda Rosa Avenue
La Jolla, California 92037

John Sidney, a United States citizen, residing at
4218 Corte de la Siena
San Diego, California 92130

Scott Southwood, a United States citizen, residing at
10679 Strathmore Drive
Santee, California 92071

Brian D. Livingston, a United States citizen, residing at
13555 Chaco Court
San Diego, California 92129

Robert Chesnut, a United States citizen, residing at
1473 Kings Cross Drive
Cardiff-by-the-Sea, California 92007

Denise Marie Baker, a United States citizen, residing at
11575 Caminito LaBar #21
San Diego, California 92126

Esteban Celis, a United States citizen, residing at
3683 Wright Road S.W.
Rochester, Minnesota 55902

Ralph T. Kubo, a United States citizen, residing at
6921 Pear Tree Drive
Carlsbad, California 92009

Howard M. Grey, a United States citizen, residing at
1461 Caminito Batea
La Jolla, California 92037

PATENT

Attorney Docket No.: 018623-014100US

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**INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN
IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID
COMPOSITIONS****CROSS-REFERENCES TO RELATED APPLICATIONS**

10 This application is a Continuation-In-Part ("CIP") of U.S.S.N. 09/189,702, filed
11/10/98, which is a CIP of U.S.S.N. 08/205,713 filed 3/4/94, which is a CIP of abandoned
U.S.S.N. 08/159,184 filed 11/29/93, which is a CIP of abandoned U.S.S.N. 08/073,205 filed
6/4/93 which is a CIP of abandoned U.S.S.N. 08/027,146 filed 3/5/93. The present
application is also related to U.S.S.N. 09/226,775, which is a CIP of abandoned U.S.S.N.
15 08/815,396, which claims benefit of abandoned U.S.S.N. 60/013,113. Furthermore, the
present application is related to U.S.S.N. 09/017,735, which is a CIP of abandoned U.S.S.N.
08/589,108; U.S.S.N. 08/454,033; and U.S.S.N. 08/349,177. The present application is also
related to U.S.S.N. 09/017,524, U.S.S.N. 08/821,739, which claims benefit of abandoned
U.S.S.N. 60/013,833; and U.S.S.N. 08/347,610, which is a CIP of U.S.S.N. 08/159,339,
20 which is a CIP of abandoned U.S.S.N. 08/103,396, which is a CIP of abandoned U.S.S.N.
08/027,746, which is a CIP of abandoned U.S.S.N. 07/926,666. The present application is
also related to U.S.S.N. 09/017,743, which is a CIP of abandoned U.S.S.N. 08/590,298; and
U.S.S.N. 08/452,843, which is a CIP of U.S.S.N. 08/344,824, which is a CIP of abandoned
U.S.S.N. 08/278,634. The present application is also related to PCT application 99/12066
25 filed 5/28/99 which claims benefit of provisional U.S.S.N. 60/087,192; U.S.S.N. 09/009,953,
which is a CIP of abandoned U.S.S.N. 60/036,713; and abandoned U.S.S.N. 60/037,432. In
addition, the present application is related to U.S.S.N. 09/098,584; U.S.S.N. 09/239,043;
U.S.S.N. 60/117,486; U.S.S.N. 09/350,401; U.S.S.N. 09/357,737; and U.S.S.N. 09/390,061.
All of the above applications are incorporated herein by reference.

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FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

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I. BACKGROUND OF THE INVENTION

Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.

The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant virus. Moreover, replication competent HIV persists in the lymphoid tissue of patients who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV infection.

Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814, 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982). HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens, epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of interferon, that inhibit viral replication.

While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, *Nature* 370:463, 1994; Walker *et al.*, *Proc. Natl.*

Acad. Sci. 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g., Tsubota et al., J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al.*, *Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g., Borrow et al., Nature Med.* 3:205-211, 1997; Price *et al., Proc. Nat. Acad. Sci.* 94:12890-12895, 1997; Koenig *et al., Nature Med.* 1:330-336, 1995; and Haas *et al., J. Immunol.* 157:4212-4221, 1996)

Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al., New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g., Rosenberg et al., Science* 278:1447, 1997).

A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like other retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape anti-viral therapy and immune recognition (Borrow *et al., Nature Med.* 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g., Lukashov et al., AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of sufficient breadth and vigor to prevent and/or clear HIV infection.

The epitope approach, as we have described, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine compositions. Such a composition may

simultaneously target multiple dominant and subdominant epitopes and thereby be used to achieve effective immunization in a diverse population.

The information provided in this section is intended to disclose the presently understood state of the art as of the filing date of the present application. Information is included in this section which was generated subsequent to the priority date of this application. Accordingly, information in this section is not intended, in any way, to delineate the priority date for the invention.

II. SUMMARY OF THE INVENTION

This invention applies our knowledge of the mechanisms by which antigen is recognized by T cells, for example, to develop epitope-based vaccines directed towards HIV. More specifically, this application communicates our discovery of specific epitope pharmaceutical compositions and methods of use in the prevention and treatment of HIV infection.

Upon development of appropriate technology, the use of epitope-based vaccines has several advantages over current vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The epitopes for inclusion in an epitope-based vaccine may be selected from conserved regions of viral or tumor-associated antigens, which thereby reduces the likelihood of escape mutants. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

An additional advantage of an epitope-based vaccine approach is the ability to combine selected epitopes (CTL and HTL), and further, to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion

of epitopes from multiple antigens from the pathogen in a vaccine composition. In the case of HIV, epitopes derived from multiple strains may also be included. A “pathogen” may be an infectious agent or a tumor associated molecule.

One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics, however, has been the extreme polymorphism of HLA molecules. To date, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used that are specific for HLA molecules corresponding to each individual HLA allele. Impractically large numbers of epitopes would therefore have to be used in order to cover ethnically diverse populations. Thus, there has existed a need for peptide epitopes that are bound by multiple HLA antigen molecules for use in epitope-based vaccines. The greater the number of HLA antigen molecules bound, the greater the breadth of population coverage by the vaccine.

Furthermore, as described herein in greater detail, a need has existed to modulate peptide binding properties, *e.g.*, so that peptides that are able to bind to multiple HLA antigens do so with an affinity that will stimulate an immune response. Identification of epitopes restricted by more than one HLA allele at an affinity that correlates with immunogenicity is important to provide thorough population coverage, and to allow the elicitation of responses of sufficient vigor to prevent or clear an infection in a diverse segment of the population. Such a response can also target a broad array of epitopes. The technology disclosed herein provides for such favored immune responses.

In a preferred embodiment, epitopes for inclusion in vaccine compositions of the invention are selected by a process whereby protein sequences of known antigens are evaluated for the presence of motif or supermotif-bearing epitopes. Peptides corresponding to a motif- or supermotif-bearing epitope are then synthesized and tested for the ability to bind to the HLA molecule that recognizes the selected motif. Those peptides that bind at an intermediate or high affinity *i.e.*, an IC_{50} (or a K_D value) of 500 nM or less for HLA class I molecules or an IC_{50} of 1000 nM or less for HLA class II molecules, are further evaluated for their ability to induce a CTL or HTL response.

Immunogenic peptide epitopes are selected for inclusion in vaccine compositions.

Supermotif-bearing peptides may additionally be tested for the ability to bind to multiple alleles within the HLA supertype family. Moreover, peptide epitopes may be analogued to modify binding affinity and/or the ability to bind to multiple alleles within an HLA supertype.

The invention also includes embodiments comprising methods for monitoring or evaluating an immune response to HIV in a patient having a known HLA-type. Such methods comprise incubating a T lymphocyte sample from the patient with a peptide composition comprising an HIV epitope that has an amino acid sequence described in Tables VII to Table XX which binds the product of at least one HLA allele present in the patient, and detecting for the presence of a T lymphocyte that binds to the peptide. A CTL peptide epitope may, for example, be used as a component of a tetrameric complex for this type of analysis.

An alternative modality for defining the peptide epitopes in accordance with the invention is to recite the physical properties, such as length; primary structure; or charge, which are correlated with binding to a particular allele-specific HLA molecule or group of allele-specific HLA molecules. A further modality for defining peptide epitopes is to recite the physical properties of an HLA binding pocket, or properties shared by several allele-specific HLA binding pockets (*e.g.* pocket configuration and charge distribution) and reciting that the peptide epitope fits and binds to the pocket or pockets.

As will be apparent from the discussion below, other methods and embodiments are also contemplated. Further, novel synthetic peptides produced by any of the methods described herein are also part of the invention.

III. BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Figure 1 provides a graph of total frequency of genotypes as a function of the number of PF candidate epitopes bound by HLA-A and B molecules, in an average population.

Figure 2: Figure 2 illustrates the position of peptide epitopes in an experimental model minigene construct.

IV. DETAILED DESCRIPTION OF THE INVENTION

The peptide epitopes and corresponding nucleic acid compositions of the present invention are useful for stimulating an immune response to HIV by stimulating the production of CTL or HTL responses. The peptide epitopes, which are derived directly or indirectly from native HIV protein amino acid sequences, are able to bind to HLA molecules and stimulate an immune response to HIV. The complete sequence of the HIV proteins to be analyzed can be obtained from Genbank. Peptide epitopes and analogs thereof can also be readily determined from sequence information that may subsequently

be discovered for heretofore unknown variants of HIV, as will be clear from the disclosure provided below.

The peptide epitopes of the invention have been identified in a number of ways, as will be discussed below. Also discussed in greater detail is that analog peptides have been derived and the binding activity for HLA molecules modulated by modifying specific amino acid residues to create peptide analogs exhibiting altered immunogenicity. Further, the present invention provides compositions and combinations of compositions that enable epitope-based vaccines that are capable of interacting with HLA molecules encoded by various genetic alleles to provide broader population coverage than prior vaccines.

IV.A. Definitions

The invention can be better understood with reference to the following definitions, which are listed alphabetically:

A "computer" or "computer system" generally includes: a processor; at least one information storage/retrieval apparatus such as, for example, a hard drive, a disk drive or a tape drive; at least one input apparatus such as, for example, a keyboard, a mouse, a touch screen, or a microphone; and display structure. Additionally, the computer may include a communication channel in communication with a network. Such a computer may include more or less than what is listed above.

"Cross-reactive binding" indicates that a peptide is bound by more than one HLA molecule; a synonym is degenerate binding.

A "cryptic epitope" elicits a response by immunization with an isolated peptide, but the response is not cross-reactive *in vitro* when intact whole protein which comprises the epitope is used as an antigen.

A "dominant epitope" is an epitope that induces an immune response upon immunization with a whole native antigen (see, *e.g.*, Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993). Such a response is cross-reactive *in vitro* with an isolated peptide epitope.

With regard to a particular amino acid sequence, an "epitope" is a set of amino acid residues which is involved in recognition by a particular immunoglobulin, or in the context of T cells, those residues necessary for recognition by T cell receptor proteins and/or Major Histocompatibility Complex (MHC) receptors. In an immune system setting, *in vivo* or *in vitro*, an epitope is the collective features of a molecule, such as

primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

"Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g., Stites, et al., IMMUNOLOGY*, 8TH ED., Lange Publishing, Los Altos, CA (1994).

An "HLA supertype or family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where xx denotes a particular HLA type), are synonyms.

Throughout this disclosure, results are expressed in terms of "IC₅₀'s." IC₅₀ is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.,* limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. Assays for determining binding are described in detail, *e.g.,* in PCT publications WO 94/20127 and WO 94/03205. It should be noted that IC₅₀ values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.,* HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC₅₀ of a given ligand.

Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC₅₀'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC₅₀ of the reference peptide increases 10-fold, the IC₅₀ values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC₅₀, relative to the IC₅₀ of a standard peptide.

Binding may also be determined using other assay systems including those using: live cells (*e.g., Ceppellini et al., Nature* 339:392, 1989; Christnick *et al., Nature* 352:67, 1991; Busch *et al., Int. Immunol.* 2:443, 19990; Hill *et al., J. Immunol.* 147:189, 1991; del

Guercio *et al.*, *J. Immunol.* 154:685, 1995), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, *J. Immunol.* 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890, 1994; Marshall *et al.*, *J. Immunol.* 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829, 1992), surface plasmon resonance (*e.g.*, Khilko *et al.*, *J. Biol. Chem.* 268:15425, 1993); high flux soluble phase assays (Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476, 1990; Schumacher *et al.*, *Cell* 62:563, 1990; Townsend *et al.*, *Cell* 62:285, 1990; Parker *et al.*, *J. Immunol.* 149:1896, 1992).

As used herein, "high affinity" with respect to HLA class I molecules is defined as binding with an IC_{50} , or K_D value, of 50 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM.

The terms "identical" or percent "identity," in the context of two or more peptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T cell response, or a helper T cell response, to the antigen from which the immunogenic peptide is derived.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment.

"Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses. In humans, the MHC complex is also known as the HLA complex. For a detailed

description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3RD ED., Raven Press, New York, 1993.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.

The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α -amino and carboxyl groups of adjacent amino acids. The preferred CTL-inducing peptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues. The preferred HTL-inducing oligopeptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues.

"Pharmaceutically acceptable" refers to a non-toxic, inert, and/or physiologically compatible composition.

A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment, for example, the primary anchor residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 9-residue peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif are set forth in Table 1. For example, analog peptides can be created by altering the presence or absence of particular

residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif.

"Promiscuous recognition" is where a distinct peptide is recognized by the same T cell clone in the context of various HLA molecules. Promiscuous recognition or binding is synonymous with cross-reactive binding.

A "protective immune response" or "therapeutic immune response" refers to a CTL and/or an HTL response to an antigen derived from an infectious agent or a tumor antigen, which prevents or at least partially arrests disease symptoms or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.

The term "residue" refers to an amino acid or amino acid mimetic incorporated into an oligopeptide by an amide bond or amide bond mimetic.

A "secondary anchor residue" is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst bound peptides than would be expected by random distribution of amino acids at one position. The secondary anchor residues are said to occur at "secondary anchor positions." A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of a peptide comprising a particular motif or supermotif.

A "subdominant epitope" is an epitope which evokes little or no response upon immunization with whole antigens which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole protein is used to recall the response *in vitro* or *in vivo*.

A "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

"Synthetic peptide" refers to a peptide that is not naturally occurring, but is man-made using such methods as chemical synthesis or recombinant DNA technology.

The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G.

Symbols for the amino acids are shown below.

Single Letter Symbol	Three Letter Symbol	Amino Acids
A	Ala	Alanine
C	Cys	Cysteine
D	Asp	Aspartic Acid
E	Glu	Glutamic Acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
Y	Tyr	Tyrosine

IV.B. Stimulation of CTL and HTL responses

The mechanism by which T cells recognize antigens has been delineated during the past ten years. Based on our understanding of the immune system we have developed efficacious peptide epitope vaccine compositions that can induce a therapeutic or prophylactic immune response to HIV in a broad population. For an understanding of the value and efficacy of the claimed compositions, a brief review of immunology-related technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P. *et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601,

1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are described herein and are set forth in Tables I, II, and III (see also, e.g., Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via web at : <http://134.2.96.221/scripts.blserver.dll/home.htm>; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics*, in press, 1999).

Furthermore, x-ray crystallographic analysis of HLA-peptide complexes has revealed pockets within the peptide binding cleft of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (See, e.g., Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al.*, *Nature* 360:364, 1992; Silver, M. L. *et al.*, *Nature* 360:367, 1992; Matsumura, M. *et al.*, *Science* 257:927, 1992; Madden *et al.*, *Cell* 70:1035, 1992; Fremont, D. H. *et al.*, *Science* 257:919, 1992; Saper, M. A., Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that have the potential of binding particular HLA antigen(s).

The present inventors have found that the correlation of binding affinity with immunogenicity, which is disclosed herein, is an important factor to be considered when evaluating candidate peptides. Thus, by a combination of motif searches and HLA-peptide binding assays, candidates for epitope-based vaccines have been identified. After determining their binding affinity, additional confirmatory work can be performed to select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, antigenicity, and immunogenicity.

Various strategies can be utilized to evaluate immunogenicity, including:

1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.,* Wentworth, P. A. *et al.*, *Mol. Immunol.* 32:603, 1995; Celis, E. *et al.*, *Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al.*, *J. Immunol.* 158:1796, 1997; Kawashima, I. *et al.*, *Human Immunol.* 59:1, 1998); This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the peptide become activated during this time and are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells.

2) Immunization of HLA transgenic mice (*see, e.g.,* Wentworth, P. A. *et al.*, *J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al.*, *Int. Immunol.* 8:651, 1996; Alexander, J. *et al.*, *J. Immunol.* 159:4753, 1997); In this method, peptides in incomplete Freund's adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.

3) Demonstration of recall T cell responses from immune individuals who have effectively been vaccinated, recovered from infection, and/or from chronically infected patients (*see, e.g.,* Rehmann, B. *et al.*, *J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al.*, *Immunity* 7:97, 1997; Bertoni, R. *et al.*, *J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al.*, *J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al.*, *J. Virol.* 71:6011, 1997); In applying this strategy, recall responses are detected by culturing PBL from subjects that have been naturally exposed to the antigen, for instance through infection, and thus have generated an immune response "naturally", or from patients who were vaccinated against the infection. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays for T cell activity including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

The following describes the peptide epitopes and corresponding nucleic acids of the invention.

IV.C. Binding Affinity of Peptide Epitopes for HLA Molecules

As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to vaccine development. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules.

CTL-inducing peptides of interest for vaccine compositions preferably include those that have an IC_{50} or binding affinity value for class I HLA molecules of 500 nM or better (*i.e.*, the value is ≤ 500 nM). HTL-inducing peptides preferably include those that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, (*i.e.*, the value is $\leq 1,000$ nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or vaccines.

As disclosed herein, higher HLA binding affinity is correlated with greater immunogenicity. Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to be immunogenic, as contrasted with about 50% of the peptides which bind with intermediate affinity. Moreover, higher binding affinity peptides lead to more vigorous immunogenic responses. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used. Thus, in preferred embodiments of the invention, high affinity binding epitopes are particularly useful.

The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens has been determined for the first time in the art by the present inventors. The correlation between binding affinity and immunogenicity was analyzed in two different experimental approaches (*see, e.g.*,

Sette, *et al.*, *J. Immunol.* 153:5586-5592, 1994). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the shaping of T cell responses (*see, e.g., Schaeffer et al. Proc. Natl. Acad. Sci. USA* 86:4649-4653, 1989).

An affinity threshold associated with immunogenicity in the context of HLA class II DR molecules has also been delineated (*see, e.g., Southwood et al. J. Immunology* 160:3363-3373, 1998, and co-pending U.S.S.N. 09/009,953 filed 1/21/98). In order to define a biologically significant threshold of DR binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the motif) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC_{50} of 1000 nM or greater. Thus, 1000 nM can be defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

The binding affinity of peptides for HLA molecules can be determined as described in Example 1, below.

IV.D. Peptide Epitope Binding Motifs and Supermotifs

Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues required for allele-specific binding to HLA molecules have been identified. The presence of these residues correlates with binding affinity for HLA molecules. The identification of motifs and/or supermotifs that correlate with high and intermediate affinity binding is an important issue with respect to the identification of immunogenic peptide epitopes for

the inclusion in a vaccine. Kast *et al.* (*J. Immunol.* 152:3904-3912, 1994) have shown that motif-bearing peptides account for 90% of the epitopes that bind to allele-specific HLA class I molecules. In this study all possible peptides of 9 amino acids in length and overlapping by eight amino acids (240 peptides), which cover the entire sequence of the E6 and E7 proteins of human papillomavirus type 16, were evaluated for binding to five allele-specific HLA molecules that are expressed at high frequency among different ethnic groups. This unbiased set of peptides allowed an evaluation of the predictive value of HLA class I motifs. From the set of 240 peptides, 22 peptides were identified that bound to an allele-specific HLA molecule with high or intermediate affinity. Of these 22 peptides, 20 (*i.e.* 91%) were motif-bearing. Thus, this study demonstrates the value of motifs for the identification of peptide epitopes for inclusion in a vaccine: application of motif-based identification techniques will identify about 90% of the potential epitopes in a target antigen protein sequence.

Such peptide epitopes are identified in the Tables described below.

Peptides of the present invention may also comprise epitopes that bind to MHC class II DR molecules. A greater degree of heterogeneity in both size and binding frame position of the motif, relative to the N and C termini of the peptide, exists for class II peptide ligands. This increased heterogeneity of HLA class II peptide ligands is due to the structure of the binding groove of the HLA class II molecule which, unlike its class I counterpart, is open at both ends. Crystallographic analysis of HLA class II DRB*0101-peptide complexes showed that the major energy of binding is contributed by peptide residues complexed with complementary pockets on the DRB*0101 molecules. An important anchor residue engages the deepest hydrophobic pocket (*see, e.g.*, Madden, D.R. *Ann. Rev. Immunol.* 13:587, 1995) and is referred to as position 1 (P1). P1 may represent the N-terminal residue of a class II binding peptide epitope, but more typically is flanked towards the N-terminus by one or more residues. Other studies have also pointed to an important role for the peptide residue in the 6th position towards the C-terminus, relative to P1, for binding to various DR molecules.

In the past few years evidence has accumulated to demonstrate that a large fraction of HLA class I and class II molecules can be classified into a relatively few supertypes, each characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus, peptides of the present invention are identified by any one of several HLA-specific amino acid motifs (*see, e.g.*, Tables I-III), or if the presence of the motif corresponds to the ability to bind several

allele-specific HLA antigens, a supermotif. The HLA molecules that bind to peptides that possess a particular amino acid supermotif are collectively referred to as an HLA “supertype.”

The peptide motifs and supermotifs described below, and summarized in Tables I-III, provide guidance for the identification and use of peptide epitopes in accordance with the invention.

Examples of peptide epitopes bearing a respective supermotif or motif are included in Tables as designated in the description of each motif or supermotif below. The Tables include a binding affinity ratio listing for some of the peptide epitopes. The ratio may be converted to IC_{50} by using the following formula: IC_{50} of the standard peptide/ratio = IC_{50} of the test peptide (*i.e.*, the peptide epitope). The IC_{50} values of standard peptides used to determine binding affinities for Class I peptides are shown in Table IV. The IC_{50} values of standard peptides used to determine binding affinities for Class II peptides are shown in Table V. The peptides used as standards for the binding assays described herein are examples of standards; alternative standard peptides can also be used when performing binding studies.

To obtain the peptide epitope sequences listed in each Table, protein sequence data for all of the HIV-1 isolates present in the 1999 Los Alamos database (<http://hiv-web.lanl.gov>) were evaluated for the presence of the designated supermotif or motif. A listing of the strains is provided in Table XXVI. Nine HIV-1 structural and regulatory proteins, gag, pol, env, nef, rev, tat, vif, vpr, and vpu, were included in the analysis. Peptide epitopes were additionally evaluated on the basis of their conservancy (*i.e.*, the amount of variance) among the available protein sequences for each HIV antigen. A criterion for conservancy used to generate the peptides set out in Tables VII-XX requires that the entire sequence of an HLA class I binding peptide be totally conserved in 15% of the sequences available for a specific HIV antigen. Similarly, a criterion for conservancy requires that the entire 9-mer core region of an HLA class II binding peptide be totally conserved in 15% of the sequences available for a specific protein. The percent conservancy of the selected peptide epitopes is indicated on the Tables. The frequency, *i.e.* the number of sequences of the HIV protein antigen in which the totally conserved peptide sequence was identified, is also shown. The “pos” (position) column in the Tables designates the amino acid position in the HIV protein that corresponds to the first amino acid residue of the epitope. The “number of amino acids” indicates the number of residues in the epitope sequence.

HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes:

The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs delineated below are summarized in Table I. The HLA class I motifs set out in Table I(a) are those most particularly relevant to the invention claimed here. Primary and secondary anchor positions are summarized in Table II. Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table VI. In some cases, peptide epitopes may be listed in both a motif and a supermotif Table. The relationship of a particular motif and respective supermotif is indicated in the description of the individual motifs.

IV.D.1. HLA-A1 supermotif

The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A*0101, A*2601, A*2602, A*2501, and A*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamly are shown in Table VI. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A1 supermotif are set forth on the attached Table VII.

IV.D.2. HLA-A2 supermotif

Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993) and cross-reactive binding among HLA-A2 and -A28 molecules have been described. (*See, e.g.*, Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor

residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table VI. As explained in detail below, binding to each of the individual allele-specific HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise an A2 supermotif are set forth on the attached Table VIII. The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.3. HLA-A3 supermotif

The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (*see, e.g.*, Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-specific HLA molecules predicted to be members of the A3 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A3 supermotif are set forth on the attached Table IX.

IV.D.4. HLA-A24 supermotif

The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (*see, e.g., Sette and Sidney, Immunogenetics, in press, 1999*). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e., the A24 supertype*) includes at least A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A24 supermotif are set forth on the attached Table X.

IV.D.5. HLA-B7 supermotif

The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e., the HLA-B7 supertype*) is comprised of at least twenty six HLA-B proteins including: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g., Sidney, et al., J. Immunol. 154:247, 1995; Barber, et al., Curr. Biol. 5:179, 1995; Hill, et al., Nature 360:434, 1992; Rammensee, et al., Immunogenetics 41:178, 1995 for reviews of relevant data*). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B7 supermotif are set forth on the attached Table XI.

IV.D.6. HLA-B27 supermotif

The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.,* the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B27 supermotif are set forth on the attached Table XII.

IV.D.7. HLA-B44 supermotif

The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.,* the B44 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

IV.D.8. HLA-B58 supermotif

The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.,* the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific

HLA molecules predicted to be members of the B58 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B58 supermotif are set forth on the attached Table XIII.

IV.D.9. HLA-B62 supermotif

The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g., Sidney and Sette, Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e., the B62 supertype*) include at least: B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B62 supermotif are set forth on the attached Table XIV.

IV.D.10. HLA-A1 motif

The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., DiBrino et al., J. Immunol.*, 152:620, 1994; Kondo *et al., Immunogenetics* 45:249, 1997; and Kubo *et al., J. Immunol.* 152:3913, 1994 for reviews of relevant data). Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise either A1 motif are set forth on the attached Table XV. Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also included in the listing of HLA-A1 supermotif-bearing peptide epitopes listed in Table VII, as these residues are a subset of the A1 supermotif primary anchors.

IV.D.11. HLA-A*0201 motif

An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g., Falk et al., Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g., Hunt et al., Science* 255:1261-1263, March 6, 1992; Parker *et al., J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kast et al., J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g., Del Guercio et al., J. Immunol.* 154:685-693, 1995; Ruppert *et al., Cell* 74:929-937, 1993; Sidney *et al., Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g., Ruppert et al., Cell* 74:929-937, 1993). These are shown in Table II. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise an A*0201 motif are set forth on the attached Table VIII. The A*0201 motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.12. HLA-A3 motif

The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (see, e.g., DiBrino *et al.*, *Proc. Natl. Acad. Sci USA* 90:1508, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A3 motif are set forth on the attached Table XVI. Those peptide epitopes that also comprise the A3 supermotif are also listed in Table IX. The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.

IV.D.13. HLA-A11 motif

The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Zhang *et al.*, *Proc. Natl. Acad. Sci USA* 90:2217-2221, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A11 motif are set forth on the attached Table XVII; peptide epitopes comprising the A3 allele-specific motif are also present in this Table because of the extensive overlap between the A3 and A11 motif primary anchor specificities. Further, those peptide epitopes that comprise the A3 supermotif are also listed in Table IX.

IV.D.14. HLA-A24 motif

The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or

secondary anchor positions; preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A24 motif are set forth on the attached Table XVIII. These epitopes are also listed in Table X, which sets forth HLA-A24-supermotif-bearing peptide epitopes, as the primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.

Motifs Indicative of Class II HTL Inducing Peptide Epitopes

The primary and secondary anchor residues of the HLA class II peptide epitope supermotifs and motifs delineated below are summarized in Table III.

IV.D.15. HLA DR-1-4-7 supermotif

Motifs have also been identified for peptides that bind to three common HLA class II allele-specific HLA molecules: HLA DRB1*0401, DRB1*0101, and DRB1*0701 (see, e.g., the review by Southwood *et al. J. Immunology* 160:3363-3373,1998).

Collectively, the common residues from these motifs delineate the HLA DR-1-4-7 supermotif. Peptides that bind to these DR molecules carry a supermotif characterized by a large aromatic or hydrophobic residue (Y, F, W, L, I, V, or M) as a primary anchor residue in position 1, and a small, non-charged residue (S, T, C, A, P, V, I, L, or M) as a primary anchor residue in position 6 of a 9-mer core region. Allele-specific secondary effects and secondary anchors for each of these HLA types have also been identified (Southwood *et al., supra*). These are set forth in Table III. Peptide binding to HLA-DRB1*0401, DRB1*0101, and/or DRB1*0701 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Conserved 9-mer core regions (*i.e.*, sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis), comprising the DR-1-4-7 supermotif, wherein position 1 of the supermotif is at position 1 of the nine-residue core, are set forth in Table XIXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in section "a" of the Table. Cross-reactive binding data for exemplary 15-residue supermotif-bearing peptides are shown in Table XIXb.

IV.D.16. HLA DR3 motifs

Two alternative motifs (*i.e.*, submotifs) characterize peptide epitopes that bind to HLA-DR3 molecules (*see, e.g.*, Geluk *et al.*, *J. Immunol.* 152:5742, 1994). In the first motif (submotif DR3A) a large, hydrophobic residue (L, I, V, M, F, or Y) is present in anchor position 1 of a 9-mer core, and D is present as an anchor at position 4, towards the carboxyl terminus of the epitope. As in other class II motifs, core position 1 may or may not occupy the peptide N-terminal position.

The alternative DR3 submotif provides for lack of the large, hydrophobic residue at anchor position 1, and/or lack of the negatively charged or amide-like anchor residue at position 4, by the presence of a positive charge at position 6 towards the carboxyl terminus of the epitope. Thus, for the alternative allele-specific DR3 motif (submotif DR3B): L, I, V, M, F, Y, A, or Y is present at anchor position 1; D, N, Q, E, S, or T is present at anchor position 4; and K, R, or H is present at anchor position 6. Peptide binding to HLA-DR3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Conserved 9-mer core regions (*i.e.*, those sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) corresponding to a nine residue sequence comprising the DR3A submotif (wherein position 1 of the motif is at position 1 of the nine residue core) are set forth in Table XXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in Table XXa. Table XXb shows binding data of exemplary DR3 submotif A-bearing peptides.

Conserved 9-mer core regions (*i.e.*, those that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) comprising the DR3B submotif and respective exemplary 15-mer peptides comprising the DR3 submotif-B epitope are set forth in Table XXc. Table XXd shows binding data of exemplary DR3 submotif B-bearing peptides.

Each of the HLA class I or class II peptide epitopes set out in the Tables herein are deemed singly to be an inventive aspect of this application. Further, it is also an inventive aspect of this application that each peptide epitope may be used in combination with any other peptide epitope.

IV.E. Enhancing Population Coverage of the Vaccine

Vaccines that have broad population coverage are preferred because they are more commercially viable and generally applicable to the most people. Broad population coverage can be obtained using the peptides of the invention (and nucleic acid compositions that encode such peptides) through selecting peptide epitopes that bind to HLA alleles which, when considered in total, are present in most of the population. Table XXI lists the overall frequencies of the HLA class I supertypes in various ethnicities (Table XXIa) and the combined population coverage achieved by the A2-, A3-, and B7-supertypes (Table XXIb). The A2-, A3-, and B7 supertypes are each present on the average of over 40% in each of these five major ethnic groups. Coverage in excess of 80% is achieved with a combination of these supermotifs. These results suggest that effective and non-ethnically biased population coverage is achieved upon use of a limited number of cross-reactive peptides. Although the population coverage reached with these three main peptide specificities is high, coverage can be expanded to reach 95% population coverage and above, and more easily achieve truly multispecific responses upon use of additional supermotif or allele-specific motif bearing peptides.

The B44-, A1-, and A24-supertypes are each present, on average, in a range from 25% to 40% in these major ethnic populations (Table XXIa). While less prevalent overall, the B27-, B58-, and B62 supertypes are each present with a frequency >25% in at least one major ethnic group (Table XXIa). Table XXIb summarizes the estimated prevalence of combinations of HLA supertypes that have been identified in five major ethnic groups. The incremental coverage obtained by the inclusion of A1-, A24-, and B44-supertypes to the A2, A3, and B7 coverage and coverage obtained with all of the supertypes described herein, is shown.

The data presented herein, together with the previous definition of the A2-, A3-, and B7-supertypes, indicates that all antigens, with the possible exception of A29, B8, and B46, can be classified into a total of nine HLA supertypes. By including epitopes from the six most frequent supertypes, an average population coverage of 99% is obtained for five major ethnic groups..

IV.F. Immune Response-Stimulating Peptide Analogs

In general, CTL and HTL responses are not directed against all possible epitopes. Rather, they are restricted to a few "immunodominant" determinants (Zinkernagel, *et al.*, *Adv. Immunol.* 27:1519, 1979; Bennink, *et al.*, *J. Exp. Med.* 168:1935-1939, 1988; Rawle,

et al., *J. Immunol.* 146:3977-3984, 1991). It has been recognized that immunodominance (Benacerraf, *et al.*, *Science* 175:273-279, 1972) could be explained by either the ability of a given epitope to selectively bind a particular HLA protein (determinant selection theory) (Vitiello, *et al.*, *J. Immunol.* 131:1635, 1983); Rosenthal, *et al.*, *Nature* 267:156-158, 1977), or to be selectively recognized by the existing TCR (T cell receptor) specificities (repertoire theory) (Klein, J., IMMUNOLOGY, THE SCIENCE OF SELF/NONSELF DISCRIMINATION, John Wiley & Sons, New York, pp. 270-310, 1982). It has been demonstrated that additional factors, mostly linked to processing events, can also play a key role in dictating, beyond strict immunogenicity, which of the many potential determinants will be presented as immunodominant (Sercarz, *et al.*, *Annu. Rev. Immunol.* 11:729-766, 1993).

The concept of dominance and subdominance is relevant to immunotherapy of both infectious diseases and cancer. For example, in the course of chronic viral disease, recruitment of subdominant epitopes can be important for successful clearance of the infection, especially if dominant CTL or HTL specificities have been inactivated by functional tolerance, suppression, mutation of viruses and other mechanisms (Franco, *et al.*, *Curr. Opin. Immunol.* 7:524-531, 1995). In the case of cancer and tumor antigens, CTLs recognizing at least some of the highest binding affinity peptides might be functionally inactivated. Lower binding affinity peptides are preferentially recognized at these times, and may therefore be preferred in therapeutic or prophylactic anti-cancer vaccines.

In particular, it has been noted that a significant number of epitopes derived from known non-viral tumor associated antigens (TAA) bind HLA class I with intermediate affinity (IC_{50} in the 50-500 nM range). For example, it has been found that 8 of 15 known TAA peptides recognized by tumor infiltrating lymphocytes (TIL) or CTL bound in the 50-500 nM range. (These data are in contrast with estimates that 90% of known viral antigens were bound by HLA class I molecules with IC_{50} of 50 nM or less, while only approximately 10% bound in the 50-500 nM range (Sette, *et al.*, *J. Immunol.*, 153:558-5592, 1994). In the cancer setting this phenomenon is probably due to elimination or functional inhibition of the CTL recognizing several of the highest binding peptides, presumably because of T cell tolerization events.

Without intending to be bound by theory, it is believed that because T cells to dominant epitopes may have been clonally deleted, selecting subdominant epitopes may allow existing T cells to be recruited, which will then lead to a therapeutic or prophylactic

response. However, the binding of HLA molecules to subdominant epitopes is often less vigorous than to dominant ones. Accordingly, there is a need to be able to modulate the binding affinity of particular immunogenic epitopes for one or more HLA molecules, and thereby to modulate the immune response elicited by the peptide, for example to prepare analog peptides which elicit a more vigorous response. This ability would greatly enhance the usefulness of peptide epitope-based vaccines and therapeutic agents.

Although peptides with suitable cross-reactivity among all alleles of a superfamily are identified by the screening procedures described above, cross-reactivity is not always as complete as possible, and in certain cases procedures to increase cross-reactivity of peptides can be useful; moreover, such procedures can also be used to modify other properties of the peptides such as binding affinity or peptide stability. Having established the general rules that govern cross-reactivity of peptides for HLA alleles within a given motif or supermotif, modification (*i.e.*, analoging) of the structure of peptides of particular interest in order to achieve broader (or otherwise modified) HLA binding capacity can be performed. More specifically, peptides which exhibit the broadest cross-reactivity patterns, can be produced in accordance with the teachings herein. The present concepts related to analog generation are set forth in greater detail in co-pending U.S.S.N. 09/226,775 filed 1/6/99.

In brief, the strategy employed utilizes the motifs or supermotifs which correlate with binding to certain HLA molecules. The motifs or supermotifs are defined by having primary anchors, and in many cases secondary anchors. Analog peptides can be created by substituting amino acid residues at primary anchor, secondary anchor, or at primary and secondary anchor positions. Generally, analogs are made for peptides that already bear a motif or supermotif. Preferred secondary anchor residues of supermotifs and motifs that have been defined for HLA class I and class II binding peptides are shown in Tables II and III, respectively.

For a number of the motifs or supermotifs in accordance with the invention, residues are defined which are deleterious to binding to allele-specific HLA molecules or members of HLA supertypes that bind the respective motif or supermotif (Tables II and III). Accordingly, removal of such residues that are detrimental to binding can be performed in accordance with the present invention. For example, in the case of the A3 supertype, when all peptides that have such deleterious residues are removed from the population of peptides used in the analysis, the incidence of cross-reactivity increased from 22% to 37% (*see, e.g.*, Sidney, J. *et al.*, *Hu. Immunol.* 45:79, 1996). Thus, one

strategy to improve the cross-reactivity of peptides within a given supermotif is simply to delete one or more of the deleterious residues present within a peptide and substitute a small "neutral" residue such as Ala (that may not influence T cell recognition of the peptide). An enhanced likelihood of cross-reactivity is expected if, together with
 5 elimination of detrimental residues within a peptide, "preferred" residues associated with high affinity binding to an allele-specific HLA molecule or to multiple HLA molecules within a superfamily are inserted.

To ensure that an analog peptide, when used as a vaccine, actually elicits a CTL response to the native epitope *in vivo* (or, in the case of class II epitopes, elicits helper T
 10 cells that cross-react with the wild type peptides), the analog peptide may be used to immunize T cells *in vitro* from individuals of the appropriate HLA allele. Thereafter, the immunized cells' capacity to induce lysis of wild type peptide sensitized target cells is evaluated. It will be desirable to use as antigen presenting cells, cells that have been either infected, or transfected with the appropriate genes, or, in the case of class II
 15 epitopes only, cells that have been pulsed with whole protein antigens, to establish whether endogenously produced antigen is also recognized by the relevant T cells.

Another embodiment of the invention is to create analogs of weak binding peptides, to thereby ensure adequate numbers of cross-reactive cellular binders. Class I binding peptides exhibiting binding affinities of 500-5000 nM, and carrying an acceptable
 20 but suboptimal primary anchor residue at one or both positions can be "fixed" by substituting preferred anchor residues in accordance with the respective supertype. The analog peptides can then be tested for crossbinding activity.

Another embodiment for generating effective peptide analogs involves the substitution of residues that have an adverse impact on peptide stability or solubility in,
 25 *e.g.*, a liquid environment. This substitution may occur at any position of the peptide epitope. For example, a cysteine (C) can be substituted out in favor of α -amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α -amino butyric acid for C not only alleviates this problem, but actually improves binding
 30 and crossbinding capability in certain instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999). Substitution of cysteine with α -amino butyric acid may occur at any residue of a peptide epitope, *i.e.* at either anchor or non-anchor positions.

IV.G. Computer Screening of Protein Sequences from Disease-Related Antigens for Supermotif- or Motif-Bearing Peptides

In order to identify supermotif- or motif-bearing epitopes in a target antigen, a native protein sequence, *e.g.*, a tumor-associated antigen, or sequences from an infectious organism, or a donor tissue for transplantation, is screened using a means for computing, such as an intellectual calculation or a computer, to determine the presence of a supermotif or motif within the sequence. The information obtained from the analysis of native peptide can be used directly to evaluate the status of the native peptide or may be utilized subsequently to generate the peptide epitope.

Computer programs that allow the rapid screening of protein sequences for the occurrence of the subject supermotifs or motifs are encompassed by the present invention; as are programs that permit the generation of analog peptides. These programs are implemented to analyze any identified amino acid sequence or operate on an unknown sequence and simultaneously determine the sequence and identify motif-bearing epitopes thereof; analogs can be simultaneously determined as well. Generally, the identified sequences will be from a pathogenic organism or a tumor-associated peptide. For example, the target molecules considered herein include, without limitation, the gag, pol, env, nef, rev, tat, vif, vpr, and vpu proteins of HIV.

In cases where the sequence of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide, be conserved in a designated percentage, of the sequences evaluated for a specific protein antigen.

Because HIV rapidly mutates thereby resulting in the generation of virus strains that have divergent amino acid sequences, an alternative method of selecting epitopes for inclusion in a vaccine composition is employed herein. In order to target a broad population that may be infected with a number of different strains, it is preferable to include in vaccine compositions epitopes that are representative of HIV antigen sequences from different HIV strains. For example, by selecting 5 epitopes from the same region, each of which is 20% conserved among HIV strains, the combination of the epitopes achieves 100% coverage of that region. As appreciated by those in the art, lower or higher degrees of conservancy, such as the 15% conservancy used for identification of

the epitopes set out in Tables VII-XX, can be employed as appropriate for a given antigenic target.

It is important that the selection criteria utilized for prediction of peptide binding are as accurate as possible, to correlate most efficiently with actual binding. Prediction of peptides that bind, for example, to HLA-A*0201, on the basis of the presence of the appropriate primary anchors, is positive at about a 30% rate (see, e.g., Ruppert, J. *et al. Cell* 74:929, 1993). However, by extensively analyzing peptide-HLA binding data disclosed herein, data in related patent applications, and data in the art, the present inventors have developed a number of allele-specific polynomial algorithms that dramatically increase the predictive value over identification on the basis of the presence of primary anchor residues alone. These algorithms take into account not only the presence or absence of primary anchors, but also consider the positive or deleterious presence of secondary anchor residues (to account for the impact of different amino acids at different positions). The algorithms are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where a_{ji} is a coefficient that represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. An important assumption of this method is that the effects at each position are essentially independent of each other. This assumption is justified by studies that demonstrated that peptides are bound to HLA molecules and recognized by T cells in essentially an extended conformation. Derivation of specific algorithm coefficients has been described, for example, in Gulukota, K. *et al.*, *J. Mol. Biol.* 267:1258, 1997.

Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (see, e.g., Milik *et al.*, *Nature Biotechnology* 16:753, 1998; Altuvia *et al.*, *Hum. Immunol.* 58:1, 1997; Altuvia *et al.*, *J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al.*, *Bioinformatics* 14:121-130, 1998; Parker *et al.*, *J. Immunol.* 152:163, 1993; Meister *et al.*, *Vaccine* 13:581, 1995; Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994; Sturniolo *et al.*, *Nature Biotechnol.* 17:555 1999).

For example, it has been shown that in sets of A*0201 motif-bearing peptides containing at least one preferred secondary anchor residue while avoiding the presence of

any deleterious secondary anchor residues, 69% of the peptides will bind A*0201 with an IC_{50} less than 500 nM (Ruppert, J. *et al. Cell* 74:929, 1993). These algorithms are also flexible in that cut-off scores may be adjusted to select sets of peptides with greater or lower predicted binding properties, as desired.

In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS" program (Devereux, *et al. Nucl. Acids Res.* 12:387-395, 1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs of the invention in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

In accordance with the procedures described above, HIV peptide epitopes and analogs thereof that are able to bind HLA supertype groups or allele-specific HLA molecules have been identified (Tables VII-XX).

IV.H. Preparation of Peptide Epitopes

Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or from natural sources such as native tumors or pathogenic organisms. Peptide epitopes may be synthesized individually or as polyepitopic peptides. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to native fragments or particles.

The peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in accordance with the invention are either free of modifications such as glycosylation, side chain oxidation, or phosphorylation; or they contain these modifications, subject to the condition that modifications do not destroy the biological activity of the peptides as described herein.

Desirably, the peptide epitope will be as small as possible while still maintaining substantially all of the immunologic activity of the native protein. When possible, it may be desirable to optimize HLA class I binding peptide epitopes of the invention to a length of about 8 to about 13 amino acid residues, preferably 9 to 10. HLA class II binding peptide epitopes may be optimized to a length of about 6 to about 30 amino acids in length, preferably to between about 13 and about 20 residues. Preferably, the peptide epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules.

The identification and preparation of peptides of other lengths can also be carried out using the techniques described herein. Moreover, it is preferred to identify native peptide regions that contain a high concentration of class I and/or class II epitopes. Such a sequence is generally selected on the basis that it contains the greatest number of epitopes per amino acid length. It is to be appreciated that epitopes can be present in a frame-shifted manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope; upon intracellular processing, each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. This larger, preferably multi-epitopic, peptide can be generated synthetically, recombinantly, or via cleavage from the native source.

The peptides of the invention can be prepared in a wide variety of ways. For the preferred relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (*See, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984*). Further, individual peptide epitopes can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, *MOLECULAR CLONING, A LABORATORY MANUAL*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant polypeptides which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

The nucleotide coding sequence for peptide epitopes of the preferred lengths contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981). Peptide analogs can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode the native peptide sequence; exemplary nucleic acid substitutions are those that encode an amino acid defined by the motifs/super motifs herein. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

IV.I. Assays to Detect T-Cell Responses

Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to the appropriate HLA proteins. These assays may involve evaluating the binding of a peptide of the invention to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* lacking peptide therein) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can

give rise to CTL populations capable of reacting with selected target cells associated with a disease. Corresponding assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

Conventional assays utilized to detect T cell responses include proliferation assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells or dendritic cells. Alternatively, mutant non-human mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides and that have been transfected with the appropriate human class I gene, may be used to test for the capacity of the peptide to induce *in vitro* primary CTL responses.

Peripheral blood mononuclear cells (PBMCs) may be used as the responder cell source of CTL precursors. The appropriate antigen-presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that kill radio-labeled target cells, both specific peptide-pulsed targets as well as target cells expressing endogenously processed forms of the antigen from which the peptide sequence was derived.

More recently, a method has been devised which allows direct quantification of antigen-specific T cells by staining with Fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*, *Science* 274:94, 1996). Other relatively recent technical developments include staining for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998).

HTL activation may also be assessed using such techniques known to those in the art such as T cell proliferation and secretion of lymphokines, *e.g.* IL-2 (*see, e.g.* Alexander *et al.*, *Immunity* 1:751-761, 1994).

Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse models including mice with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized and others (e.g., transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed. Additional transgenic mouse models with other HLA alleles may be generated as necessary. Mice may be immunized with peptides emulsified in Incomplete Freund's Adjuvant and the resulting T cells tested for their capacity to recognize peptide-pulsed target cells and target cells transfected with appropriate genes. CTL responses may be analyzed using cytotoxicity assays described above. Similarly, HTL responses may be analyzed using such assays as T cell proliferation or secretion of lymphokines.

Exemplary immunogenic peptide epitopes are set out in Table XXIII.

IV.J. Use of Peptide Epitopes as Diagnostic Agents and for Evaluating Immune Responses

HLA class I and class II binding peptides as described herein can be used, in one embodiment of the invention, as reagents to evaluate an immune response. The immune response to be evaluated may be induced by using as an immunogen any agent that may result in the production of antigen-specific CTLs or HTLs that recognize and bind to the peptide epitope(s) to be employed as the reagent. The peptide reagent need not be used as the immunogen. Assay systems that may be used for such an analysis include relatively recent technical developments such as tetramers, staining for intracellular lymphokines and interferon release assays, or ELISPOT assays.

For example, a peptide of the invention may be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs (see, e.g., Ogg *et al.*, *Science* 279:2103-2106, 1998; and Altman *et al.*, *Science* 174:94-96, 1996) and determine the frequency of the antigen-specific CTL population in a sample of peripheral blood mononuclear cells. A tetramer reagent using a peptide of the invention may be generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and β_2 -microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the heavy chain at a site that was previously

engineered into the protein. Tetramer formation is then induced by the addition of streptavidin. By means of fluorescently labeled streptavidin, the tetramer can be used to stain antigen-specific cells. The cells may then be identified, for example, by flow cytometry. Such an analysis may be used for diagnostic or prognostic purposes.

Peptides of the invention may also be used as reagents to evaluate immune recall responses. (see, e.g., Bertoni *et al.*, *J. Clin. Invest.* 100:503-513, 1997 and Penna *et al.*, *J. Exp. Med.* 174:1565-1570, 1991.) For example, patient PBMC samples from individuals infected with HIV may be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells may be evaluated by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.

The peptides may also be used as reagents to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed using, for example, either of the methods described above. The patient is HLA typed, and peptide epitope reagents that recognize the allele-specific molecules present in that patient are selected for the analysis. The immunogenicity of the vaccine is indicated by the presence of HIV epitope-specific CTLs and/or HTLs in the PBMC sample.

The peptides of the invention may also be used to make antibodies, using techniques well known in the art (see, e.g. *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual* Harlow, Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989), which may be useful as reagents to diagnose HIV infection. Such antibodies include those that recognize a peptide in the context of an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

IV.K. Vaccine Compositions

Vaccines that contain an immunogenically effective amount of one or more peptides as described herein are a further embodiment of the invention. Once appropriately immunogenic epitopes have been defined, they can be delivered by various means, herein referred to as "vaccine" compositions. Such vaccine compositions can include, for example, lipopeptides (e.g., Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide

compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (see e.g., Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (e.g., Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Faló, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Furthermore, vaccines in accordance with the invention encompass compositions of one or more of the claimed peptide(s). The peptide(s) can be individually linked to its own carrier; alternatively, the peptide(s) can exist as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition may be a naturally occurring region of an antigen or may be prepared, e.g., recombinantly or by chemical synthesis.

Furthermore, useful carriers that can be used with vaccines of the invention are well known in the art, and include, e.g., thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (i.e., acceptable) diluent such as water, or saline, preferably

phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS).

As disclosed in greater detail herein, upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later infection, or at least partially resistant to developing an ongoing chronic infection, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some instances it may be desirable to combine the class I peptide vaccines of the invention with vaccines which induce or facilitate neutralizing antibody responses to the target antigen of interest, particularly to viral envelope antigens. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE™ (Epimmune, San Diego, CA) molecule (described, for example, in U.S. Patent Number 5,736,142). Furthermore, any of these embodiments can be administered as a nucleic acid mediated modality.

The vaccine compositions of the invention may also be used in combination with antiviral drugs such as interferon- α .

For therapeutic or prophylactic immunization purposes, the peptides of the invention can also be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL and/or HTL response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of

other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Antigenic peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat chronic infections, or tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated antigen) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (an infected cell or a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells. Alternatively, dendritic cells are transfected, *e.g.*, with a minigene construct in accordance with the invention, in order to elicit immune responses. Minigenes will be discussed in greater detail in a following section.

Vaccine compositions may also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

DNA or RNA encoding one or more of the peptides of the invention can also be administered to a patient. This approach is described, for instance, in Wolff *et al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polyepitopic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. Exemplary epitopes that may be utilized in a vaccine to treat or prevent HIV infection are set out in Tables XXXVII and XXXVIII. It is preferred that each of the following principles are balanced in order to make the selection. The multiple epitopes to

be incorporated in a given vaccine composition may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with HIV clearance. For HLA Class I this includes 3-4 epitopes that come from at least one antigen of HIV. For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one HIV antigen (*see e.g., Rosenberg et al., Science 278:1447-1450*).

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often preferred to select analogs because the patient may have developed tolerance to the native epitope. When selecting epitopes for infectious disease-related antigens it is preferable to select either native or analoged epitopes. Of particular relevance for infectious disease vaccines (but for cancer-related vaccines as well), are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A peptide comprising "transcendent nested epitopes" is a peptide that has both HLA class I and HLA class II epitopes in it.

When providing nested epitopes, it is preferable to provide a sequence that has the greatest number of epitopes per provided sequence. Preferably, one avoids providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a longer peptide sequence, such as a sequence comprising nested epitopes, it is important to screen the sequence in order to insure that it does not have pathological or other deleterious biological properties.

5.) When creating a minigene, as disclosed in greater detail in the following section, an objective is to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same as those employed when selecting a peptide comprising nested epitopes. Furthermore, upon

determination of the nucleic acid sequence to be provided as a minigene, the peptide encoded thereby is analyzed to determine whether any "junctional epitopes" have been created. A junctional epitope is an actual binding epitope, as predicted, *e.g.*, by motif analysis, that only exists because two discrete peptide sequences are encoded directly next to each other. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

IV.K.1. Minigene Vaccines

A growing body of experimental evidence demonstrates that a number of different approaches are available which allow simultaneous delivery of multiple epitopes.

Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according

to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention. The use of multi-epitope minigenes is described below and in, *e.g.*, co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.*

71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding nine dominant HLA-A*0201- and A11-restricted epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), the PADRE™ universal helper T cell (HTL) epitope, and

an endoplasmic reticulum-translocating signal sequence was engineered. Immunization of HLA transgenic mice with this plasmid construct resulted in strong CTL induction responses against the nine epitopes tested, similar to those observed with a lipopeptide of known immunogenicity in humans, and significantly greater than immunization in oil-based adjuvants. Moreover, the immunogenicity of DNA-encoded epitopes *in vivo*

correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. Thus, these data show that the minigene served to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the

encoded epitopes. A similar approach may be used to develop minigenes encoding HIV epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in the minigene sequence include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and

sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (e.g., IL-2, IL-12, GM-CSF), cytokine-inducing molecules (e.g., LeIF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF- β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile

phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytotoxicity, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytotoxicity of peptide-loaded, ^{51}Cr -labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA

vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles
5 comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

IV.K.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising the peptides of the present invention, or analogs
10 thereof, which have immunostimulatory activity may be modified to provide desired attributes, such as improved serum half life, or to enhance immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. The use of T helper epitopes in conjunction with CTL
15 epitopes to enhance immunogenicity is illustrated, for example, in the co-pending applications U.S.S.N. 08/820,360, U.S.S.N. 08/197,484, and U.S.S.N. 08/464,234.

Particularly preferred CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under
20 physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues. Alternatively, the CTL
25 peptide may be linked to the T helper peptide without a spacer.

The CTL peptide epitope may be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated. The HTL peptide epitopes used in the invention can be modified in the same
30 manner as CTL peptides. For instance, they may be modified to include D-amino acids or be conjugated to other molecules such as lipids, proteins, sugars and the like.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in the majority of the population. This can be accomplished by selecting amino acid sequences that bind to many, most, or all of the HLA class II molecules.

These are known as "loosely HLA-restricted" or "promiscuous" T helper sequences. Examples of amino acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE), *Plasmodium falciparum* CS protein at positions 378-398 (DIEKKIAKMEKASSVFNVNS), and

5 Streptococcus 18kD protein at positions 116 (GAVDSILGGVATYGAA). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (see, e.g., PCT publication WO 95/07707). These synthetic compounds

10 called Pan-DR-binding epitopes (e.g., PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVWANTLKAAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the

15 response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, peptides comprising HTL epitopes can contain D-amino acids to increase their

20 resistance to proteases and thus extend their serum half-life. Also, the epitope peptides of the invention can be conjugated to other molecules such as lipids, proteins or sugars, or any other synthetic compounds, to increase their biological activity. Specifically, the T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α -amino groups of a lysine residue and then linked, e.g., via one or more linking residues

30 such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic comprises

palmitic acid attached to ϵ - and α - amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P_3CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide. (*See, e.g., Deres, et al., Nature* 342:561, 1989). Peptides of the invention can be coupled to P_3CSS , for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3CSS -conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses to infection.

As noted herein, additional amino acids can be added to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C_1 - C_{20}) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

IV.L. Administration of Vaccines for Therapeutic or Prophylactic Purposes

The peptides of the present invention and pharmaceutical and vaccine compositions of the invention are useful for administration to mammals, particularly humans, to treat and/or prevent HIV infection. Vaccine compositions containing the peptides of the invention are administered to a patient infected with HIV or to an individual susceptible to, or otherwise at risk for, HIV infection to elicit an immune response against HIV antigens and thus enhance the patient's own immune response capabilities. In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective CTL and/or HTL response to the virus antigen and to cure or at least partially arrest or slow symptoms

and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

The vaccine compositions of the invention may also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

As noted above, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The manner in which the peptide is contacted with the CTL or HTL is not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vivo* or *in vitro*. If the contacting occurs *in vivo*, the peptide itself can be administered to the patient, or other vehicles, *e.g.*, DNA vectors encoding one or more peptides, viral vectors encoding the peptide(s), liposomes and the like, can be used, as described herein.

For pharmaceutical compositions, the immunogenic peptides of the invention, or DNA encoding them, are generally administered to an individual already infected with HIV. The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. Those in the incubation phase or the acute phase of infection can be treated with the immunogenic peptides separately or in conjunction with other treatments, as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of HIV infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In chronic infection, loading doses followed by boosting doses may be required.

Treatment of an infected individual with the compositions of the invention may hasten resolution of the infection in acutely infected individuals and prevent development of chronic infection. Where susceptible individuals are identified prior to or during infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

The peptide or other compositions used for the treatment or prophylaxis of HIV infection can be used, *e.g.*, in persons who have not manifested symptoms of disease but who act as a disease vector. In this context, it is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to effectively stimulate a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood. The peptides and compositions of the present invention may be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

Thus, for treatment of chronic infection, a representative dose is in the range disclosed above, namely where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg , preferably from about 500 μg to about 50,000 μg per 70 kilogram patient. Initial doses followed by boosting doses at established intervals, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic infection, administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a

period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see, e.g., Remington's Pharmaceutical Sciences*, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a

molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily

propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

IV.M. Kits

The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired peptide compositions in a container, preferably in unit dosage form and instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

V. EXAMPLES

The following examples illustrate identification, selection, and use of immunogenic Class I and Class II peptide epitopes for inclusion in vaccine compositions.

Example 1. HLA Class I and Class II Binding Assays

The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.22 transfectants were used as sources of HLA class I molecules. These cells were maintained *in vitro* by culture in RPMI 1640 medium supplemented with 2mM L-glutamine (GIBCO, Grand Island, NY), 50μM 2-ME, 100μg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA). Cells were grown in 225-cm² tissue culture flasks or, for large-scale

cultures, in roller bottle apparatuses. The specific cell lines routinely used for purification of MHC class I and class II molecules are listed in Table XXIV.

Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)). Briefly, cells were lysed at a concentration of 10^8 cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at $15,000 \times g$ for 30min.

HLA molecules were purified from lysates by affinity chromatography. Lysates prepared as above were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The antibodies used for the extraction of HLA from cell lysates are listed in Table XXV. The anti-HLA column was then washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then be concentrated by centrifugation in Centrprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813, 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and $1\text{-}10\text{nM}$ ^{125}I -radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301,

which was performed at pH 4.5, and DRB1*1601 (DR2w21 β ₁) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (see Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN₃. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2 β ₁) assay makes separation of bound from unbound peaks more difficult under these conditions, all DRB1*1501 (DR2w2 β ₁) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

Radiolabeled peptides were iodinated using the chloramine-T method. Representative radiolabeled probe peptides utilized in each assay, and its assay specific IC₅₀ nM, are summarized in Tables IV and V. Typically, in preliminary experiments, each MHC preparation was titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

Since under these conditions [label]<[HLA] and IC₅₀≥[HLA], the measured IC₅₀ values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 μg/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC₅₀ of a positive control for inhibition by the IC₅₀ for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For database purposes, and inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC₅₀ nM values by dividing the IC₅₀ nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation has proven to be the most accurate and consistent for

comparing peptides that have been tested on different days, or with different lots of purified MHC.

Because the antibody used for HLA-DR purification (LB3.1) is α -chain specific, β_1 molecules are not separated from β_3 (and/or β_4 and β_5) molecules. The β_1 specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2), and DRB1*0803 (DR8w3), where no β_3 is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2 β_1), DRB5*0101 (DR2w2 β_2), DRB1*1601 (DR2w21 β_1), DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DR β molecule specificity have been described previously (*see, e.g., Southwood et al., J. Immunol.* 160:3363-3373, 1998).

Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes as, for example, described in Example 2.

Example 2. Identification of HLA Supermotif- and Motif-Bearing CTL Candidate Epitopes

Vaccine compositions of the invention may include multiple epitopes that comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage was performed using the strategy described below.

Computer searches and algorithms for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in Examples 2 and 5 employed the protein sequence data from HIV-1 clade B virus strains that were available in the 1994 Los Alamos database.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs were performed as follows. All translated HIV protein sequences were analyzed using a text string search software program, *e.g., MotifSearch 1.4* (D. Brown, San Diego)

to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally. Identified A2-, A3-, and DR-supermotif sequences were scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$“\Delta G” = a_{1j} \times a_{2i} \times a_{3j} \dots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i . For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

Complete protein sequences from nine HIV structural and regulatory proteins were aligned, then scanned, utilizing motif identification software, to identify conserved 9- and 10-mer sequences containing the HLA-A2-supermotif main anchor specificity.

- 5 The analysis included all isolates in the 1994 Los Alamos database. The conservation criteria varied according to antigen: greater than 80% of clade B isolates for gag, pol, env; greater than 70% for nef, rev, tat, vif, vpr; great than 60% for vpu.)

- A total of 233 conserved, HLA-A2 supermotif-positive sequences were identified. The peptides corresponding to the sequences were then synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a
10 prototype A2 supertype molecule). Thirty peptides bound A*0201 with IC₅₀ values ≤500 nM; of these 30, 5 bound with high binding affinities (IC₅₀ values ≤50 nM) and 25 bound with intermediate binding affinities, in the 50-500 nM range (Table XXVII).

- The thirty A*0201-binding peptides were subsequently tested for the capacity to
15 bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). As shown in Table XXVII, 20 of the 30 peptides were found to be A2-supertype cross-reactive binders, binding at least 3 of the 5 A2-supertype alleles tested.

Selection of HLA-A3 supermotif-bearing epitopes

- 20 The HIV protein sequences scanned above were also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. A total of 353 conserved 9- or 10-mer motif-containing sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the two most prevalent A3-supertype alleles. Sixty-six of the peptides were found to bind one of
25 the two alleles with binding affinities of ≤500 nM (Table XXVIII). These peptides were then tested for binding cross-reactivity to the other common A3-supertype alleles (A*3101, A*3301, and A*6801). Twenty one of the peptides bound at least three of the five HLA-A3-supertype molecules tested (Table XXVIII). Table XXVIII also includes two 11-mer peptides that were not selected using the search criteria outlined above, but
30 have been shown to be A3-supertype cross-reactive binders.

Selection of HLA-B7 supermotif bearing epitopes

When the same HIV target antigen protein sequences were also analyzed for the presence of conserved 9- or 10-mer peptides with the HLA-B7-supermotif, 54 sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-B*0702, the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Sixteen peptides bound B*0702 with IC_{50} of ≤ 500 nM (Table XXIX). These peptides were then tested for binding to other common B7-supertype molecules (B*3501, B*5101, B*5301, and B*5401). As shown in Table XXIX, eight of the sixteen peptides were capable of binding to three or more of the five B7-supertype alleles tested.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into potential vaccine constructs. An analysis of the protein sequence data from the HIV target antigens utilized above can also be performed to identify HLA-A1- and A24-motif-containing conserved sequences.

Other similar, but less extensive, studies performed by the present inventors have identified five conserved HIV-derived peptides that bind to A*0101 with an IC_{50} of 500 nM or less. (Table XXX). In a similar context, 11 conserved HLA-A*2402-binding HIV-derived peptides have also been identified, 5 of which bind with an IC_{50} of 100 nM or less (Table XXXI).

Example 3. Confirmation of Immunogenicity

*Evaluation of A*0201 immunogenicity*

It has been shown that CTL induced in A*0201/K^b transgenic mice exhibit specificity similar to CTL induced in the human system (*see, e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007-1015, 1991; Wentworth *et al.*, *Eur. J. Immunol.* 26:97-101, 1996). Accordingly, these mice were used to evaluate the immunogenicity of 19 of the 20 A2-supertype cross-reactive peptides identified in Example 2 above.

CTL induction in transgenic mice following peptide immunization has been described (Vitiello *et al.*, *J. Exp. Med.* 173:1007-1015, 1991; Alexander *et al.*; *J. Immunol.* 159:4753-4761, 1997). In these studies, mice were injected subcutaneously at the base of the tail with each peptide (50 μ g/mouse) emulsified in IFA in the presence of an excess of an IAb-restricted helper peptide (140 μ g/mouse) (HBV core 128-140, Sette *et*

al., J. Immunol. 153:5586-5592, 1994). Eleven days after injection, splenocytes were incubated in the presence of peptide-loaded syngenic LPS blasts. After six days, cultures were assayed for cytotoxic activity using peptide-pulsed targets. The data, summarized in Table XXXII, indicate that eight peptides were capable of inducing primary CTL responses in A*0201/K^b transgenic mice. (For these studies, a peptide was considered positive if it induced CTL (L.U. 30/10⁶ cells \geq 2 in at least two transgenic animals (Wentworth *et al., Eur. J. Immunol.* 26:97-101, 1996).

The cross-reactive candidate CTL epitopes were also tested for the ability to stimulate recall CTL responses HIV-infected patients. Briefly, PBMC from patients infected with HIV were cultured in the presence of 10 μ g/ml of synthetic peptide. After 10 and 14 days, the cultures were restimulated with peptide. The cultures were assayed for cytolytic activity on day 21 using target cells pulsed with the specific peptide in a ⁵¹Cr release assay. These data are also summarized in Table XXXII. As shown, 15 of the 19 peptides analyzed were recognized in recall CTL responses using PBMC from HIV-infected patients.

The set of peptides screened for immunogenicity contained two redundant peptides, 1261.14 and 1261.04, which differ in length by a single amino acid. While both peptides exhibit supertype degenerate binding, only the short of the two peptides exhibited immunogenicity. One supertype peptide not tested, 1211.09, has been reported to be recognized by CTL lines isolated from HIV-infected patients. In summary, 16 A2-supertype cross-reactive peptides have been identified that are immunogenic in humans; 53% of these peptides are also recognized in HLA-A2 transgenic mice. The sixteen peptides represent epitopes from five HIV antigens: env, gag, pol, vpr, and nef.

*Evaluation of A*03/A11 immunogenicity*

Twenty one of the A3-supertype cross-reactive peptides identified in Example 2 above were evaluated for immunogenicity (Table XXXIII). Peptides were screened using HLA-A11/K^b transgenic mice, using the protocol described above for HLA-A2 transgenic mice (Alexander *et al., J. Immunol.* 159:4753-4761, 1997) and using PBMC obtained from HIV-infected patients to test for the ability to stimulate CTL recall responses. Ten peptides that were capable of inducing CTL in HLA-A11 transgenic mice were identified.

Three peptides, 966.01, 940.03, and 1069.47, have been shown by collaborators to be immunogenic in HIV-infected patients. Peptides 966.01 and 1069.47 also induced CTL responses in transgenic mice, peptide 940.03 exhibited immunogenicity in patients only.

In summary, 11 of 23 A3-supertype cross-reactive binding peptides were found to be immunogenic in either HLA-A11 transgenic mice or HIV-infected patients. These peptides represent epitopes from three HIV antigens: pol, env, and nef.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified in Example 2 can be evaluated using HLA-B7 transgenic mice and PBMC from in HIV-infected patients in a manner analogous to the evaluation of A2-and A3-supermotif-bearing peptides. Three of these peptides have been previously reported as being immunogenic in HIV-infected patients.

Example 4. Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analogued, or “fixed” to confer upon the peptide certain characteristics, *e.g.* greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analog peptides that exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

As shown in Example 2, twenty HIV-derived, A2-supertype-restricted epitopes were identified. Peptide engineering strategies are implemented to further increase the cross-reactivity of the candidate epitopes identified above which bind 3/5 of the A2 supertype alleles tested. On the basis of the data disclosed, *e.g.*, in related and co-pending U.S.S.N 09/226,775, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide may be tested for binding to one or all supertype members and then analogued to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

Similarly, analogs of HLA-A3 supermotif-bearing epitopes may also be generated. For example, peptides binding to 3/5 of the A3-supertype molecules may be engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Those peptides that demonstrate ≤ 500 nM binding capacity are then tested for A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, peptides binding 3 or more B7-supertype alleles may be improved, where possible, to achieve increased cross-reactive binding. B7 supermotif-bearing peptides may, for example, be engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

20 *Analoging at Secondary Anchor Residues*

Moreover, HLA supermotifs are of value in engineering highly cross-reactive peptides and/or peptides that bind HLA molecules with increased affinity by identifying particular residues at secondary anchor positions that are associated with such properties. For example, the binding capacity of a B7 supermotif-bearing peptide representing a discreet single amino acid substitution at position 1 can be analyzed. A peptide such as t Peptide 1261.01 (Table XXIX), can, for example, be analogued to substitute L for F at position 1 and subsequently be evaluated for increased binding affinity/ and or increased cross-reactivity. This procedure will identify analogued peptides with modulated binding affinity.

Engineered analogs with sufficiently improved binding capacity or cross-reactivity are tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. The analogued peptides may be additionally tested for the ability to stimulate a recall response using PBMC from HIV-infected patients. In conclusion, these data demonstrate that by the use of even single

amino acid substitutions, it is possible to increase the binding affinity and/or cross-reactivity of peptide ligands for HLA supertype molecules.

Example 5. Identification of HIV-derived sequences with HLA-DR binding motifs

Peptide epitopes bearing an HLA class II supermotif or motif may also be identified as outlined below using methodology similar to that described in Examples 1-3.

Selection of HLA-DR-supermotif-bearing epitopes.

To identify HIV-derived, HLA class II HTL epitopes, the protein sequences from the same HIV antigens used for the identification of HLA Class I supermotif/motif sequences were analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences were selected comprising a DR-supermotif, further comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates sequences for the presence of secondary anchors Δ . Using allele specific selection tables (see, e.g., Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule. Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The HIV-derived peptides identified above were tested for their binding capacity for various common HLA-DR molecules. All peptides were initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least 2 of these 3 DR molecules were then tested for binding to DR2w2 β 1, DR2w2 β 2, DR6w19, and DR9 molecules in secondary assays. Finally, peptides binding at least 2 of the 4 secondary panel DR molecules, and thus cumulatively at least 4 of 7 different DR molecules, were screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least 7 of the 10 DR molecules comprising the primary, secondary, and tertiary screening assays were considered cross-reactive DR

binders. The composition of these screening panels, and the phenotypic frequency of associated antigens, are shown in Table XXXIV.

Thirteen HIV-derived peptides were found to bind at least 7 of 10 common HLA-DR alleles. The sequence of these 13 peptides, and their binding capacity for each assay
 5 in the primary through tertiary panels, are shown in Table XXXV. This set of peptide epitopes is predominantly derived from pol, but also includes epitopes from gag and env.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic
 10 populations, DR3 binding capacity is an important criterion in the selection of HTL epitopes. However, data generated previously indicated that DR3 only rarely cross-reacts with other DR alleles (Sidney *et al.*, *J. Immunol.* 149:2634-2640, 1992; Geluk *et al.*, *J. Immunol.* 152:5742-5748, 1994; Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). This is not entirely surprising in that the DR3 peptide-binding motif appears to be distinct
 15 from the specificity of most other DR alleles. For maximum efficiency in developing vaccine candidates it would be desirable for DR3 motifs to be clustered in proximity with DR supermotif regions. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the distinct binding specificity of the DR3 motif, peptides binding only to DR3 can also be considered as candidates for
 20 inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, the nine target HIV antigens were analyzed for conserved sequences carrying one of the two DR3 specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides were then synthesized and tested for the ability to bind DR3 with an affinity of 1 μ M or
 25 better, i.e., less than 1 μ M. Five peptides were found that met this binding criterion (Table XXXVI), and thereby qualify as HLA class II high affinity binders. Of these five, four represent epitopes from pol, and one is from vpu.

DR3 binding epitopes identified in this manner may then be included in vaccine compositions with DR supermotif-bearing peptide epitopes.

30

Example 6. Immunogenicity of HIV-derived HTL epitopes

Immunogenicity of HTL epitopes can be evaluated in a manner analogous to the determination of immunogenicity of CTL epitopes using appropriate transgenic mice

models and/or assessing the ability to stimulate recall responses using PBMC isolated from HIV-infected individuals.

The immunogenicity of 11 of the 13 HLA class II DR-supermotif binding epitopes identified in Example 5 was evaluated in a study testing PBMC isolated from HIV-
 5 infected individuals for recall proliferative responses. All eleven of these peptides were found to stimulate DR-restricted proliferative responses (Table XXXVII).

The DR3-motif bearing peptides can also be evaluated in a similar manner. Such studies demonstrate the immunogenicity of class II epitopes derived from HIV proteins.

10 Example 7. Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

15 In order to analyze population coverage, gene frequencies of HLA alleles were determined. Gene frequencies for each HLA allele were calculated from antigen or allele frequencies utilizing the binomial distribution formulae $gf=1-(\text{SQRT}(1-af))$ (see, e.g., Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies were calculated, and the cumulative antigen
 20 frequencies derived by the use of the inverse formula $[af=1-(1-Cgf)^2]$.

Where frequency data was not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies was assumed. To obtain total potential supertype population coverage no linkage disequilibrium was assumed, and only alleles confirmed to belong to each of the supertypes were included (minimal
 25 estimates). Estimates of total potential coverage achieved by inter-loci combinations were made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., $\text{total}=A+B*(1-A)$). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34, A66, and A*7401, these alleles
 30 were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups (see Table XXI). Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%. An analogous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Summary of candidate HLA class I epitopes

In summary, on the basis of the data presented in the above examples, 47 candidate CTL peptide epitopes derived from HIV have been identified (see, Table XXXVIII). Of these 47 epitopes, 6 are derived from gag, 22 from pol, 10 from env, 3 from nef, and one epitope each from rev, vif, and vpr. This set of epitopes includes 16 HLA-A2 supermotif-bearing epitopes (two from gag, eight from pol, three from env, two from vpr, and one from nef), all of which are recognized in HIV-infected patients. The 10 HLA-A3 supermotif-bearing candidate epitopes include 6 pol-derived epitopes, two env-derived epitopes and one epitope each from gag, vif, and nef. With the exception of peptides 1273.08 and 1273.03, all of the epitopes are immunogenic in HLA transgenic mice. The two additional peptides are included to enhance antigen diversity.

The CTL candidate epitope set also includes 8 B7-restricted peptides. Of these eight, 3 epitopes have been reported as immunogenic in patients. Five B7-supermotif-bearing peptides were included as candidates based on supertype binding. Immunogenicity studies in humans (e.g., Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. Given these results, and in view of the limited immunogenicity data available for B7 supermotif-bearing peptides, the use of B7-supertype binding affinity is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

Similarly, A1- and A24-restricted peptides were included on the basis of both demonstrated immunogenicity of the candidate epitopes and on the basis of binding

- affinity. Five of the candidate epitopes have been reported to be recognized in recall CTL responses from HIV-infected patients. Because a high percentage of the peptides with binding affinities ≤ 100 nM are found to be immunogenic, four A24-restricted peptides were included as vaccine candidates. An additional five A24-restricted epitopes and four
- 5 A1-restricted epitopes that bound their respective alleles with an IC_{50} of ≤ 500 nM were also included to provide a greater degree of population coverage.

- With these 47 CTL epitopes (as disclosed herein and from the art), an average population coverage is predicted to be greater than 95% in each of five major ethnic populations. Using the game theory Monte Carlo simulation analysis, which is known in the art (see *e.g.*, Osborne, M.J. and Rubinstein, A. "A course in game theory" MIT Press, 1994), it is estimated that 90% of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize 7 or more of the vaccine epitopes described herein (Figure 1)
- 10

15 *Summary of candidate HLA class II epitopes*

- A list of HIV-derived HTL epitopes that would be preferred for use in the design of minigene constructs or other vaccine formulations is summarized in Table XXXIX. The set of HTL epitopes includes 13 DR supermotif-bearing peptides and 5 DR3 motif-bearing peptides. The majority of the epitopes are derived from pol, 3 are from gag, 2 are
- 20 from env and one is derived from vpu. The total estimated population coverage represented by this panel of HTL epitopes is estimated to be greater than 91% in each of five major ethnic groups (Table XL).

Example 8. CTL Recognition Of Endogenous Processed Antigens After Priming

- 25 This example determines that CTL induced by native or analogued peptide epitopes identified and selected as described in Examples 1-6 recognize endogenously synthesized, *i.e.*, native antigens.

- Effector cells isolated from transgenic mice that are immunized with peptide epitopes as in Example 3, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of
- 30

peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with HIV expression vectors.

The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that is being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

Example 9. Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise a lipidated HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope selected from Table XXVI-XXIX, or an analog of that epitope. The HTL epitope is, for example, selected from Table XXXII.

Lipopeptide preparation: Lipopeptides are prepared by coupling the appropriate fatty acid to the amino terminus of the resin bound peptide. A typical procedure is as follows: A dichloromethane solution of a four-fold excess of a pre-formed symmetrical anhydride of the appropriate fatty acid is added to the resin and the mixture is allowed to react for two hours. The resin is washed with dichloromethane and dried. The resin is then treated with trifluoroacetic acid in the presence of appropriate scavengers [*e.g.* 5% (v/v) water] for 60 minutes at 20°C. After evaporation of excess trifluoroacetic acid, the crude peptide is washed with diethyl ether, dissolved in methanol and precipitated by the addition of water. The peptide is collected by filtration and dried.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-

bearing epitopes, are primed subcutaneously (base of the tail) with 0.1 ml of peptide conjugate formulated in saline, or DMSO/saline. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

5 Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (e.g., Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991)

In vitro CTL activation: One week after priming, spleen cells (30x10⁶ cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated
10 lymphoblasts (10x10⁶ cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to 1.5x10⁶) are incubated at 37°C in the presence of 200 µl of ⁵¹Cr. After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1
15 µg/ml. For the assay, 10⁴ ⁵¹Cr-labeled target cells are added to different concentrations of effector cells (final volume of 200 µl) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = 100 x
20 (experimental release - spontaneous release)/(maximum release - spontaneous release). To facilitate comparison between separate CTL assays run under the same conditions, % ⁵¹Cr release data is expressed as lytic units/10⁶ cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6
25 hour ⁵¹Cr release assay. To obtain specific lytic units/10⁶, the lytic units/10⁶ obtained in the absence of peptide is subtracted from the lytic units/10⁶ obtained in the presence of peptide. For example, if 30% ⁵¹Cr release is obtained at the effector (E): target (T) ratio of 50:1 (i.e., 5x10⁵ effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., 5x10⁴ effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: [(1/50,000)-(1/500,000)] × 10⁶ = 18 LU.

30 The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in Example 3. Analyses similar to this may be performed to evaluate the

immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 10. Selection of CTL and HTL epitopes for inclusion in an HIV-specific vaccine.

This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition may be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or may be single and/or polypeptidic peptides.

The following principles are utilized when selecting an array of epitopes for inclusion in a vaccine composition. Each of the following principles are balanced in order to make the selection.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with HIV clearance. For HLA Class I this includes 3-4 epitopes that come from at least one antigen of HIV. In other words, it has been observed that patients who spontaneously clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen. For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one HIV antigen.

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art and discussed herein, can be employed to assess breadth, or redundancy, of population coverage.

4.) When selecting epitopes for HIV antigens it may be preferable to select native epitopes. Therefore, of particular relevance for infectious disease vaccines, are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A peptide comprising "transcendent nested epitopes" is a peptide that has both HLA class I and HLA class II epitopes in it.

When providing nested epitopes, a sequence that has the greatest number of epitopes per provided sequence is provided. A limitation on this principle is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a longer peptide sequence, such as a sequence comprising nested epitopes, the sequence is screened in order to insure that it does not have pathological or other deleterious biological properties.

5.) When creating a minigene, as disclosed in greater detail in Example 11, an objective is to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same as those employed when selecting a peptide comprising nested epitopes. Additionally, however, upon determination of the nucleic acid sequence to be provided as a minigene, the peptide encoded thereby is analyzed to determine whether any "junctional epitopes" have been created. A junctional epitope is an actual binding epitope, as predicted, *e.g.*, by motif analysis. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that epitope, which is not present in a native HIV protein sequence. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables XXVI-XXIX and Table XXXII. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

Example 11. Construction of Minigene Multi-Epitope DNA Plasmids

This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.

A minigene expression plasmid may include multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are identified, for example, in Tables XXVI-XXIX and XXXII. HLA class I supermotif or motif-bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multipitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing

temperature (5° below the lowest calculated Tm of each primer pair) for 30 sec, and 72°C for 1 min.

For the first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 12. The plasmid construct and the degree to which it induces immunogenicity.

The degree to which the plasmid construct prepared using the methodology outlined in Example 11 is able to induce immunogenicity is evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994. To assess the capacity of the pMin minigene construct to induce CTLs *in vivo*, HLA-A11/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ⁵¹Cr release assay. The results indicate the magnitude of the CTL response directed against the A3-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A3 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A2 and HLA-B7

transgenic mouse models to assess CTL induction by HLA-A2 and HLA-B7 motif or supermotif epitopes.

To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, I-A^b restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant.

CD4+ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene).

The HTL response is measured using a ³H-thymidine incorporation proliferation assay, (*see, e.g.,* Alexander et al. *Immunity* 1:751-761, 1994). the results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in Example 11, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The

boosting agent may consist of recombinant protein (*e.g.,* Barnett *et al., Aids Res. and Human Reotroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.,* Hanke et al., *Vaccine* 16:439-445, 1998; Sedegah *et al., Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al., Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene may be evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 µg of the DNA minigene encoding the immunogenic peptides. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10⁷ pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN-γ ELISA. It is found that the minigene utilized in a prime-boost mode elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis is also performed

using other HLA-A11 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

Example 13. Peptide Composition for Prophylactic Uses

5 Vaccine compositions of the present invention are used to prevent HIV infection in persons who are at risk for such infection. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in Examples 9 and/or 10, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV
10 infection. The composition is provided as a single lipidated polypeptide that encompasses multiple epitopes. The vaccine is administered in an aqueous carrier comprised of Freund's Incomplete Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 µg, generally 100-5,000 µg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks
15 followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

20 Alternatively, the polyepitopic peptide composition can be administered as a nucleic acid in accordance with methodologies known in the art and disclosed herein.

Example 14. Polyepitopic Vaccine Compositions Derived from Native HIV Sequences

A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify
25 "relatively short" regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The "relatively short" peptide is generally
30 less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping

(i.e., frame shifted relative to one another). For example, with frame shifted overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

5 The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity
10 properties of the polyepitopic peptide.

The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for
15 the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native HIV antigens thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

20 Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

Example 15. Polyepitopic Vaccine Compositions Directed To Multiple Diseases

25 The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

30 For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the

various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

Example 16. Use of peptides to evaluate an immune response

Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be performed in a manner as that described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, HIV HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β 2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300g for 5 minutes and resuspended in 50 μ l of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby

readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

5 Example 17. Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected with HIV, or who have been vaccinated with an HIV vaccine.

10 For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals
15 who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM)
20 containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4×10^5 PBMC are stimulated with peptide in 8
25 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response
30 requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al.*, *Nature Med.* 2:1104,1108, 1996; Rehermann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al.* *J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al. J. Virol.* 66:2670-2678, 1992).

5 Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 μ M, and labeled with 100 μ Ci of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

10 Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: $100 \times [(\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})]$. Maximum release is determined by
 15 lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

The class II restricted HTL responses may also be analyzed. Purified PBMC are
 20 cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 $\mu\text{g/ml}$ synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μCi ^3H -thymidine is added to each well and incubation is continued for an additional 18
 25 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^3H -thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^3H -thymidine incorporation in the presence of antigen divided by the ^3H -thymidine incorporation in the absence of antigen.

30 Example 18. Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried

out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μ g of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μ g peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μ g of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

The vaccine is found to be both safe and efficacious.

Example 19. Phase II Trials In Patients Infected With HIV

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to patients having chronic HIV infection. The main objectives of the trials are to determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in CD4⁺ cells counts. Such a study is designed, for example, as follows:

The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as

a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

- There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic backgrounds. All of them are infected with HIV for over five years and are HCV, HBV and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.
- The viral load and CD4⁺ levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

Example 20. Induction of CTL Responses Using a Prime Boost Protocol

- A prime boost protocol similar in its underlying principle to that used to evaluate the efficacy of a DNA vaccine in transgenic mice, which was described in Example 12, may also be used for the administration of the vaccine to humans. Such a vaccine regimen may include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

- For example, the initial immunization may be performed using an expression vector, such as that constructed in Example 11, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 µg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polypeptidic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples will be obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results will indicate that a magnitude of sufficient response to achieve protective immunity against HIV is generated.

Example 21. Administration of Vaccine Compositions Using Dendritic Cells

Vaccines comprising peptide epitopes of the invention may be administered using dendritic cells. In this example, the immunogenic peptide epitopes are used to elicit a CTL and/or HTL response *ex vivo*.

Ex vivo CTL or HTL responses to a particular antigen (infectious or tumor-associated antigen) are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptides. After an appropriate incubation time (typically about 14 weeks), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cells, *i.e.*, HIV-infected cells.

Example 22. Alternative Method of Identifying Motif-Bearing Peptides

Another way of identifying motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing, have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can then be infected with a pathogenic organism or transfected with nucleic acids that express the antigen of interest, *e.g.* HIV regulatory or structural proteins. Thereafter, peptides produced by endogenous antigen processing of peptides produced consequent to infection (or as a result of transfection) will bind to HLA molecules within the cell and be transported and displayed on the cell surface.

The peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, *e.g.*, by mass spectral analysis (*e.g.*, Kubo *et al.*, *J. Immunol.* 152:3913, 1994). Because, as disclosed herein, the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express any endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells

may then be used as described, *i.e.*, they may be infected with a pathogenic organism or transfected with nucleic acid encoding an antigen of interest to isolate peptides corresponding to the pathogen or antigen of interest that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than infection or transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

The above examples are provided to illustrate the invention but not to limit its scope. For example, the human terminology for the Major Histocompatibility Complex, namely HLA, is used throughout this document. It is to be appreciated that these principles can be extended to other species as well. Thus, other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent application cited herein are hereby incorporated by reference for all purposes.

TABLE I

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	TILVMS		FWY
A2	LIVMATQ		IVMATL
A3	VSMATLI		RK
A24	YFWIVLMT		FIYWLM
B7	P		VILFMWYA
B27	RHK		FYLWMIVA
B44	ED		FWYLMIVA
B58	ATS		FWYLMIVA
B62	QLIVMP		FWYMIVLA
MOTIFS			
A1	TSM		Y
A1		DEAS	Y
A2.1	LMVQIAT		VLIMAT
A3	LMVISATFCGD		KYRHFA
A11	VTMLISAGNCDF		KRYH
A24	YFWM		FLIW
A*3101	MVTALIS		RK
A*3301	MVALFIST		RK
A*6801	AVTMSLI		RK
B*0702	P		LMFWYALV
B*3501	P		LMFWYIVA
B51	P		LIVFWYAM
B*5301	P		IMFWYALV
B*5401	P		ATIVLMFWY

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE Ia

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T <i>ILVMS</i>		FWY
A2	<i>VQAT</i>		<i>VLIMAT</i>
A3	V <i>SMA</i> T <i>LI</i>		RK
A24	Y <i>FWIVLMT</i>		FIYWLM
B7	P		VILFMWYA
B27	RHK		FYLWMIVA
B58	ATS		FWYLIVMA
B62	Q <i>LIVMP</i>		FWYMIVLA
MOTIFS			
A1	TSM		Y
A1		DEAS	Y
A2.1	<i>VQAT</i> *		<i>VLIMAT</i>
A3.2	LMVISAT <i>FCGD</i>		KYR <i>HFA</i>
A11	V <i>TMLISAGNCDF</i>		KRHY
A24	YFW		FLIW

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

1

	1	2	3	4	5	6	7	8	C-terminus
SUPERMOTIFS									
A1		1° Anchor TLVMS							1° Anchor FWY
A2		1° Anchor LIVMAIQ							1° Anchor LIVMAT
A3	preferred	1° Anchor VSMATLI	YFW (4/5)			YFW (3/5)	YFW (4/5)	P (4/5)	1° Anchor RK
	deleterious	DE (3/5), P (5/5)	DE (4/5)						
A24		1° Anchor YFWVLM T							1° Anchor FYWVLM
B7	preferred	FWY (5/5) LIVM (3/5)	FWY (4/5) P					FWY (3/5)	1° Anchor VILEMIVIA
	deleterious	DE (3/5); P(5/5); G(4/5); A(3/5); QN (3/5)			DE (3/5)	G (4/5)	QN (4/5)	DE (4/5)	
B27		1° Anchor RHK							1° Anchor FYLVIMIVA
B44		1° Anchor ED							1° Anchor FWYLVIMVA
B58		1° Anchor ATS							1° Anchor FWYLVIMVA
B62		1° Anchor QLIVMP							1° Anchor FWYMIVLA

POSITION

	1	2	3	4	5	6	7	8	
C-terminus									

POSITION

	1	2	3	4	5	6	7	8	
C-terminus									

MOTIFS1°Anchor
YA1 preferred
9-mer

deleterious

1°Anchor
STM

DEA

YFW

P

DEQN

YFW

A

A

RHKLIVM
P

DE

1°Anchor
YA1 preferred
9-mer

deleterious

ASTCLIV
M1°Anchor
DEAS

GSTC

ASTC

LIVM

DE

GP

PG

RHK

PQN

DE

RHKDEPY
FW

POSITION

	1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A1 preferred	YFW	^{1°Anchor} STM	DEAQN	A	YFWQN		PASTC	GDE	P	^{1°Anchor} Y
deleterious	GP		RHKGIV M	DE	RHK	QNA	RHKYFW	RHK	A	
A1 preferred	YFW	STCLVM	^{1°Anchor} DEAS	A	YFW		PG	G	YFW	^{1°Anchor} Y
deleterious	RHK	RHKDEPY FW			P	G		PRHK	QN	
A2.1 preferred	YFW	^{1°Anchor} LMIVQAT	YFW	STC	YFW		A	P	^{1°Anchor} VLLIMAT	
deleterious	DEP		DERKH			RKH	DERKH			
A2.1 preferred	AYFW	^{1°Anchor} LMIVQAT	LVM	G		G		FYWL VM		^{1°Anchor} VLLIMAT
deleterious	DEP		DE	RKHA	P		RKH	DERK H	RKH	

POSITION

	1	2	3	4	5	6	7	8	9 or C-terminus
A3 preferred	RHK	1°Anchor LMVISAT FCGD	YFW	PRHKYFW	A	YFW		P	1°Anchor KYRHPA
deleterious	DEP		DE						
A11 preferred	A	1°Anchor VTLMISA GNCDF	YFW	YFW	A	YFW	YFW	P	1°Anchor KRVH
deleterious	DEP						A	G	
A24 preferred 9-mer	YFWRHK	1°Anchor YFWM		STC			YFW	YFW	1°Anchor FLIW
deleterious	DEG		DE	G	QNP	DERHK	G	AQN	
A24 preferred 10-mer		1°Anchor YFWM		P	YFWP		P		1°Anchor FLIW
deleterious			GDE	QN	RHK	DE	A	QN	DEA

POSITION

ii	1	2	3	4	5	6	7	8	9 or C-terminus 1°Anchor RK
A3101	preferred	RHK	YFW	P	YFW	YFW	YFW	AP	
	deleterious	DEP	DE		ADE	DE	DE	DE	
A3301	preferred	1°Anchor MVALFIS T	YFW				AYFW		1°Anchor RK
	deleterious	GP	DE						
A6801	preferred	YFWSTC	1°Anchor AVTMSLI		YFWLIIV M		YFW	P	1°Anchor RK
	deleterious	GP	DEG		RHK			A	
B0702	preferred	RHKFWY	1°Anchor P	RHK	RHK	RHK	RHK	PA	1°Anchor LMFWY/IV
	deleterious	DEQNP	DEP	DE	DE	GDE	QN	DE	
B3501	preferred	FWYLIIVM	1°Anchor P	FWY			FWY		1°Anchor LMFWY/IV
	deleterious	AGP			G	G			

POSITION

	1	2	3	4	5	6	7	8	9 or C-terminus
B51 preferred	LIVMF ^W Y	^{1°} Anchor P	FWY	STC	FWY		G	FWY	^{1°} Anchor LIVF ^W Y ^{AM}
deleterious	AGPDERHKSTC				DE	G	DEQN	GDE	
B5301 preferred	LIVMF ^W Y	^{1°} Anchor P	FWY	STC	FWY		LIVMF ^W Y	FWY	^{1°} Anchor IMF ^W Y ^{ALV}
deleterious	AGPQN					G	RHKQN	DE	
B5401 preferred	FWY	^{1°} Anchor P	FWYLIVM		LIVM		ALIVM	FWYAP	^{1°} Anchor ATTVL ^W MF ^W Y
deleterious	GPQNDE		GDESTC		RHKDE	DE	QNDGE	DE	

Italicized residues indicate less preferred or "tolerated" residues.
The information in Table II is specific for 9-mers unless otherwise specified.

TABLE III

MOTIFS	POSITION					
	1° anchor 1	2	3	4	5	6
DR4 preferred deleterious	FMYLIVW	M	T	W	I	VSTCPALIM
DR1 preferred deleterious	MFLLVWY	C	CH	PAMQ FD	CWD	VMATSP/LC
DR7 preferred deleterious	MFLLVWY	M	W	A	G	IVMSACTPL
DR Supermotif	MFLLVWY	C				GRD N
						VMSTACPLI
DR3 MOTIFS	1° anchor 1	2	3	4	5	6
motif a preferred	LIVMFY			D		
motif b preferred	LIVMFAY			DNQUEST		KRH

Italicized residues indicate less preferred or "tolerated" residues.

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Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	25
A*0201	941.01	FLPSDYFPSV	5.0
A*0202	941.01	FLPSDYFPSV	4.3
A*0203	941.01	FLPSDYFPSV	10
A*0205	941.01	FLPSDYFPSV	4.3
A*0206	941.01	FLPSDYFPSV	3.7
A*0207	941.01	FLPSDYFPSV	23
A*6802	1141.02	FTQAGYPAL	40
A*0301	941.12	KVFPYALINK	11
A*1101	940.06	AVDLYHFLK	6.0
A*3101	941.12	KVFPYALINK	18
A*3301	1083.02	STLPETYVRR	29
A*6801	941.12	KVFPYALINK	8.0
A*2402	979.02	AYIDNYNKF	12
B*0702	1075.23	APRTLVL	5.5
B*3501	1021.05	FPFKYAAAF	7.2
B51	1021.05	FPFKYAAAF	5.5
B*5301	1021.05	FPFKYAAAF	9.3
B*5401	1021.05	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNIV TPRTPPP	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table VI

HLA-supertype	Allele-specific HLA-supertype members	
	Verified ^a	Predicted ^b
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0206, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6601	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1504, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2102, B*2703, B*2704, B*2705, B*2706, B*3001, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	B*1901, B*1902, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4801, B*5001
B58	B*5701, B*5702, B*5801, B*5802, B*1516, B*1517	
D62	B*1501, B*1502, B*1513, B*5201	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1510

a. Verified alleles includes alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.

b. Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specificity.

Table VII
 HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101 Frequency	SEQ ID NO
ENV	KLWTVYY	44	8	11	17		1
ENV	NLWTVYY	44	8	35	56		2
ENV	DTVINWV	75	8	19	30		3
ENV	VTEFNWV	102	8	34	53		4
ENV	RIGPGQTF	357	8	11	17		5
ENV	SGSGQTF	360	8	01	33		6
ENV	SGSGQTF	360	8	01	33		7
ENV	KLREIQE	405	8	01	25		8
ENV	STNGTET	537	8	01	17		9
ENV	AVGIGAVF	595	8	11	17		10
ENV	ILLKLTVW	650	8	13	20		11
ENV	ILLQLTVW	650	8	34	53		12
ENV	IMLQLTVW	650	8	10	16		13
ENV	RYLQLTVW	650	8	33	52		14
ENV	NVFNSSW	693	8	13	20		15
ENV	EWDNMTW	716	8	13	20		16
ENV	DLALDKW	754	8	21	33		17
ENV	ELLELDKW	754	8	20	31		18
ENV	DTNWLWY	769	8	10	16		19
ENV	NLWYIKF	773	8	40	50		20
ENV	KLRLIKF	787	8	10	25		21
ENV	LIGLRVF	787	8	29	45		22
ENV	SIRLVNGF	842	8	13	20		23
ENV	SIRLVSGF	842	8	13	20		24
ENV	DLRLCLF	856	8	17	27		25
ENV	DLRLCLF	856	8	38	59		26
ENV	ISLCLFSY	858	8	35	55		27
ENV	ISLCLFSY	858	8	33	53		28
ENV	TVYGVPRW	48	9	55	86		29
ENV	NVTENFMW	101	9	34	53		30
ENV	DSNSTGNY	218	9	01	20		31
ENV	ILKCNDDKF	271	9	12	19		32
ENV	RIGPGQTF	357	9	11	17		33
ENV	RIGPGQTF	360	9	01	33		34
ENV	SGSGQTF	360	9	01	33		35
ENV	DLHTTISE	428	9	21	33		36
ENV	ISFNCGEF	434	9	36	56		37
ENV	ISFNCGEF	434	9	16	25		38
ENV	RIKQINMW	488	9	30	47		39
ENV	RIKQINMW	488	9	12	19		40
ENV	GSNGTET	538	9	18	28		41
ENV	GSNGTET	538	9	11	18		42
ENV	MILGAMELGE	599	9	64	36		43
ENV	TIGAMELGE	599	9	03	27		44
ENV	LICTTAVPW	688	9	19	30		45
ENV	LICTTAVPW	688	9	17	27		46
ENV	LICTTVPW	757	9	12	19		47
ENV	ALDKWASLW	757	9	11	18		48
ENV	ALDKWASLW	757	9	15	23		49
ENV	GLIGLRIF	786	9	15	23		50

Table VII
 HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101 Frequency	SEQ ID NO
ENV	GLGLMVF	786	9	29	45		51
ENV	IVNRVROGY	799	9	38	59		52
ENV	RSRLVNGF	841	9	12	19		53
ENV	RSRLVSGF	841	9	13	20		54
ENV	YSGLTALAW	846	9	16	25		55
ENV	YSGLTALAW	846	9	16	25		56
ENV	SLAGLHLDW	889	9	18	30		57
ENV	SLAGLORGW	889	9	11	18		58
ENV	RLGWGLKY	894	9	05	18		59
ENV	RLGWGLKY	894	9	09	29		60
ENV	VLVYGVVPW	47	10	55	86		61
ENV	QMIIDISLW	116	10	29	45		62
ENV	IQAGPKYSF	245	10	29	45		63
ENV	QMIIDISLW	116	10	29	45		64
ENV	PHVCTPAGF	260	10	28	42		65
ENV	PHVCTPAGF	260	10	10	16		66
ENV	AILKCNKKF	270	10	12	19		67
ENV	NTSPRSVAY	376	10	01	33		68
ENV	HSFNCGEFF	434	10	35	55		69
ENV	HSFNCGEFF	434	10	16	25		70
ENV	NTSPRSVAY	376	10	01	33		71
ENV	NITGNLTLEF	537	10	17	30		72
ENV	KLICITVVPW	687	10	19	30		73
ENV	KLICITVVPW	687	10	17	27		74
ENV	KLICITVVPW	687	10	12	19		75
ENV	TTNVPWSS	691	10	11	17		76
ENV	SVARVROGY	798	10	36	56		77
ENV	YSGLTALAW	846	10	16	25		78
ENV	YSGLTALAW	846	10	16	25		79
ENV	DUISCLFESY	856	10	35	55		80
ENV	IVELLGREGW	879	10	22	34		81
ENV	SSLGKRLGW	886	10	10	16		82
ENV	WVTVYGVVP	46	11	55	86		83
ENV	PWKKEATTL	54	11	22	34		84
ENV	HLKASDAVAA	244	11	40	64		85
ENV	KVSEPHPIHY	252	11	12	22		86
ENV	GTAGNSRAA	375	11	28	42		87
ENV	TTISFNCGE	432	11	01	33		88
ENV	TTISFNCGE	432	11	16	25		89
ENV	TTISFNCGE	432	11	12	19		90
ENV	VMIISFNCGE	432	11	13	20		91
ENV	HSFNCGEFF	434	11	35	55		92
ENV	HSFNCGEFF	434	11	16	25		93
ENV	NMWQVEYKA	494	11	15	23		94
ENV	DMRDNAWSEL	552	11	37	58		95
ENV	AVGIGAFLGF	595	11	11	17		96
ENV	YLRDQQLGI	672	11	27	42		97
ENV	YLRDQQLGI	672	11	18	28		98
ENV	CTTRVPWSS	690	11	11	17		99
ENV	YLRDQQLGI	672	11	10	16		100
ENV	LALDKWSEL	755	11	11	17		

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	LLELDKASL	755	11	18	28		101
ENV	ALDKWASLW	757	11	10	16		102
ENV	ELDKWASLW	757	11	16	25		103
ENV	LSKLVKKE	770	11	11	17		104
ENV	LSKLVKKE	770	11	12	17		105
ENV	ITNWLWYKIF	770	11	14	22		106
ENV	LSIVNRVQGY	797	11	34	53		107
ENV	RVKQGYSLSF	802	11	47	73		108
ENV	RLVSFGLALA	844	11	16	25		109
ENV	CLFSYRLRDF	861	11	18	28		110
ENV	RVHLLGRRL	878	11	22	34		111
ENV	RLVHLLGRRL	878	11	22	34		112
ENV	RLVHLLGRRL	884	11	22	34		113
ENV	RLVHLLGRRL	884	11	22	34		114
ENV	RLVHLLGRRL	884	11	22	34		115
GAG	ASRELERF	38	8	46	72		116
GAG	SSQVSQNY	145	8	15	31		117
GAG	KVVEEKAF	178	8	24	38		118
GAG	KVVEEKAF	178	8	28	44		119
GAG	TLQEQDAW	263	8	12	19		120
GAG	TLQEQDAW	263	8	12	19		121
GAG	PIPVGYNY	279	8	35	55		122
GAG	PIPVGYNY	279	8	35	55		123
GAG	ASQEVKNW	333	8	11	17		124
GAG	ATQDVKNW	333	8	15	23		125
GAG	ATQDVKNW	333	8	18	28		126
GAG	IMMQKSNF	408	8	11	17		127
GAG	IMMQKSNF	408	8	11	17		128
GAG	CTEIQDAW	459	8	52	82		129
GAG	ETIDKQLY	537	8	01	23		130
GAG	ETIDKQLY	537	8	01	23		131
GAG	ETIDKQLY	537	8	01	23		132
GAG	ETIDKQLY	537	8	01	23		133
GAG	ETIDKQLY	537	8	01	23		134
GAG	ETIDKQLY	537	8	01	23		135
GAG	ETIDKQLY	537	8	01	23		136
GAG	ETIDKQLY	537	8	01	23		137
GAG	ETIDKQLY	537	8	01	23		138
GAG	ETIDKQLY	537	8	01	23		139
GAG	ETIDKQLY	537	8	01	23		140
GAG	ETIDKQLY	537	8	01	23		141
GAG	ETIDKQLY	537	8	01	23		142
GAG	ETIDKQLY	537	8	01	23		143
GAG	ETIDKQLY	537	8	01	23		144
GAG	ETIDKQLY	537	8	01	23		145
GAG	ETIDKQLY	537	8	01	23		146
GAG	ETIDKQLY	537	8	01	23		147
GAG	ETIDKQLY	537	8	01	23		148
GAG	ETIDKQLY	537	8	01	23		149
GAG	ETIDKQLY	537	8	01	23		150

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
GAG	PLTSLKSLF	548	9	12	19		151
GAG	PLTSLRSIF	548	9	12	19		152
GAG	VLSGGKLDW	7	10	15	23		153
GAG	RLRPGKKKY	20	10	34	53		154
GAG	SLPNTVATLY	79	10	35	55		155
GAG	SLPNTVATLY	79	10	35	55		156
GAG	ALSRLTNAW	167	10	29	45		157
GAG	ALSRLTNAW	167	10	29	45		158
GAG	WVKVVEEKAF	176	10	24	38		159
GAG	WVKVVEEKAF	176	10	28	44		160
GAG	DTINEEAAEW	224	10	31	48		161
GAG	DTINEEAAEW	224	10	31	48		162
GAG	TSYLQEQW	261	10	27	43		163
GAG	TSYLQEQW	261	10	27	43		164
GAG	DIKGGPKPEF	308	10	19	30		165
GAG	DIKGGPKPEF	308	10	41	64		166
GAG	ATIMMQRGNF	406	10	11	28		167
GAG	PSIKGRPGNF	475	10	23	36		168
GAG	PSIKGRPGNF	475	10	14	14		169
GAG	SLSSGKGLA	475	10	17	17		170
GAG	SLSSGKGLA	475	10	15	23		171
GAG	IYWASRELERF	35	11	19	30		172
GAG	IYWASRELERF	35	11	25	39		173
GAG	LSLYNTVATL	78	11	15	24		174
GAG	TSYTLQEQIA	260	11	11	17		175
GAG	TSYTLQEQIA	260	11	27	43		176
GAG	IYVWVWVW	299	11	27	43		177
GAG	IYVWVWVW	299	11	57	89		178
GAG	ASAQDLKGG	392	11	01	50		179
GAG	ATAQDLKGG	392	11	01	50		180
GAG	PTAPPAESTGF	495	11	10	16		181
GAG	PTAPPAESTGF	495	11	14	22		182
GAG	PTAPPAESTGF	507	11	02	67		183
GAG	PTAPPAESTGF	507	11	03	68		184
NEF	ANALW	71	8	12	22		185
NEF	PMYKGF	105	8	12	19		186
NEF	DILDLVWY	185	8	20	31		187
NEF	DILDLVWY	185	8	33	52		188
NEF	WYHTQGF	191	8	13	20		189
NEF	WYHTQGF	191	8	21	33		190
NEF	GRKELT	213	8	13	20		191
NEF	GRKELT	213	8	13	20		192
NEF	PLTFCWCF	219	8	43	193		193
NEF	WSKSSIVGW	5	9	20	31		194
NEF	QVLRPMTF	100	9	10	16		195
NEF	QVLRPMTF	100	9	46	72	0.0008	196
NEF	WYHTQGF	191	9	13	20		197
NEF	WYHTQGF	191	9	14	23		198
NEF	WYHTQGF	191	9	14	23		199
NEF	HTQGYFDW	194	9	25	39		200

Table VII
HIV-1 A1 Super-Motif Profiles with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
NEF	NTQGYFDW	194	9	12	19		201
NEF	YTPGGRHY	207	9	17	27		202
NEF	YTPGGRHY	207	9	13	20		203
NEF	DLWVYHTQGF	188	10	13	20		204
NEF	DLWVYHTQGF	188	10	13	20		205
NEF	DLWVYHTQGF	211	10	11	20		206
NEF	GTGPRFLTGW	213	10	12	19		207
NEF	IMARELIPEY	320	10	10	16		208
NEF	NTAATNAUCA	68	11	12	19		209
NEF	PLRPMYTKGA	102	11	12	19		210
NEF	DLWVYHTQGF	188	11	13	20		211
NEF	DLWVYHTQGF	188	11	21	33		212
NEF	DLWVYHTQGF	188	11	13	20		213
POL	DLNLSKSW	122	8	13	20		214
POL	ENLPSKSW	122	8	12	19		215
POL	MGGHGGF	133	8	62	97		216
POL	QIGCTLNF	179	8	41	64		217
POL	QIGCTLNF	179	8	16	25		218
POL	KIGPENNY	238	8	11	20		219
POL	KIGPENNY	238	8	11	20		220
POL	VLDVGDAY	297	8	60	94		221
POL	SVPLDKDF	306	8	18	28		222
POL	M1KLEIF	353	8	44	69		223
POL	Q1PEKDSW	434	8	13	20		224
POL	V1PEKDSW	434	8	13	20		225
POL	KLVRGLNW	448	8	12	20		226
POL	KLVRGLNW	448	8	12	20		227
POL	ETWVTDYW	508	8	10	16		228
POL	PVGAETIF	625	8	28	44		229
POL	IVGAETIF	626	8	12	20		230
POL	KTELQATY	668	8	12	19		231
POL	NIVTDQY	686	8	62	97		232
POL	LIKKKQY	717	8	35	55		233
POL	LIKKKQY	717	8	35	55		234
POL	ETGQATY	844	8	59	92		235
POL	ILKLGRW	853	8	34	53		236
POL	LLKLGRW	853	8	25	39		237
POL	IITDNGSNF	866	8	51	80		238
POL	TTVKAACW	876	8	15	23		239
POL	AVKAAACW	877	8	32	50		240
POL	AVKAAACW	877	8	32	50		241
POL	QIKQDNF	968	8	12	22		242
POL	QIKQDNF	968	8	35	55		243
POL	KIONERVY	971	8	52	81		244
POL	PTIRRELQW	30	9	13	20		245
POL	FSEFQTLW	85	9	14	22		246
POL	KMIGGIGGF	132	9	62	97		247
POL	LNKRRTQDF	268	9	57	88		248
POL	TLVQVQW	295	9	57	89	0.0180	249
POL	VLDVGDAY	297	9	60	94		250

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	PSVPLDKDF	305	9	18	28		251
POL	ELRQILRW	308	9	19	30		252
POL	ETKNGVY	312	9	42	81	0.0052	253
POL	SMTKLEFF	352	9	43	27		254
POL	ELRQILRW	393	9	17	23		255
POL	ELRQILRW	393	9	15	23		256
POL	ILNPEKDSW	433	9	13	20		257
POL	KLWASQY	452	9	60	94	0.0070	258
POL	ELRQILRW	573	9	47	73		259
POL	KLPEKETW	582	9	25	31		260
POL	KLPEKETW	582	9	25	22		261
POL	WTDYWGQATW	594	9	14	38		262
POL	WTDYWGQATW	594	9	24	26		263
POL	ATWPEWEF	600	9	52	81		264
POL	NTPPLVKLW	610	9	57	89		265
POL	ELRQILRW	625	9	28	44	0.0007	266
POL	ETKNGVY	641	9	35	55	0.0010	267
POL	QLKKKKY	716	9	26	41	0.0007	268
POL	SSGIRKVL	745	9	57	80		269
POL	QVDCSPGIW	805	9	57	89		270
POL	ETGQETAYF	844	9	57	89		271
POL	FLKLAGRW	852	9	32	50		272
POL	FLKLAGRW	852	9	25	39		273
POL	ETKNGVY	875	9	15	23		274
POL	STVKAACW	876	9	15	23		275
POL	ETKNGVY	925	9	57	89		276
POL	KTAVQMAVF	929	9	60	94		277
POL	QMAVFHNF	971	9	52	81	0.0056	278
POL	KIQNFRVY	971	9	41	64		279
POL	LIQIGCLNF	177	10	15	23		280
POL	LIQIGCLNF	177	10	15	23		281
POL	GMGPKYKQ	216	10	41	80	0.0130	282
POL	ISGRHPNY	236	10	11	17		283
POL	ISGRHPNY	236	10	11	19		284
POL	AIKKKDSIKW	251	10	57	91		285
POL	STKWRKLDF	257	10	58	91		286
POL	ELNRRQDFW	268	10	57	89	0.2000	287
POL	WTDYWGQATW	295	10	56	88		288
POL	WTDYWGQATW	295	10	56	88		289
POL	SMTKLEFF	352	10	33	32	0.2500	290
POL	VIQYVMDLY	368	10	51	20		291
POL	PIQLPEKDSW	432	10	13	20		292
POL	PIQLPEKDSW	432	10	13	20		293
POL	ILKEPVHGVY	498	10	40	63	0.0017	294
POL	ELRQILRW	520	10	13	23		295
POL	ELRQILRW	520	10	13	23		296
POL	WTDYWGQATW	573	10	12	42		297
POL	KLWASQY	573	10	12	42		298
POL	KLWASQY	573	10	12	42		299
POL	IVWGRKTF	584	10	15	23		300
POL	PIQKETWEAW	584	10	15	23		301
POL	PIQKETWEAW	584	10	27	42		302

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	ETWETWTD	588	10	10	16		301
POL	ETWETWTD	588	10	10	16		302
POL	ETWETWTD	588	10	10	16		303
POL	ETWETWTD	588	10	10	16		304
POL	ETWETWTD	588	10	10	16		305
POL	ETWETWTD	588	10	10	16		306
POL	ETWETWTD	588	10	10	16		307
POL	ETWETWTD	588	10	10	16		308
POL	ETWETWTD	588	10	10	16		309
POL	ETWETWTD	588	10	10	16		310
POL	ETWETWTD	588	10	10	16		311
POL	ETWETWTD	588	10	10	16		312
POL	ETWETWTD	588	10	10	16		313
POL	ETWETWTD	588	10	10	16		314
POL	ETWETWTD	588	10	10	16		315
POL	ETWETWTD	588	10	10	16		316
POL	ETWETWTD	588	10	10	16		317
POL	ETWETWTD	588	10	10	16		318
POL	ETWETWTD	588	10	10	16		319
POL	ETWETWTD	588	10	10	16		320
POL	ETWETWTD	588	10	10	16		321
POL	ETWETWTD	588	10	10	16		322
POL	ETWETWTD	588	10	10	16		323
POL	ETWETWTD	588	10	10	16		324
POL	ETWETWTD	588	10	10	16		325
POL	ETWETWTD	588	10	10	16		326
POL	ETWETWTD	588	10	10	16		327
POL	ETWETWTD	588	10	10	16		328
POL	ETWETWTD	588	10	10	16		329
POL	ETWETWTD	588	10	10	16		330
POL	ETWETWTD	588	10	10	16		331
POL	ETWETWTD	588	10	10	16		332
POL	ETWETWTD	588	10	10	16		333
POL	ETWETWTD	588	10	10	16		334
POL	ETWETWTD	588	10	10	16		335
POL	ETWETWTD	588	10	10	16		336
POL	ETWETWTD	588	10	10	16		337
POL	ETWETWTD	588	10	10	16		338
POL	ETWETWTD	588	10	10	16		339
POL	ETWETWTD	588	10	10	16		340
POL	ETWETWTD	588	10	10	16		341
POL	ETWETWTD	588	10	10	16		342
POL	ETWETWTD	588	10	10	16		343
POL	ETWETWTD	588	10	10	16		344
POL	ETWETWTD	588	10	10	16		345
POL	ETWETWTD	588	10	10	16		346
POL	ETWETWTD	588	10	10	16		347
POL	ETWETWTD	588	10	10	16		348
POL	ETWETWTD	588	10	10	16		349
POL	ETWETWTD	588	10	10	16		350

Table VII
HIV Δ01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	LIKKEKVILA	717	11	20	31		351
POL	LVSGIRKVF	743	11	13	20		352
POL	LVSGIRKVF	743	11	13	20		353
POL	LVSGIRKVF	743	11	26	41		354
POL	ILSNWRAMAS	768	11	32	50		355
POL	ILVAVIVASGY	825	11	53	83		356
POL	KVHTIDGNSNF	863	11	21	33		357
POL	TSMAVAKMC	873	11	27	42		358
POL	TSMAVAKMC	873	11	27	42		359
POL	TSMAVAKMC	874	11	14	22		360
POL	TSMAVAKMC	874	11	27	42		361
POL	TSTIVKACW	874	11	14	22		362
POL	ILKTAQVMAN	923	11	57	89		363
POL	AVQMAVFHIN	927	11	60	94		364
POL	QHKQNFVY	968	11	12	19		365
POL	QHKQNFVY	968	11	35	55		366
POL	QHKQNFVY	969	11	12	19		367
POL	QHKQNFVY	969	11	35	55		368
POL	QHKQNFVY	985	11	35	55	0 0 1 1 0	369
POL	PLWKGPAKLL	985	11	18	28		370
REV	ILYQSNPY	23	8	27	42		371
REV	AVRIKSLY	17	9	13	20		372
REV	KILYQSNPY	22	9	26	41		373
TAT	ILYQSNPY	20	9	18	28		374
TAT	PVDNPLFPW	3	9	26	41		375
TAT	PVDNPLFPW	3	9	14	22		376
TAT	FLNKGGLSY	41	10	14	22		377
VIF	SLVKHIIMY	23	8	44	69		378
VIF	RLVITTYW	65	8	12	19		379
VIF	QLHLIYF	110	8	14	22		380
VIF	QLHLIYF	110	8	14	22		381
VIF	ILYIYDFC	113	8	15	23		382
VIF	ILMIDYDCF	113	8	15	23		383
VIF	IVSPRCEY	133	8	14	22		384
VIF	KSLVKHIIMY	22	9	18	28		385
VIF	NSLVKHIIMY	22	9	24	34		386
VIF	GLHTIGRDW	73	9	22	34		387
VIF	GLHTIGRDW	73	9	12	19		388
VIF	SVENRLELY	89	9	11	17		389
VIF	QVDRMKRTW	12	10	12	19		390
VIF	QVDRMKRTW	12	10	16	24		391
VIF	QVDRMKRTW	12	10	31	48		392
VIF	ILGLIGVSIEW	83	10	26	41		393
VIF	ILGLIGVSIEW	83	10	25	39		394
VIF	ILGLIGVSIEW	88	10	11	17		395
VIF	LIHMIFDFC	111	10	15	23		396
VIF	LIHMIFDFC	111	10	15	23		397
VIF	SVKKLTEDRW	174	10	13	20		398
VIF	GVSEWRLLR	87	10	16	24		399
VIF	GLADQLIIMH	106	11	11	17		400
VIF	QLHLIYDFC	110	11	13	20		401

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
VIF	QLIMITYFDCF	110	11	14	22		401
VIF	KSEAVRHR	173	11	13	20		402
VPR	KSEAVRHR	27	8	15	23		403
VPR	WHLIGGY	38	8	11	17		404
VPR	RILQQLF	62	8	45	70		405
VPR	AVRIIPRIW	30	9	14	22		406
VPR	AVRIIPRIW	30	9	34	53		407
VPR	ELKNEAVRIIF	25	10	17	27		408
VPR	ELKNEAVRIIF	25	10	15	23		409
VPR	WHLIGGY	38	10	20	31		410
VPR	WHLIGGY	45	10	17	27		411
VPR	IIYNYGDTW	45	10	14	22		412
VPR	IIYNYGDTW	45	10	14	22		413
VPR	IIYNYGDTW	45	10	14	22		414
VPR	IIYNYGDTW	60	10	41	64		415
VPR	IIYNYGDTW	63	10	35	55		416
VPR	IIYNYGDTW	59	11	38	59		417
VPR	IIYNYGDTW	52	11	34	53		418
VPR	IIYNYGDTW	26	8	15	23		419
VPU	IIYNYGDTW	30	8	15	23		420
VPU	IIYNYGDTW	34	8	12	19		421
VPU	EMGIIAFW	89	8	11	17		422
VPU	AVVWTFV	29	9	14	22		423
VPU	AVVWTFV	31	10	12	19		424
VPU	AVVWTFV	7	11	01	50		425
VPU	AVVWTFV	7	11	01	50		426
VPU	AVVWTFV	30	11	12	19		427
VPU	RIKRDSDSY	64	11	01	50		428
VPU	RIKRDSDSY	64	11	01	50		429

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LILGLVII	21	8	09	15						429
ENV	GLVIVKVA	28	8	10	16						430
ENV	GLVIMESA	28	8	11	16						431
ENV	GLVATVYA	34	8	01	50						432
ENV	WYIVYGV	41	8	58	91						433
ENV	WYIVYGV	48	8	55	86						434
ENV	GVVWKEA	52	8	34	53						435
ENV	PVWKEATT	54	8	22	34						436
ENV	WYIVYGV	59	8	24	38						437
ENV	TLGLSDA	69	8	54	86						438
ENV	EVINWVAT	77	8	36	56						439
ENV	ATHACVPT	83	8	56	88						440
ENV	NYTEVENM	101	8	34	53						441
ENV	NWWRNDMV	107	8	12	19						442
ENV	NWWRNDMV	107	8	34	53						443
ENV	WYIVYGV	115	8	24	38						444
ENV	DGSLKCPV	121	8	55	86						445
ENV	SKKPCYKL	128	8	55	86						446
ENV	KLTPLCVT	134	8	53	84						447
ENV	LTPLCVTL	135	8	54	84						448
ENV	VTSIGNSA	161	8	01	20						449
ENV	ALFYKLDV	202	8	10	16						450
ENV	ALFYKLDV	202	8	12	19						451
ENV	ALFYKLDV	202	8	01	31						452
ENV	LINGNTSA	217	8	17	27						453
ENV	NTSATQQA	241	8	14	22						454
ENV	NTSVITQA	241	8	13	20						455
ENV	ITQACPKV	245	8	37	58						456
ENV	PHIHYCA	258	8	40	63						457
ENV	PHIHYCA	258	8	38	58						458
ENV	PHIYCAFA	264	8	18	28						459
ENV	PHIYCTPA	260	8	18	28						460
ENV	CAPAGFAI	264	8	29	45						461
ENV	CTPAGFAI	264	8	10	16						462
ENV	GTGPKCNV	281	8	17	27						463
ENV	NYSTVQC I	287	8	51	80						464
ENV	YQCHHFI	290	8	31	50						465
ENV	CTGKIRPV	294	8	26	41						466
ENV	CTGKIRPV	294	8	26	41						467
ENV	GKPVVST	297	8	33	52						468
ENV	GKPVVST	297	8	26	41						469
ENV	PVSTQLL	300	8	60	94						470
ENV	VYSTQLL	301	8	60	94						471
ENV	QILLNGSL	305	8	57	89						472
ENV	SLAREEVI	306	8	15	25						473
ENV	SLAREEVI	311	8	14	24						474
ENV	LAEEEVVI	312	8	13	20						475
ENV	IRSENLIT	319	8	10	16						476
ENV	CTPPNNIT	345	8	29	45						477
ENV	NTRKSIRI	351	8	10	16						478

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*5802	SEQ ID NO
ENV	NTSPKSRV	376	8	01	33						439
ENV	TAGNSIRA	376	8	01	33						480
ENV	IIGDIRQA	437	8	00	30						481
ENV	YAGNSIRA	437	8	01	17						482
ENV	ITEGNTIL	478	8	01	50						483
ENV	NTLPCRI	482	8	11	17						484
ENV	TITLPCRI	482	8	14	22						485
ENV	RIKQIRIM	488	8	30	47						486
ENV	RIKQIVIM	488	8	12	19						487
ENV	IIRIMQEV	492	8	12	28						488
ENV	WVQVQGM	496	8	18	28						489
ENV	WVQVQGM	496	8	11	17						490
ENV	EVGKAMYA	498	8	18	28						491
ENV	RVCQAMYA	498	8	10	16						492
ENV	KAMVAIPI	502	8	23	36						493
ENV	QAMYAPPI	502	8	14	22						494
ENV	RAMYAPPI	502	8	12	30						495
ENV	YAGNSIRA	510	8	11	17						496
ENV	NTIGILLT	519	8	11	17						497
ENV	NTIGILLT	519	8	35	55						498
ENV	ELYKYKVV	560	8	56	89						499
ENV	KVKKIEPL	565	8	25	39						500
ENV	KIEPLGVA	568	8	23	37						501
ENV	PIKAKIRV	576	8	22	34						502
ENV	YVQEKRAV	588	8	32	50						503
ENV	VQEKRAV	588	8	17	27						504
ENV	VQEKRAV	589	8	17	27						505
ENV	RAVGIGAV	594	8	12	19						506
ENV	GAFLFLGL	601	8	12	19						507
ENV	GAFLFLGL	601	8	13	20						508
ENV	GAFLFLGL	601	8	22	34						509
ENV	FLGASGIA	608	8	48	75						510
ENV	FLGASGIA	608	8	55	86						511
ENV	AAGSTMGIA	611	8	58	91						512
ENV	STMGAAST	614	8	39	61						513
ENV	TMGAAST	615	8	39	61						514
ENV	GAASITLT	617	8	39	61						515
ENV	GAASITLT	618	8	39	61						516
ENV	LTQVARGQL	623	8	38	59						517
ENV	LTQVARGQL	623	8	36	56						518
ENV	LTQVARGQL	628	8	49	77						519
ENV	IVQQQNNL	634	8	26	41						520
ENV	IVQQQNNL	634	8	32	50						521
ENV	VQQQNNLL	635	8	26	41						522
ENV	VQQQNNLL	637	8	32	50						523
ENV	QSSNLLRA	640	8	26	41						524
ENV	QSSNLLRA	640	8	26	41						525
ENV	NLRRAIEA	640	8	51	80						526
ENV	ALIEAQQUIL	644	8	49	77						527
ENV	ALIEAQQUIL	644	8	49	77						528

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	AQIILLKL	647	8	13	20						529
ENV	AQIILLQL	647	8	35	55						530
ENV	AQIIMLQL	647	8	10	16						531
ENV	QQIILKLT	648	8	13	20						532
ENV	QQIILQLT	648	8	34	53						533
ENV	QQIILQLT	648	8	10	16						534
ENV	QQIILQLT	648	8	10	16						535
ENV	TVWGIKQL	655	8	59	92						536
ENV	KOLQARVL	660	8	41	64						537
ENV	QLQARVLA	661	8	41	64						538
ENV	QLQARVLA	662	8	33	52						539
ENV	VLQARVLA	666	8	34	53						540
ENV	VLQARVLA	672	8	31	48	0.0001					541
ENV	VLQARVLA	672	8	31	48						542
ENV	KLICITAV	687	8	18	28						543
ENV	KLICITAV	687	8	17	27						544
ENV	KLICITTV	687	8	12	19						545
ENV	WMWEVERI	723	8	12	19						546
ENV	LLALDKWA	723	8	19	30						547
ENV	LLALDKWA	755	8	19	30						548
ENV	LLALDKWA	755	8	21	33						549
ENV	LLALDKWA	755	8	18	27						550
ENV	ELDKWASL	757	8	18	27						551
ENV	SLWAWFDI	763	8	17	27						552
ENV	ITKWLVYI	770	8	16	25						553
ENV	ITNWLVYI	770	8	19	30						554
ENV	YKIFIMI	776	8	43	67						555
ENV	FMIVGGLL	780	8	44	69						556
ENV	FMIVGGLL	780	8	45	70						557
ENV	FMIVGGLL	781	8	45	70						558
ENV	FMIVGGLL	783	8	45	70						559
ENV	IVGGLVGL	783	8	10	16						560
ENV	IVGGLVGL	786	8	15	23						561
ENV	GLIGLRIV	786	8	32	50						562
ENV	GLIGLRIV	789	8	18	28						563
ENV	GLRIFAV	789	8	29	45						564
ENV	GLRIFAV	792	8	15	23						565
ENV	IVFVLSI	792	8	31	51						566
ENV	VLSINRV	796	8	38	59						567
ENV	PLSFQTL	809	8	10	16						568
ENV	PLSFQTL	809	8	13	20						569
ENV	GLDRPGGT	823	8	01	33						570
ENV	GLYNGFLA	844	8	13	20						571
ENV	GLYNGFLA	845	8	10	16						572
ENV	LVSGELAL	845	8	20	32						573
ENV	LALAWDDL	850	8	25	39						574
ENV	CLFSYIHL	861	8	42	66						575
ENV	RLRDULLI	867	8	13	20	0.0001					576
ENV	IAARTVEL	874	8	12	19						577
ENV	IAARTVEL	876	8	11	17						578
ENV	ELGHSLSL	881	8	09	15						579

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*5802	SEQ ID NO
ENV	LQYWSQEL	907	8	16	25						579
ENV	GQELKNSA	911	8	12	19						580
ENV	SOELKNSA	911	8	12	19						581
ENV	SAVSLINA	917	8	11	17						582
ENV	AVSLINAT	917	8	11	17						583
ENV	AVSLINAT	921	8	14	22						584
ENV	LLNKATAA	921	8	15	23						585
ENV	DTIAIAVA	923	8	10	16						586
ENV	NATAIAVA	923	8	14	22						587
ENV	AIATAAEG	926	8	32	50						588
ENV	VAEGTDRI	929	8	19	26						589
ENV	VAEGTDRI	929	8	16	22						590
ENV	VAEGTDRI	932	8	11	17						591
ENV	ILIPREPI	947	8	13	20						592
ENV	PTIRIQGL	951	8	12	19						593
ENV	RQGLEKAL	955	8	35	55						594
ENV	VIVVYGVVP	47	9	55	86	0.0003					595
ENV	GVVPVKLAT	52	9	22	34	0.0002					596
ENV	PVKEATTT	58	9	24	38	0.0002					597
ENV	PTIRIRQEL	58	9	24	38	0.0002					598
ENV	TLIFLQSDA	61	9	52	81	0.0002					599
ENV	DAKAYDIEV	70	9	17	27	0.0002					600
ENV	DTEVINVA	75	9	18	28	0.0001					601
ENV	NVWATIACV	80	9	49	77	0.0002					602
ENV	WATIAACVPT	82	9	36	54	0.0002					603
ENV	PTIRIRQEL	89	9	23	33	0.0002					604
ENV	PTIRIRQEL	89	9	21	33	0.0002					605
ENV	MYEAGNEDI	113	9	23	36	0.0002					606
ENV	QMIIDISL	116	9	29	45	0.0002					607
ENV	ISLWIDQSL	121	9	38	59	0.0180					608
ENV	ISLWIDQSL	121	9	10	16	0.0001					609
ENV	SLKPCVKLT	128	9	55	86	0.0001					610
ENV	CYKLTILCY	132	9	52	81	0.0002					611
ENV	PLCYLNCIT	137	9	22	34	0.1600					612
ENV	PLCYLNCIT	137	9	22	34	0.0005					613
ENV	IRKNSFNI	181	9	13	20						614
ENV	ALFYRLDVP	202	9	11	17						615
ENV	VQNNNNNSIT	202	9	01	20						616
ENV	RLNCNNTSA	236	9	17	27						617
ENV	RLNCNNTSA	237	9	13	20						618
ENV	WQVQKCPK	244	9	15	23						619
ENV	KYSFEPIH	252	9	30	47						620
ENV	CAPAGFAL	264	9	29	45	0.0001					621
ENV	STVQCITHGI	289	9	51	80	0.0001					622
ENV	CTHIGIRPVP	294	9	32	50						623
ENV	CTHIGIRPVP	294	9	26	44	0.0001					624
ENV	PVYSTQLLL	304	9	66	94	0.0001					625
ENV	QVYQLEKSL	304	9	57	89	0.0001					626
ENV	QLLNGSLA	305	9	55	86	0.0001					627
ENV	QLLNGSLA	305	9								628

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SEQ ID NO
ENV	SLAEVEVI	311	9	13	20	0.0020					629
ENV	NAKTIIVQL	329	9	14	22						630
ENV	ATGDHGD	369	9	12	19						631
ENV	YVYVYVYV	372	9	12	19						632
ENV	ETGDIRDA	372	9	09	15						633
ENV	GTAGNSSRA	375	9	01	33						634
ENV	NTSPRSRVA	376	9	01	33						635
ENV	TAGNSRRAA	376	9	01	33						636
ENV	DIRQAICNV	380	9	15	23						637
ENV	DIRQAICNV	380	9	10	20						638
ENV	QVNSWQV	404	9	20	44						639
ENV	QVNSWQV	404	9	17	27	0.0026					640
ENV	NMQVEVGA	494	9	15	23	0.0022					641
ENV	QGMAYAPPI	501	9	14	22						642
ENV	QIRCSNNI	511	9	11	17						643
ENV	QIRCSNNI	512	9	11	17	0.0001					644
ENV	NIETNKET	537	9	01	17						645
ENV	NIETNKET	537	9	01	17						646
ENV	VYKLEPLGV	546	9	23	36						647
ENV	PLGVAPTKA	571	9	23	36	0.0001					648
ENV	PTKAKRRVV	576	9	22	34	0.0001					649
ENV	RVVEREKRA	587	9	32	50	0.0001					650
ENV	RVVEREKRA	587	9	17	27	0.0001					651
ENV	VVERLKRVA	588	9	25	39						652
ENV	VVERLKRVA	588	9	25	39						653
ENV	VVERLKRVA	598	9	16	25						654
ENV	AVGELGEL	602	9	11	17						655
ENV	AVGELGEL	602	9	11	17	0.0950					656
ENV	AMFLGELGA	602	9	12	19						657
ENV	AVFLGELGA	602	9	19	30						658
ENV	FLGAAGSTM	608	9	55	86	0.0190					659
ENV	FLGAAGTMGA	610	9	55	86	0.0009					660
ENV	FLGAAGTMGA	611	9	75	111	0.0001					661
ENV	FLGAAGTMGA	614	9	39	61						662
ENV	TMGAASITL	615	9	39	61						663
ENV	GAASITLIV	617	9	36	56						664
ENV	TLTVQARQL	622	9	37	58						665
ENV	LTVMARQLL	623	9	36	56						666
ENV	QARQLLSGI	626	9	38	59						667
ENV	QARQLLSGI	626	9	38	59						668
ENV	IVQQSNNLL	633	9	32	50	0.0001					669
ENV	IVQQSNNLL	634	9	26	41	0.0001					670
ENV	IVQQSNNLL	634	9	32	50						671
ENV	QQQNLLIRA	636	9	25	35						672
ENV	QQQNLLIRA	636	9	26	41						673
ENV	QQQNLLIRA	637	9	26	41						674
ENV	QQQNLLIRA	637	9	26	41						675
ENV	QVNSWQV	643	9	45	70						676
ENV	EAQQILLKL	644	9	48	75						677
ENV	EAQQILLKL	646	9	12	19						678
ENV	EAQQILLKL	646	9	35	56						679

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency (%)	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
ENV	AQQLIKLT	647	9	13	20						679
ENV	AQQLIKLT	647	9	34	53						680
ENV	AQQLIKLT	647	9	10	20						681
ENV	AQQLIKLT	647	9	13	53						682
ENV	AQQLIKLT	648	9	34	53						683
ENV	LLQLIKWT	651	9	13	20						684
ENV	LLQLIKWT	651	9	34	53						685
ENV	MLQLIKWT	651	9	10	16						686
ENV	LTWGRQL	654	9	59	92	0.5100	0.0200	0.2300	0.1500	0.0620	687
ENV	GRQLQARV	658	9	40	64	0.0001					688
ENV	QQLQARVA	660	9	40	64	0.0001					689
ENV	ELQLQARV	665	9	33	52	0.0085					690
ENV	ELQLQARV	665	9	33	52	0.0009					691
ENV	ELQLQARV	665	9	33	52	0.0011					692
ENV	ELQLQARV	665	9	33	52	0.0011					693
ENV	ELQLQARV	665	9	33	52	0.0011					694
ENV	ELQLQARV	665	9	33	52	0.0011					695
ENV	ELQLQARV	665	9	33	52	0.0011					696
ENV	ELQLQARV	665	9	33	52	0.0011					697
ENV	ELQLQARV	665	9	33	52	0.0011					698
ENV	ELQLQARV	665	9	33	52	0.0011					699
ENV	ELQLQARV	665	9	33	52	0.0011					700
ENV	ELQLQARV	665	9	33	52	0.0011					701
ENV	ELQLQARV	665	9	33	52	0.0011					702
ENV	ELQLQARV	665	9	33	52	0.0011					703
ENV	ELQLQARV	665	9	33	52	0.0011					704
ENV	ELQLQARV	665	9	33	52	0.0011					705
ENV	ELQLQARV	665	9	33	52	0.0011					706
ENV	ELQLQARV	665	9	33	52	0.0011					707
ENV	ELQLQARV	665	9	33	52	0.0011					708
ENV	ELQLQARV	665	9	33	52	0.0011					709
ENV	ELQLQARV	665	9	33	52	0.0011					710
ENV	ELQLQARV	665	9	33	52	0.0011					711
ENV	ELQLQARV	665	9	33	52	0.0011					712
ENV	ELQLQARV	665	9	33	52	0.0011					713
ENV	ELQLQARV	665	9	33	52	0.0011					714
ENV	ELQLQARV	665	9	33	52	0.0011					715
ENV	ELQLQARV	665	9	33	52	0.0011					716
ENV	ELQLQARV	665	9	33	52	0.0011					717
ENV	ELQLQARV	665	9	33	52	0.0011					718
ENV	ELQLQARV	665	9	33	52	0.0011					719
ENV	ELQLQARV	665	9	33	52	0.0011					720
ENV	ELQLQARV	665	9	33	52	0.0011					721
ENV	ELQLQARV	665	9	33	52	0.0011					722
ENV	ELQLQARV	665	9	33	52	0.0011					723
ENV	ELQLQARV	665	9	33	52	0.0011					724
ENV	ELQLQARV	665	9	33	52	0.0011					725
ENV	ELQLQARV	665	9	33	52	0.0011					726
ENV	ELQLQARV	665	9	33	52	0.0011					727
ENV	ELQLQARV	665	9	33	52	0.0011					728

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
ENV	ELKNSAISL	913	9	10	16						729
ENV	ELKNSAVSL	913	9	12	16						730
ENV	SAVSLNAT	917	9	11	17	0.0001					731
ENV	AVSLNATA	918	9	14	17						732
ENV	SLLSAVAN	920	9	14	22						733
ENV	ELKNSAVN	921	9	15	23						734
ENV	IAVAAGT	925	9	10	16						735
ENV	IAVAAGT	925	9	10	16						736
ENV	TAIAVAEGT	925	9	22	34						737
ENV	AVAEGTDRI	928	9	16	25	0.0008					738
ENV	AVAEGTDRI	928	9	14	22						739
ENV	VAEGTDRI	929	9	16	25	0.0001					740
ENV	VAEGTDRI	942	9	12	19						741
ENV	RIOGLEIRA	953	9	34	53	0.0003					742
ENV	ROGLEIRALL	955	9	34	53						743
ENV	ILGLVICS	26	10	10	16						744
ENV	LLGLMICS	26	10	10	16						745
ENV	QLYATVYAGV	34	10	11	17	0.0150					746
ENV	KLWVTVYGV	44	10	34	54						747
ENV	WVTVYGV	44	10	34	54						748
ENV	WVTVYGV	46	10	55	86	0.0009					749
ENV	WVTVYGV	46	10	55	86						750
ENV	GVFWKGLAT	52	10	22	34	0.0001					751
ENV	PWKELATTL	54	10	22	34	0.0001					752
ENV	KTLFCASDA	60	10	32	19						753
ENV	TTLFCASDA	60	10	32	19	0.0001					754
ENV	TTLFCASDA	60	10	32	19	0.0160					755
ENV	TTLFCASDA	67	10	44	72						756
ENV	TTLFCASDA	67	10	19	30	0.0006					757
ENV	KAVDEVHVV	72	10	17	27	0.0013					758
ENV	DEVHNVWAT	75	10	18	28	0.0001					759
ENV	EVHNVWAT	75	10	35	55						760
ENV	PTDNIQEV	89	10	13	20	0.0001					761
ENV	NMVEQMIEDI	112	10	20	31	0.0001					762
ENV	NMVEQMIEDI	112	10	22	36						763
ENV	NMVEQMIEDI	115	10	22	34	0.0001					764
ENV	DISLWDQSL	120	10	38	59						765
ENV	DISLWDQSL	120	10	10	16	0.0001					766
ENV	DQSLKPCVKL	126	10	47	73						767
ENV	CVKALPLCVT	132	10	53	83	0.0001					768
ENV	STSNSSNST	159	10	01	52						769
ENV	VISTQISAGT	161	10	01	20						770
ENV	SVGNNSNST	181	10	12	19						771
ENV	SVGNNSNST	217	10	01	33						772
ENV	RLNCNLSAI	236	10	15	24						773
ENV	LINCNLSAI	237	10	14	22						774
ENV	SAITQACPKV	243	10	13	20						775
ENV	SVITQACPKV	243	10	15	25						776
ENV	PIPHIYCAPA	258	10	36	56						777
ENV	PIPHIYCAPA	258	10	18	28						778
ENV	GTGRCVNST	281	10	12	19	0.0002					779
ENV	CTNVSTVQCT	285	10	13	20						780

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*1201	A*0202	A*0203	A*0206	A*4802	SHQ ID NO
ENV	VQCTHGRPV	292	10	32	56						779
ENV	VQCTHGRPV	292	10	33	35						780
ENV	GRVAVSTQL	297	10	33	52						781
ENV	STOLLNLSGL	303	10	26	41						782
ENV	TQLLNGSLA	304	10	57	89	0.0002					783
ENV	RIGRQITFYA	357	10	55	86	0.0001					784
ENV	GIGRQITFYA	360	10	01	16						785
ENV	SIGRQITFYA	360	10	33	33						786
ENV	QVGRQITFYA	360	10	11	17						787
ENV	GTAGNSRRAA	375	10	01	33						788
ENV	MQNGTITST	458	10	01	17						789
ENV	NANITPCIKI	478	10	01	50						790
ENV	ITLPCRIKQI	483	10	25	39						791
ENV	TLPCRIKQI	484	10	15	23						792
ENV	TLPCRIKQV	484	10	16	16						793
ENV	WQVQGRKAMV	494	10	17	27						794
ENV	NQVQGRKAMV	494	10	15	23						795
ENV	WQVQGRKAMV	496	10	18	28	0.0004					796
ENV	WQVQGRKAMV	496	10	10	16						797
ENV	QVQRCSSNIT	511	10	11	17						798
ENV	ETFRPGGDDM	544	10	17	27	0.0001					799
ENV	ETFRPGGDDM	544	10	31	58						800
ENV	ELVYKXVYKI	560	10	13	21	0.0001					801
ENV	ELVYKXVYKI	560	10	29	46						802
ENV	KVVKIEPLGV	565	10	23	36						803
ENV	VVKIEPLGVA	566	10	23	36						804
ENV	KIEPLGVAPT	568	10	23	37						805
ENV	APTKAKKRRV	584	10	17	27						806
ENV	RVVFERKRAV	587	10	25	39						807
ENV	RVVQREKRAV	587	10	16	25	0.0001					808
ENV	RVVQREKRAV	587	10	16	25						809
ENV	RVVQREKRAV	587	10	16	25						810
ENV	RVVQREKRAV	587	10	16	25						811
ENV	RVVQREKRAV	587	10	16	25						812
ENV	RVVQREKRAV	587	10	16	25						813
ENV	RVVQREKRAV	587	10	16	25						814
ENV	RVVQREKRAV	587	10	16	25						815
ENV	RVVQREKRAV	587	10	16	25						816
ENV	RVVQREKRAV	587	10	16	25						817
ENV	RVVQREKRAV	587	10	16	25						818
ENV	RVVQREKRAV	587	10	16	25						819
ENV	RVVQREKRAV	587	10	16	25						820
ENV	RVVQREKRAV	587	10	16	25						821
ENV	RVVQREKRAV	587	10	16	25						822
ENV	RVVQREKRAV	587	10	16	25						823
ENV	RVVQREKRAV	587	10	16	25						824
ENV	RVVQREKRAV	587	10	16	25						825
ENV	RVVQREKRAV	587	10	16	25						826
ENV	RVVQREKRAV	587	10	16	25						827
ENV	RVVQREKRAV	587	10	16	25						828

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
ENV	QARQLISGIV	626	10	38	59						829
ENV	GIWQGNLL	633	10	39	41						830
ENV	QVQGNLLRA	635	10	35	50						831
ENV	VOQGNLLRA	635	10	25	39						832
ENV	VOQGNLLRA	635	10	26	41						833
ENV	QVQGNLLRAI	636	10	25	39						834
ENV	QVQGNLLRAI	636	10	26	41						835
ENV	BAIEAQHILL	643	10	44	69						836
ENV	EAQHILLKLT	646	10	42	67						837
ENV	EAQHILLKLT	646	10	34	54						838
ENV	EAQHILLKLT	647	10	13	20						839
ENV	EAQHILLKLT	647	10	34	53						840
ENV	EAQHILLKLT	647	10	13	20						841
ENV	EAQHILLKLT	650	10	13	20						842
ENV	EAQHILLKLT	650	10	34	53						843
ENV	EAQHILLKLT	653	10	13	20						844
ENV	EAQHILLKLT	653	10	44	69	0.0015					845
ENV	EAQHILLKLT	658	10	40	77	0.0150					846
ENV	EAQHILLKLT	658	10	40	63	0.0002					847
ENV	EAQHILLKLT	660	10	33	52						848
ENV	EAQHILLKLT	672	10	27	42						849
ENV	EAQHILLKLT	672	10	18	28						850
ENV	EAQHILLKLT	680	10	48	75	0.0004					851
ENV	EAQHILLKLT	721	10	12	19						852
ENV	EAQHILLKLT	746	10	15	23						853
ENV	EAQHILLKLT	747	10	16	25						854
ENV	EAQHILLKLT	747	10	18	28						855
ENV	EAQHILLKLT	755	10	11	17						856
ENV	EAQHILLKLT	755	10	18	28						857
ENV	EAQHILLKLT	761	10	17	27						858
ENV	EAQHILLKLT	761	10	15	23						859
ENV	EAQHILLKLT	770	10	14	22						860
ENV	EAQHILLKLT	773	10	43	67	0.0002					861
ENV	EAQHILLKLT	778	10	38	59	0.0003					862
ENV	EAQHILLKLT	781	10	34	54						863
ENV	EAQHILLKLT	783	10	42	66						864
ENV	EAQHILLKLT	786	10	15	23						865
ENV	EAQHILLKLT	787	10	21	33						866
ENV	EAQHILLKLT	787	10	16	25						867
ENV	EAQHILLKLT	787	10	21	33						868
ENV	EAQHILLKLT	791	10	14	22						869
ENV	EAQHILLKLT	791	10	17	27	0.0007					870
ENV	EAQHILLKLT	794	10	31	48	0.0002					871
ENV	EAQHILLKLT	842	10	12	19						872
ENV	EAQHILLKLT	851	10	19	25						873
ENV	EAQHILLKLT	851	10	19	25						874
ENV	EAQHILLKLT	859	10	11	17						875
ENV	EAQHILLKLT	859	10	31	48						876
ENV	EAQHILLKLT	873	10	11	17						877
ENV	EAQHILLKLT	881	10	10	16						878

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SEQ ID NO
ENV	LLGRGWEAL	882	10	09	15						879
ENV	RLQWEGKYL	894	10	09	29						880
ENV	NLLQVWSQEL	905	10	16	25	0.0059					881
ENV	ELKNSAVSL	913	10	11	16						882
ENV	SAVSLNATA	917	10	11	17						883
ENV	AVSLNATAI	918	10	14	17						884
ENV	AVSLNATAI	919	10	14	22	0.0650					885
ENV	LNATMAVA	921	10	14	22	0.0740					886
ENV	ATAVAEFT	924	10	14	22		0.0074				887
ENV	IAVAEFTDRI	927	10	16	25						888
ENV	IAVAEFTDRI	927	10	14	22	0.0001					889
ENV	IAVAEFTDRI	928	10	15	23						890
ENV	IAVAEFTDRI	928	10	14	22	0.0004					891
ENV	IAVAEFTDRI	928	10	14	22						892
ENV	IAVAEFTDRI	928	10	14	22						893
ENV	IAVAEFTDRI	928	10	14	22						894
ENV	IAVAEFTDRI	928	10	14	22						895
ENV	IAVAEFTDRI	928	10	14	22						896
ENV	IAVAEFTDRI	928	10	14	22						897
ENV	IAVAEFTDRI	928	10	14	22						898
ENV	IAVAEFTDRI	928	10	14	22						899
ENV	IAVAEFTDRI	928	10	14	22						900
ENV	IAVAEFTDRI	928	10	14	22						901
ENV	IAVAEFTDRI	928	10	14	22						902
ENV	IAVAEFTDRI	928	10	14	22						903
ENV	IAVAEFTDRI	928	10	14	22						904
ENV	IAVAEFTDRI	928	10	14	22						905
ENV	IAVAEFTDRI	928	10	14	22						906
ENV	IAVAEFTDRI	928	10	14	22						907
ENV	IAVAEFTDRI	928	10	14	22						908
ENV	IAVAEFTDRI	928	10	14	22						909
ENV	IAVAEFTDRI	928	10	14	22						910
ENV	IAVAEFTDRI	928	10	14	22						911
ENV	IAVAEFTDRI	928	10	14	22						912
ENV	IAVAEFTDRI	928	10	14	22						913
ENV	IAVAEFTDRI	928	10	14	22						914
ENV	IAVAEFTDRI	928	10	14	22						915
ENV	IAVAEFTDRI	928	10	14	22						916
ENV	IAVAEFTDRI	928	10	14	22						917
ENV	IAVAEFTDRI	928	10	14	22						918
ENV	IAVAEFTDRI	928	10	14	22						919
ENV	IAVAEFTDRI	928	10	14	22						920
ENV	IAVAEFTDRI	928	10	14	22						921
ENV	IAVAEFTDRI	928	10	14	22						922
ENV	IAVAEFTDRI	928	10	14	22						923
ENV	IAVAEFTDRI	928	10	14	22						924
ENV	IAVAEFTDRI	928	10	14	22						925
ENV	IAVAEFTDRI	928	10	14	22						926
ENV	IAVAEFTDRI	928	10	14	22						927
ENV	IAVAEFTDRI	928	10	14	22						928

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*0402	SEQ ID NO
ENV	EINCRPNNT	342	11	10	16						979
ENV	RIGPGOTFYAT	357	11	10	16						930
ENV	GIKPGOTFYAT	360	11	10	33						931
ENV	SIKPGOTFYAT	360	11	01	33						932
ENV	ENKPGOTFYAT	360	11	01	33						933
ENV	ENLPCRIKQI	438	11	01	17						934
ENV	ENLPCRIKQI	482	11	11	17						935
ENV	TITLPCRIKQI	482	11	13	20						936
ENV	ITLPCRIKQI	483	11	15	23						937
ENV	IRIMQVEVGKA	492	11	12	29						938
ENV	EVGKAYAYAPI	498	11	10	28						939
ENV	KVGKAYAYAPI	498	11	10	16						940
ENV	EVGKAYAYAPI	512	11	11	17						941
ENV	KVYKPIEPLVA	565	11	23	36						942
ENV	GVAPTKAKRRV	573	11	17	27						943
ENV	VAPTKAKRRV	574	11	17	27						944
ENV	NHITPIREKRA	586	11	01	50						945
ENV	STRITIREKRAV	586	11	11	50						946
ENV	VYEREKRAVGI	601	11	11	17						947
ENV	GVAPTKAKRRV	601	11	12	19						948
ENV	GVAPTKAKRRV	601	11	19	30						949
ENV	FLGFLGAA	601	11	48	75						950
ENV	FLGFLGAAAGST	604	11	48	75						951
ENV	FLGFLGAAAGST	608	11	35	86						952
ENV	AAGSTMAGASI	611	11	44	53						953
ENV	STMGASITLT	611	11	39	61						954
ENV	STMGASITLT	615	11	36	56						955
ENV	GAASITLTVA	617	11	28	44						956
ENV	STLTVQARQL	620	11	27	42						957
ENV	ITLTVQARQL	621	11	27	42						958
ENV	TVQARQLLSGI	624	11	36	56						959
ENV	VQARQLLSGI	625	11	25	39						960
ENV	IVQQNQLIRA	634	11	26	41						961
ENV	IVQQNQLIRA	634	11	26	41						962
ENV	VQQQNQLIRA	635	11	25	39						963
ENV	VQQQNQLIRA	635	11	26	41						964
ENV	QNNLLRAIEA	637	11	26	41						965
ENV	QNNLLRAIEA	637	11	23	36						966
ENV	LLRAIEAQIIL	641	11	12	19						967
ENV	LLRAIEAQIIL	641	11	12	19						968
ENV	EAQIILKLTIV	646	11	35	55						969
ENV	EAQIILKLTIV	646	11	12	19						970
ENV	EAQIILKLTIV	646	11	34	54						971
ENV	LQTVNGIKQL	652	11	44	69						972
ENV	LQTVNGIKQL	652	11	49	77						973
ENV	GRKQARVLA	654	11	40	62						974
ENV	QARVLAVERTL	658	11	33	52						975
ENV	QARVLAVERTL	668	11	33	36						976
ENV	AVKYLIRIQQL	668	11	11	17						977
ENV	LLGWGCSGKL	678	11	46	72						978
ENV	NMTWNEWEREI	720	11	12	19						979

HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SHQ ID NO
ENV	NOQKNEQDILL	746	11	13	20						970
ENV	NOQKNEQDILL	746	11	15	23						980
ENV	NOQKNEQDILL	747	11	16	25						981
ENV	NOQKNEQDILL	752	11	12	19						982
ENV	NOQKNEQDILL	752	11	15	22						983
ENV	NOQKNEQDILL	752	11	15	22						984
ENV	NOQKNEQDILL	752	11	15	22						985
ENV	NOQKNEQDILL	761	11	13	20						986
ENV	NOQKNEQDILL	773	11	43	67						987
ENV	NOQKNEQDILL	778	11	31	48						988
ENV	NOQKNEQDILL	780	11	34	53						989
ENV	NOQKNEQDILL	782	11	36	56						990
ENV	NOQKNEQDILL	782	11	36	56						991
ENV	NOQKNEQDILL	783	11	30	47						992
ENV	NOQKNEQDILL	786	11	15	23						993
ENV	NOQKNEQDILL	786	11	21	33						994
ENV	NOQKNEQDILL	787	11	15	23						995
ENV	NOQKNEQDILL	787	11	20	31						996
ENV	NOQKNEQDILL	787	11	20	31						997
ENV	NOQKNEQDILL	789	11	19	30						998
ENV	NOQKNEQDILL	804	11	45	70						999
ENV	NOQKNEQDILL	842	11	11	17						1000
ENV	NOQKNEQDILL	850	11	19	30						1001
ENV	NOQKNEQDILL	852	11	20	31						1002
ENV	NOQKNEQDILL	881	11	11	18						1003
ENV	NOQKNEQDILL	881	11	10	16						1004
ENV	NOQKNEQDILL	917	11	11	17						1005
ENV	NOQKNEQDILL	918	11	11	17						1006
ENV	NOQKNEQDILL	920	11	13	20						1007
ENV	NOQKNEQDILL	926	11	16	25						1008
ENV	NOQKNEQDILL	926	11	14	22						1009
ENV	NOQKNEQDILL	927	11	15	23						1010
ENV	NOQKNEQDILL	927	11	14	22						1011
ENV	NOQKNEQDILL	927	11	14	22						1012
ENV	NOQKNEQDILL	951	11	11	17						1013
ENV	NOQKNEQDILL	953	11	13	22						1014
ENV	NOQKNEQDILL	953	11	13	22						1015
ENV	NOQKNEQDILL	953	11	13	22						1016
ENV	NOQKNEQDILL	953	11	13	22						1017
ENV	NOQKNEQDILL	953	11	13	22						1018
ENV	NOQKNEQDILL	953	11	13	22						1019
ENV	NOQKNEQDILL	953	11	13	22						1020
ENV	NOQKNEQDILL	953	11	13	22						1021
ENV	NOQKNEQDILL	953	11	13	22						1022
ENV	NOQKNEQDILL	953	11	13	22						1023
ENV	NOQKNEQDILL	953	11	13	22						1024
ENV	NOQKNEQDILL	953	11	13	22						1025
ENV	NOQKNEQDILL	953	11	13	22						1026
ENV	NOQKNEQDILL	953	11	13	22						1027
ENV	NOQKNEQDILL	953	11	13	22						1028

0.2700

Table VIII
HIV-1 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SHQ ID NO
GAG	GTEELSL	73	8	12	19						1029
GAG	ELRSLNLT	76	8	17	27						1030
GAG	SLFNTVAT	79	8	16	25						1031
GAG	SLYNTVAT	79	8	22	34						1032
GAG	TVATLYCV	83	8	41	64						1033
GAG	EVKTLKEA	85	8	11	17						1034
GAG	EVKTLKEA	85	8	22	34						1035
GAG	ADQAAADI	119	8	10	16						1036
GAG	ADQAAADI	132	8	01	33						1037
GAG	KYSQNYPI	148	8	15	27						1038
GAG	KYSQNYPI	148	8	27	48						1039
GAG	VQNAQQQM	156	8	21	33						1040
GAG	QVQNAQQM	156	8	29	44						1041
GAG	QVQNAQQM	161	8	29	44						1042
GAG	QVQNAQQM	161	8	29	44						1043
GAG	IQALSPTL	165	8	11	17						1044
GAG	IQALSPTL	165	8	29	45						1045
GAG	QALSPTLL	166	8	11	17						1046
GAG	QALSPTLL	166	8	11	17						1047
GAG	QALSPTLL	182	8	50	75						1048
GAG	KAESPVAL	182	8	50	75						1049
GAG	EVIPMFSA	188	8	46	72						1050
GAG	EVIPMTIA	188	8	14	22						1051
GAG	VIPMTIAL	189	8	46	72						1052
GAG	VIPMTIAL	189	8	14	22						1053
GAG	TALESCEGA	193	8	15	23						1054
GAG	TALESCEGA	194	8	46	72						1055
GAG	TALSSEGT	194	8	15	23						1056
GAG	ATPDNLNM	200	8	12	19						1057
GAG	ATPDQNT	200	8	42	66						1058
GAG	PDQLNNML	202	8	12	19						1059
GAG	PDQLNNML	202	8	13	67						1060
GAG	PDQLNNML	204	8	12	19						1061
GAG	DUNTMNT	204	8	44	69						1062
GAG	NIVGGIIQA	210	8	12	19						1063
GAG	NTVGGIIQA	210	8	47	73						1064
GAG	IVGGIIQA	211	8	12	19						1065
GAG	TVGGIIQA	211	8	47	73						1066
GAG	AMQMLKET	218	8	31	52						1067
GAG	AMQMLKET	218	8	26	41						1068
GAG	MQMLKDTI	219	8	33	52						1069
GAG	MQMLKDTI	219	8	26	41						1070
GAG	DTINSEAA	224	8	33	52						1071
GAG	DTINSEAA	224	8	33	52						1072
GAG	EAEIMDRV	224	8	39	64						1073
GAG	EAEIMDRV	229	8	15	23						1074
GAG	PVHAGRIA	238	8	19	30						1075
GAG	DIAGTIST	256	8	55	86						1076
GAG	DIAGTIST	257	8	48	75						1077
GAG	STLQEQIA	262	8	12	19						1078

Table VII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	LOEQIAWM	264	8	14	22						1079
GAG	LOEQIGWM	264	8	29	45						1080
GAG	WNTNPPPI	270	8	20	31						1081
GAG	WNTNPPPI	270	8	20	31						1082
GAG	WNTNPPPI	270	8	17	27						1083
GAG	WNTNPPPI	270	8	39	61						1084
GAG	WNTNPPPI	270	8	39	61						1085
GAG	WNTNPPPI	270	8	57	89						1086
GAG	WNTNPPPI	270	8	57	89						1087
GAG	WNTNPPPI	270	8	58	91						1088
GAG	WNTNPPPI	270	8	60	94						1089
GAG	WNTNPPPI	270	8	15	23						1090
GAG	WNTNPPPI	270	8	22	34						1091
GAG	WNTNPPPI	270	8	14	22						1092
GAG	WNTNPPPI	270	8	40	63						1093
GAG	WNTNPPPI	270	8	28	44						1094
GAG	WNTNPPPI	270	8	28	44						1095
GAG	WNTNPPPI	270	8	28	44						1096
GAG	WNTNPPPI	270	8	28	44						1097
GAG	WNTNPPPI	270	8	28	44						1098
GAG	WNTNPPPI	270	8	28	44						1099
GAG	WNTNPPPI	270	8	28	44						1100
GAG	WNTNPPPI	270	8	28	44						1101
GAG	WNTNPPPI	270	8	28	44						1102
GAG	WNTNPPPI	270	8	28	44						1103
GAG	WNTNPPPI	270	8	28	44						1104
GAG	WNTNPPPI	270	8	28	44						1105
GAG	WNTNPPPI	270	8	28	44						1106
GAG	WNTNPPPI	270	8	28	44						1107
GAG	WNTNPPPI	270	8	28	44						1108
GAG	WNTNPPPI	270	8	28	44						1109
GAG	WNTNPPPI	270	8	28	44						1110
GAG	WNTNPPPI	270	8	28	44						1111
GAG	WNTNPPPI	270	8	28	44						1112
GAG	WNTNPPPI	270	8	28	44						1113
GAG	WNTNPPPI	270	8	28	44						1114
GAG	WNTNPPPI	270	8	28	44						1115
GAG	WNTNPPPI	270	8	28	44						1116
GAG	WNTNPPPI	270	8	28	44						1117
GAG	WNTNPPPI	270	8	28	44						1118
GAG	WNTNPPPI	270	8	28	44						1119
GAG	WNTNPPPI	270	8	28	44						1120
GAG	WNTNPPPI	270	8	28	44						1121
GAG	WNTNPPPI	270	8	28	44						1122
GAG	WNTNPPPI	270	8	28	44						1123
GAG	WNTNPPPI	270	8	28	44						1124
GAG	WNTNPPPI	270	8	28	44						1125
GAG	WNTNPPPI	270	8	28	44						1126
GAG	WNTNPPPI	270	8	28	44						1127
GAG	WNTNPPPI	270	8	28	44						1128

HIV A02 Super Motif Peptides with Binding Information

Problem	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	PLASLKS	548	8	15	23						1179
GAG	PLTSKSL	548	8	12	19						1130
GAG	PLTSKSL	548	8	12	19						1131
GAG	SLFORDPL	554	8	12	19						1132
GAG	SLFORDPL	554	8	12	19						1133
GAG	SLFORDPL	554	8	12	19						1134
GAG	SLFORDPL	554	8	12	19						1135
GAG	SLFORDPL	554	8	12	19						1136
GAG	SLFORDPL	554	8	12	19						1137
GAG	SLFORDPL	554	8	12	19						1138
GAG	SLFORDPL	554	8	12	19						1139
GAG	SLFORDPL	554	8	12	19						1140
GAG	SLFORDPL	554	8	12	19						1141
GAG	SLFORDPL	554	8	12	19						1142
GAG	SLFORDPL	554	8	12	19						1143
GAG	SLFORDPL	554	8	12	19						1144
GAG	SLFORDPL	554	8	12	19						1145
GAG	SLFORDPL	554	8	12	19						1146
GAG	SLFORDPL	554	8	12	19						1147
GAG	SLFORDPL	554	8	12	19						1148
GAG	SLFORDPL	554	8	12	19						1149
GAG	SLFORDPL	554	8	12	19						1150
GAG	SLFORDPL	554	8	12	19						1151
GAG	SLFORDPL	554	8	12	19						1152
GAG	SLFORDPL	554	8	12	19						1153
GAG	SLFORDPL	554	8	12	19						1154
GAG	SLFORDPL	554	8	12	19						1155
GAG	SLFORDPL	554	8	12	19						1156
GAG	SLFORDPL	554	8	12	19						1157
GAG	SLFORDPL	554	8	12	19						1158
GAG	SLFORDPL	554	8	12	19						1159
GAG	SLFORDPL	554	8	12	19						1160
GAG	SLFORDPL	554	8	12	19						1161
GAG	SLFORDPL	554	8	12	19						1162
GAG	SLFORDPL	554	8	12	19						1163
GAG	SLFORDPL	554	8	12	19						1164
GAG	SLFORDPL	554	8	12	19						1165
GAG	SLFORDPL	554	8	12	19						1166
GAG	SLFORDPL	554	8	12	19						1167
GAG	SLFORDPL	554	8	12	19						1168
GAG	SLFORDPL	554	8	12	19						1169
GAG	SLFORDPL	554	8	12	19						1170
GAG	SLFORDPL	554	8	12	19						1171
GAG	SLFORDPL	554	8	12	19						1172
GAG	SLFORDPL	554	8	12	19						1173
GAG	SLFORDPL	554	8	12	19						1174
GAG	SLFORDPL	554	8	12	19						1175
GAG	SLFORDPL	554	8	12	19						1176
GAG	SLFORDPL	554	8	12	19						1177
GAG	SLFORDPL	554	8	12	19						1178

Table V.HI
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	GATPDQINT	199	9	42	66						1179
GAG	ATPDQINNM	200	9	12	19						1180
GAG	ATPDQINTM	200	9	42	66						1181
GAG	DLNMLNIN	204	9	12	19						1182
GAG	DLNMLNIN	204	9	42	66	0.0001					1183
GAG	NNGGHOAA	210	9	12	19						1184
GAG	NTVGGHOAA	210	9	47	73						1185
GAG	IVGGHOAA	211	9	12	19						1186
GAG	TVGGHOAA	211	9	47	73						1187
GAG	AMOMLKDT	217	9	33	52						1188
GAG	AMOMLKDT	217	9	33	52						1189
GAG	AMOMLKDT	218	9	33	51						1190
GAG	AMOMLKDT	218	9	26	41						1191
GAG	AMOMLKDT	218	9	26	41						1192
GAG	DIAGTSTL	256	9	48	75	0.0001					1193
GAG	TESTLOEQ	260	9	45	71						1194
GAG	TLQRQIAWM	263	9	12	19						1195
GAG	TLQRQIAWM	263	9	12	19						1196
GAG	TLQRQIAWM	264	9	12	19						1197
GAG	LOEQGWMIT	264	9	29	45						1198
GAG	MTNAPPIV	271	9	20	31	0.0300	0.0006	0.3000	0.0023	3.3000	1199
GAG	MTSNPPHV	271	9	16	25						1200
GAG	DIYKRWIL	284	9	17	27	0.0001					1201
GAG	DIYKRWIL	284	9	37	38	0.0001					1202
GAG	ILGLNKIV	290	9	57	89	0.0003					1203
GAG	KIVRMYSPT	296	9	15	23						1204
GAG	KIVRMYSPT	296	9	41	64	0.0007					1205
GAG	KIVRMYSPT	299	9	14	22						1206
GAG	RAYSPISIL	299	9	40	63						1207
GAG	RAYSPISIL	300	9	40	63						1208
GAG	YVDFPKTL	320	9	28	44	0.0010					1209
GAG	YVDFPKTL	326	9	34	53						1210
GAG	RAEQASQEV	329	9	12	19						1211
GAG	RAEQATQDV	329	9	15	23						1212
GAG	RAEQATQDV	329	9	27	42						1213
GAG	RAEQATQDV	333	9	15	23						1214
GAG	ATQEVKAWM	333	9	15	28						1215
GAG	SOEVKNWMT	334	9	11	17						1216
GAG	TQDEVKNWMT	334	9	15	23						1217
GAG	TQDEVKNWMT	334	9	18	28						1218
GAG	DVKNWMTDT	336	9	12	19						1219
GAG	DVKNWMTDT	336	9	32	39						1220
GAG	NPNDCKSI	349	9	17	25						1221
GAG	NPNDCKSI	349	9	45	70						1222
GAG	NPNDCKSI	356	9	16	25						1223
GAG	ILKALGPA	357	9	16	25	0.0001					1224
GAG	ILKALGPA	357	9	18	28						1225
GAG	ILKALGPA	357	9	18	28	0.0001					1226
GAG	PAITLEMM	359	9	16	25						1227
GAG	PAITLEMM	363	9	16	25						1228

Table V.H
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
GAG	AATLEEMMT	364	9	16	25						1229
GAG	GASLEEMT	364	9	16	16						1230
GAG	GATLEEMT	364	9	28	44						1231
GAG	ATLEEMMT	365	9	46	72						1232
GAG	EMMTACQV	369	9	59	92	0.0006					1233
GAG	EMMTACQV	370	9	59	92						1234
GAG	GGGESHKA	376	9	33	38						1235
GAG	KARVLAEM	383	9	57	89						1236
GAG	VLAEMSQV	386	9	16	25						1237
GAG	VLAEMSQV	386	9	33	52	0.1100					1238
GAG	LAEMSQV	387	9	23	37						1239
GAG	LAEMSQV	387	9	33	52						1240
GAG	CTERQNEL	459	9	51	87						1241
GAG	ROANFLGI	465	9	56	88						1242
GAG	FLQNRPEPT	486	9	10	16	0.0110	0.0004	0.3100	0.0002	0.0130	1243
GAG	FLQNRPEPT	486	9	28	44						1244
GAG	LQNRPEPT	487	9	10	16						1245
GAG	LQNRPEPT	487	9	28	44						1246
GAG	PAETKPT	493	9	01	5						1247
GAG	KQETDKEL	531	9	12	19						1248
GAG	PDKFLYPL	534	9	12	19						1249
GAG	KQETDKEL	535	9	01	25						1250
GAG	KQETDKEL	535	9	01	25						1251
GAG	PDKFLYPL	538	9	01	25						1252
GAG	TQVFLYPL	538	9	01	25						1253
GAG	TQVFLYPL	538	9	11	17						1254
GAG	RSVLSGGEL	4	10	11	22						1255
GAG	RSVLSGGEL	4	10	28	44						1256
GAG	SVLSGGELDA	6	10	15	23						1257
GAG	KLDWIKRL	12	10	16	25						1258
GAG	KLDWIKRL	12	10	16	25						1259
GAG	WASRELEEL	37	10	46	69						1260
GAG	FALNPLLEI	46	10	18	28						1261
GAG	FALNPLLEI	46	10	14	22						1262
GAG	ETSEGCRL	54	10	14	22						1263
GAG	QILGLOQRL	61	10	11	17						1264
GAG	QILGLOQRL	61	10	11	17						1265
GAG	QILGLOQRL	61	10	14	22						1266
GAG	QILGLOQRL	61	10	15	23						1267
GAG	ELSLVNTVA	76	10	15	23						1268
GAG	ATLYCVHQI	85	10	12	19						1269
GAG	ATLYCVHQI	85	10	15	23						1270
GAG	RIEVEDTKA	93	10	13	20						1271
GAG	GAAXATDSNI	123	10	01	50						1272
GAG	GAAXATDSNI	123	10	01	50						1273
GAG	SONYFVQNA	146	10	22	44						1274
GAG	SONYFVQNA	146	10	22	44						1275
GAG	SONYFVQNA	150	10	22	44						1276
GAG	SONYFVQNA	150	10	30	47						1277
GAG	PVQNAQQM	154	10	21	33						1278
GAG	PVQNAQQM	154	10	29	45						1279
GAG	PVQNAQQM	154	10	14	22						1280
GAG	PVQNAQQM	155	10	29	45						1281
GAG	WQNLQGNV	155	10	29	45						1282

Table VIII
 HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	Seq ID NO
GAG	NAQQMVFHQ	158	10	12	19						1279
GAG	NLQGMVFHQ	158	10	11	13						1280
GAG	LOGQMVFHQ	158	10	15	23						1281
GAG	LAQGMVFHQ	163	10	27	42						1282
GAG	QASPTLNA	166	10	29	45						1283
GAG	QALSPTLNA	166	10	10	16						1284
GAG	RLTNAWVKVI	171	10	30	47						1285
GAG	RTLNWVKVVI	171	10	31	48	0.0003					1286
GAG	KAFSEVPM	183	10	34	70						1287
GAG	PMFALSSEGA	191	10	45	70						1288
GAG	PMFALSSEGA	191	10	15	23						1289
GAG	GATPDLLNMI	199	10	12	19						1290
GAG	GATPDLLNMI	199	10	42	66						1291
GAG	GATPDLLNMI	200	10	12	19						1292
GAG	ATPDLLNMI	200	10	42	66						1293
GAG	PDLLNMI	202	10	11	67						1294
GAG	PDLLNMI	202	10	13	62						1295
GAG	PDLLNMI	208	10	12	19						1296
GAG	MLNTEGQIA	210	10	47	73	0.0022					1297
GAG	MLNTEGQIA	210	10	12	19						1298
GAG	NI VGHQIAAM	210	10	47	73						1299
GAG	NI VGHQIAAM	210	10	33	52						1300
GAG	QAAMQMLKDT	216	10	26	51						1301
GAG	QAAMQMLKDT	216	10	26	51						1302
GAG	QAAMQMLKDT	217	10	26	41						1303
GAG	MLKDTINEEA	221	10	32	50						1304
GAG	MLKDTINEEA	221	10	22	34						1305
GAG	AAEWRLIIPV	230	10	34	53						1306
GAG	AAEWRLIIPV	230	10	14	22						1307
GAG	RLHPVHAGPI	235	10	22	34						1308
GAG	RVHPVHAGPI	235	10	22	34						1309
GAG	RVHPVHAGPI	235	10	18	28						1310
GAG	RVHPVHAGPI	240	10	17	27						1311
GAG	RVHPVHAGPI	240	10	44	69						1312
GAG	QMBREPGSDI	248	10	44	69						1313
GAG	QMBREPGSDI	248	10	45	70						1314
GAG	QMBREPGSDI	259	10	11	17						1315
GAG	TTSLTLEQIA	262	10	12	19						1316
GAG	STLQEQIAAM	262	10	27	42						1317
GAG	STLQEQIAAM	262	10	27	42						1318
GAG	STLQEQIAAM	263	10	12	19						1319
GAG	STLQEQIAAM	263	10	27	42						1320
GAG	WMTSNRPPIV	270	10	20	31	0.0510	0.0014	0.5900	0.0002	0.0180	1321
GAG	WMTSNRPPIV	270	10	16	25						1322
GAG	GAISPVGDI	276	10	01	90						1323
GAG	GAISPVGDI	281	10	07	63						1324
GAG	PVGEIKRWI	281	10	40	63						1325
GAG	PVGEIKRWI	291	10	57	89	0.0009					1326
GAG	ILGLNGVIRM	291	10	57	89	0.0010					1327
GAG	IVRMYSFTSI	297	10	14	22						1328
GAG	IVRMYSFTSI	297	10	40	63						1329
GAG	QASQEVKNMM	332	10	11	17						1330

HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SEQ ID NO
GAG	QATQDVKNWM	332	10	15	23						1329
GAG	QATQDVKNWM	332	10	18	28						1330
GAG	ATQDVKNWMT	333	10	15	23						1331
GAG	ATQDVKNWMT	333	10	18	28						1332
GAG	DVKNWMTITL	336	10	12	19						1333
GAG	DVKNWMTITL	336	10	11	17						1334
GAG	DVKNWMTITL	336	10	25	39						1335
GAG	MTITLLVQNA	341	10	22	34						1336
GAG	MTITLLVQNA	341	10	36	56						1337
GAG	MTITLLVQNA	341	10	45	69						1338
GAG	NANPDKSIL	349	10	17	17						1339
GAG	NANPDKSIL	349	10	45	70						1340
GAG	KTILKALGPA	355	10	16	25						1341
GAG	KTILKALGPA	355	10	16	25						1342
GAG	TLKALGPA	356	10	13	20						1343
GAG	TLKALGPA	357	10	16	25						1344
GAG	TLKALGPA	357	10	16	25						1345
GAG	ATLLEEMMTA	364	10	16	25						1346
GAG	GASLEEMMTA	364	10	10	16						1347
GAG	GATLLEEMMTA	364	10	28	44						1348
GAG	RVLAEAMSSQ	385	10	16	25						1349
GAG	RVLAEAMSSQ	385	10	33	52	0.0058					1350
GAG	FMASQVNSA	389	10	10	16						1351
GAG	FMASQVNSA	389	10	11	17						1352
GAG	AMSOVYNSA	390	10	10	16						1353
GAG	QMKDCTERQA	455	10	49	77						1354
GAG	FLQNRPEPTA	486	10	10	16						1355
GAG	FLQNRPEPTA	486	10	28	44						1356
GAG	FLQNRPEPTA	486	10	32	52						1357
GAG	TTISQKPEPI	521	10	09	15	0.0013					1358
GAG	ETIDKDLVPL	537	10	01	25						1359
GAG	PUDKELYPLT	538	10	01	25						1360
GAG	RTNSLYPLT	538	10	01	25						1361
GAG	TIDKDLVPLA	538	10	01	25						1362
GAG	WASRELEFAY	577	11	12	17						1363
GAG	WASRELEFAY	577	11	17	27						1364
GAG	ELERFANVNL	42	11	14	22						1365
GAG	ELERFANVNL	42	11	15	23						1366
GAG	LLLETSEGRQI	52	11	16	25						1367
GAG	ROLQLOPQSL	60	11	11	17						1368
GAG	QIUSHELRL	70	11	11	17						1369
GAG	ELERFANVNL	42	11	11	20						1370
GAG	VATLYCVHRI	84	11	12	19						1371
GAG	VATLYCVHRI	84	11	15	23						1372
GAG	RIEVKDTREAL	93	11	12	19						1373
GAG	PIVONLQGGMV	154	11	14	22						1374
GAG	PIVONLQGGMV	154	11	29	45						1375
GAG	QMKDCTERQA	455	11	15	23						1376
GAG	QMKDCTERQA	455	11	16	25						1377
GAG	MVITQASPRTL	163	11	27	42						1378

HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*5802	SEQ ID NO
GAG	HOASPRTLNA	165	11	29	45						1379
GAG	HOASPRTLNA	165	11	10	16						1380
GAG	ALSPTLNWV	167	11	29	45						1381
GAG	ALSPTLNWV	167	11	10	16						1382
GAG	NAWVAVIEKA	174	11	25	39						1383
GAG	NAWVAVIEKA	174	11	27	42						1384
GAG	WVEKASIEVE	175	11	28	44						1385
GAG	WVEKASIEVE	179	11	28	44						1386
GAG	PMFSAISEGAT	191	11	44	69						1387
GAG	PMFSAISEGAT	191	11	58	23						1388
GAG	ALSUGATPDQL	195	11	12	19						1389
GAG	GAHQDLNMLL	199	11	12	19						1390
GAG	GAHQDLNMLL	202	11	11	17						1391
GAG	PDQLNMLNIV	202	11	41	64						1392
GAG	PDQLNMLNIV	202	11	12	19						1393
GAG	MLNIVGGHQA	207	11	43	67						1394
GAG	MLNIVGGHQA	208	11	12	19						1395
GAG	MLNIVGGHQA	211	11	17	28						1396
GAG	IVGGHQAAMQ	211	11	47	73						1397
GAG	IVGGHQAAMQ	211	11	47	73						1398
GAG	HOAAQMMLKDT	215	11	33	52						1400
GAG	HOAAQMMLKDT	215	11	26	41						1401
GAG	QAAQMMLKDT	216	11	33	52						1402
GAG	QAAQMMLKDT	216	11	33	52						1403
GAG	QMLKDTINEEA	220	11	32	50						1404
GAG	QMLKDTINEEA	220	11	22	34						1405
GAG	QMLKDTINEEA	221	11	32	50						1406
GAG	MLKDTINEEA	221	11	22	34						1407
GAG	MLKDTINEEA	221	11	22	34						1408
GAG	EAAEWDRLLIV	229	11	34	53						1409
GAG	EAAEWDRLLIV	229	11	44	69						1410
GAG	RLIPIVIAQPIA	235	11	15	22						1411
GAG	QAMREPRGSDI	247	11	44	69						1412
GAG	QAMREPRGSDI	248	11	44	69						1413
GAG	QAMREPRGSDI	248	11	11	17						1414
GAG	GTSTLQEQIA	259	11	12	19						1415
GAG	STLQEQIAWMT	262	11	12	19						1416
GAG	STLQEQIAWMT	262	11	12	19						1417
GAG	QIGWMTNPNPI	265	11	18	26						1418
GAG	QIGWMTNPNPI	267	11	10	16						1419
GAG	QIGWMTNPNPI	267	11	17	27						1420
GAG	PGYDTIKRWII	281	11	17	27						1421
GAG	PGYDTIKRWII	281	11	39	61						1422
GAG	DIYKRWIIIGL	284	11	17	27						1423
GAG	DIYKRWIIIGL	284	11	17	27						1424
GAG	IULGNLIVRM	290	11	56	88						1425
GAG	KIVRMYSPTISI	296	11	14	22						1426
GAG	KIVRMYSPTISI	296	11	39	61						1427
GAG	KIVRMYSPTISI	297	11	14	22						1428
GAG	IVRMYSPTISIL	297	11	40	63						1429
GAG	IVRMYSPTISIL	297	11	13	20						1430
GAG	IVRMYSPTISIL	299	11	38	59						1431

Table V.III
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A *0201	A *0202	A *0203	A *0206	A *6802	SEQ ID NO
GAG	YVDREFKTLRA	320	11	27	42						1479
GAG	YVDREFKTLRA	320	11	28	44						1430
GAG	TLRAQDSQEV	327	11	12	19						1431
GAG	TLRAQDSQEV	327	11	11	17						1432
GAG	TLRAQDSQEV	327	11	24	38						1433
GAG	EQASQEVKNWM	331	11	11	17						1434
GAG	EQATQDVKNWM	331	11	15	23						1435
GAG	EQATQEVKNWM	331	11	18	28						1436
GAG	QASQEVKNWMT	332	11	11	17						1437
GAG	QASQEVKNWMT	332	11	15	23						1438
GAG	QATQEVKNWMT	332	11	18	28						1439
GAG	QATQEVKNWMT	332	11	16	26						1440
GAG	QSEVKNWMTET	334	11	11	17						1441
GAG	QSEVKNWMTET	334	11	11	17						1442
GAG	QSEVKNWMTET	334	11	14	22						1443
GAG	DYKNWMTETLL	336	11	12	19						1444
GAG	QSEVKNWMTETLL	336	11	11	17						1445
GAG	QSEVKNWMTETLL	336	11	22	34						1446
GAG	QSEVKNWMTETLL	340	11	22	34						1447
GAG	WMTETLLVQNA	340	11	35	55						1448
GAG	LYQNAIPDCKT	346	11	45	70						1449
GAG	VQNAIPDCKSI	347	11	10	16						1450
GAG	QSEVKNWMTET	347	11	45	70						1451
GAG	QSEVKNWMTET	347	11	16	25						1452
GAG	QSEVKNWMTET	355	11	13	20						1453
GAG	QSEVKNWMTET	355	11	13	20						1454
GAG	QSEVKNWMTET	355	11	16	25						1455
GAG	QSEVKNWMTET	357	11	16	25						1456
GAG	QSEVKNWMTET	360	11	16	25						1457
GAG	QSEVKNWMTET	360	11	17	27						1458
GAG	QSEVKNWMTET	360	11	16	25						1459
GAG	QSEVKNWMTET	374	11	36	56						1460
GAG	QSEVKNWMTET	374	11	23	36						1461
GAG	QSEVKNWMTET	376	11	36	56						1462
GAG	QSEVKNWMTET	376	11	19	30						1463
GAG	QSEVKNWMTET	385	11	20	31						1464
GAG	QSEVKNWMTET	385	11	16	25						1465
GAG	QSEVKNWMTET	393	11	01	50						1466
GAG	QSEVKNWMTET	393	11	01	50						1467
GAG	QSEVKNWMTET	454	11	49	77						1468
GAG	QSEVKNWMTET	492	11	01	50						1469
GAG	QSEVKNWMTET	511	11	02	67						1470
GAG	QSEVKNWMTET	511	11	09	14						1471
GAG	QSEVKNWMTET	537	11	01	25						1472
GAG	QSEVKNWMTET	537	11	01	25						1473
GAG	QSEVKNWMTET	551	11	12	19						1474
NEF	QSEVKNWMTET	551	11	12	19						1475
NEF	QSEVKNWMTET	551	11	12	19						1476
NEF	QSEVKNWMTET	551	11	12	19						1477
NEF	QSEVKNWMTET	551	11	12	19						1478
NEF	QSEVKNWMTET	551	11	12	19						1479
NEF	QSEVKNWMTET	551	11	12	19						1480
NEF	QSEVKNWMTET	551	11	12	19						1481
NEF	QSEVKNWMTET	551	11	12	19						1482
NEF	QSEVKNWMTET	551	11	12	19						1483
NEF	QSEVKNWMTET	551	11	12	19						1484
NEF	QSEVKNWMTET	551	11	12	19						1485
NEF	QSEVKNWMTET	551	11	12	19						1486
NEF	QSEVKNWMTET	551	11	12	19						1487
NEF	QSEVKNWMTET	551	11	12	19						1488
NEF	QSEVKNWMTET	551	11	12	19						1489
NEF	QSEVKNWMTET	551	11	12	19						1490
NEF	QSEVKNWMTET	551	11	12	19						1491
NEF	QSEVKNWMTET	551	11	12	19						1492
NEF	QSEVKNWMTET	551	11	12	19						1493
NEF	QSEVKNWMTET	551	11	12	19						1494
NEF	QSEVKNWMTET	551	11	12	19						1495
NEF	QSEVKNWMTET	551	11	12	19						1496
NEF	QSEVKNWMTET	551	11	12	19						1497
NEF	QSEVKNWMTET	551	11	12	19						1498
NEF	QSEVKNWMTET	551	11	12	19						1499
NEF	QSEVKNWMTET	551	11	12	19						1500
NEF	QSEVKNWMTET	551	11	12	19						1501
NEF	QSEVKNWMTET	551	11	12	19						1502
NEF	QSEVKNWMTET	551	11	12	19						1503
NEF	QSEVKNWMTET	551	11	12	19						1504
NEF	QSEVKNWMTET	551	11	12	19						1505
NEF	QSEVKNWMTET	551	11	12	19						1506
NEF	QSEVKNWMTET	551	11	12	19						1507
NEF	QSEVKNWMTET	551	11	12	19						1508
NEF	QSEVKNWMTET	551	11	12	19						1509
NEF	QSEVKNWMTET	551	11	12	19						1510
NEF	QSEVKNWMTET	551	11	12	19						1511
NEF	QSEVKNWMTET	551	11	12	19						1512
NEF	QSEVKNWMTET	551	11	12	19						1513
NEF	QSEVKNWMTET	551	11	12	19						1514
NEF	QSEVKNWMTET	551	11	12	19						1515
NEF	QSEVKNWMTET	551	11	12	19						1516
NEF	QSEVKNWMTET	551	11	12	19						1517
NEF	QSEVKNWMTET	551	11	12	19						1518
NEF	QSEVKNWMTET	551	11	12	19						1519
NEF	QSEVKNWMTET	551	11	12	19						1520
NEF	QSEVKNWMTET	551	11	12	19						1521
NEF	QSEVKNWMTET	551	11	12	19						1522
NEF	QSEVKNWMTET	551	11	12	19						1523
NEF	QSEVKNWMTET	551	11	12	19						1524
NEF	QSEVKNWMTET	551	11	12	19						1525
NEF	QSEVKNWMTET	551	11	12	19						1526
NEF	QSEVKNWMTET	551	11	12	19						1527
NEF	QSEVKNWMTET	551	11	12	19						1528
NEF	QSEVKNWMTET	551	11	12	19						1529
NEF	QSEVKNWMTET	551	11	12	19						1530
NEF	QSEVKNWMTET	551	11	12	19						1531
NEF	QSEVKNWMTET	551	11	12	19						1532
NEF	QSEVKNWMTET	551	11	12	19						1533
NEF	QSEVKNWMTET	551	11	12	19						1534
NEF	QSEVKNWMTET	551	11	12	19						1535
NEF	QSEVKNWMTET	551	11	12	19						1536
NEF	QSEVKNWMTET	551	11	12	19						1537
NEF	QSEVKNWMTET	551	11	12	19						1538
NEF	QSEVKNWMTET	551	11	12	19						1539
NEF	QSEVKNWMTET	551	11	12	19						1540
NEF	QSEVKNWMTET	551	11	12	19						1541
NEF	QSEVKNWMTET	551	11	12	19						1542
NEF	QSEVKNWMTET	551	11	12	19						1543
NEF	QSEVKNWMTET	551	11	12	19						1544
NEF	QSEVKNWMTET	551	11	12	19						1545
NEF	QSEVKNWMTET	551	11	12	19						1546
NEF	QSEVKNWMTET	551	11	12	19						1547
NEF	QSEVKNWMTET	551	11	12	19						1548
NEF	QSEVKNWMTET	551	11	12	19						1549
NEF	QSEVKNWMTET	551	11	12	19						1550
NEF	QSEVKNWMTET	551	11	12	19						1551
NEF	QSEVKNWMTET	551	11	12	19						1552
NEF	QSEVKNWMTET	551	11	12	19						1553
NEF	QSEVKNWMTET	551	11	12	19						1554
NEF	QSEVKNWMTET	551	11	12	19						1555
NEF	QSEVKNWMTET	551	11	12	19						1556
NEF	QSEVKNWMTET	551	11	12	19						1557
NEF	QSEVKNWMTET	551	11	12	19						1558
NEF	QSEVKNWMTET	551	11	12	19						1559
NEF	QSEVKNWMTET	551	11	12	19						1560
NEF	QSEVKNWMTET	551	11	12	19						1561
NEF	QSEVKNWMTET	551	11	12	19						1562
NEF	QSEVKNWMTET	551	11	12	19						1563
NEF	QSEVKNWMTET	551	11	12	19						1564
NEF	QSEVKNWMTET	551	11	12	19						1565
NEF	QSEVKNWMTET	551	11	12	19						1566
NEF	QSEVKNWMTET	551	11	12	19						1567
NEF	QSEVKNWMTET	551	11	12	19						1568
NEF	QSEVKNWMTET	551	11	12	19						1569
NEF	QSEVKNWMTET	551	11	12	19						1570
NEF	QSEVKNWMTET	551	11	12	19						1571
NEF	QSEVKNWMTET	551	11	12	19						1572
NEF	QSEVKNWMTET	551	11	12	19						1573
NEF	QSEVKNWMTET	551	11	12	19						1574
NEF	QSEVKNWMTET	551	11	12	19						1575
NEF	QSEVKNWMTET	551	11	12	19						1576
NEF	QSEVKNWMTET	551	11	12	19						15

Table V.III
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1201	A*1202	A*1203	A*1206	A*4802	SIQ ID NO
NEF	AAEGVGAV	42	8	17	28						1479
NEF	DLERIGAI	57	8	14	22						1480
NEF	GATSSNT	62	8	32	50						1481
NEF	ATSSNTAA	63	8	10	16						1482
NEF	ATSSNTAA	63	8	27	42						1483
NEF	ITSSNTAA	64	8	15	23						1484
NEF	AATNADCA	70	8	12	22						1485
NEF	EAQBEVEV	82	8	16	25						1486
NEF	PYRQYPL	95	8	48	75						1487
NEF	QAPPAAGV	95	8	17	27						1488
NEF	QAPPAAGV	95	8	56	89						1489
NEF	QAPPAAGV	100	8	17	27	0.0001					1490
NEF	ALDLSHFL	111	8	11	17						1491
NEF	AVDLSHFL	111	8	15	23						1492
NEF	FLKEKGGL	117	8	56	88						1493
NEF	SQKRQDIL	177	8	12	19						1494
NEF	QAPPAAGV	32	9	01	17						1495
NEF	RAQAPAAA	32	9	01	17						1496
NEF	RAQAPAAA	32	9	01	17						1497
NEF	RTETPAAGV	32	9	01	17						1498
NEF	QAPPAAGV	33	9	01	17						1499
NEF	QAPPAAGV	33	9	01	17						1500
NEF	QAPPAAGV	34	9	01	17						1501
NEF	PADEGVAV	41	9	11	18						1502
NEF	PAEGVGAV	41	9	12	19						1503
NEF	GVGAASQDL	45	9	11	17						1504
NEF	GVGAASQDL	45	9	21	33						1505
NEF	GVGAASQDL	45	9	17	27						1506
NEF	GVGAASQDL	45	9	14	22						1507
NEF	GVGAASQDL	45	9	27	42						1508
NEF	GATSSNTAA	63	9	14	22						1509
NEF	ITSSNTAA	64	9	13	20						1510
NEF	TAATNADCA	69	9	12	19						1511
NEF	ATNADCAWL	71	9	12	22						1512
NEF	QAPPAAGV	95	9	17	27						1513
NEF	QAPPAAGV	99	9	56	88						1514
NEF	PLAPMTYKA	102	9	21	33						1515
NEF	MTYKGAIDL	106	9	12	19						1516
NEF	GAFLDSFEL	110	9	10	16						1517
NEF	QAPPAAGV	182	9	20	31						1518
NEF	QAPPAAGV	182	9	35	55						1519
NEF	ILDLSHFL	186	9	34	55						1520
NEF	ILDLSHFL	186	9	19	30						1521
NEF	ITFGWCKFL	221	9	39	61	0.1400	0.1300	0.0022	0.0180	7.2000	1522
NEF	LPVDDPREV	229	9	11	17						1523
NEF	QAPPAAGV	32	10	01	17						1524
NEF	QAPPAAGV	32	10	01	17						1525
NEF	QAPPAAGV	33	10	01	17						1526
NEF	GATSSNTAA	63	10	14	22						1527
NEF	ATSSNTAA	63	10	13	20						1528
NEF	NTAATNADCA	68	10	12	19						1529

Table VH
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
NEF	AATNADCAWL	70	10	12	22						1529
NEF	WLEAGLEEEV	79	15	15	24						1530
NEF	EVGPVPTQV	91	10	40	33						1531
NEF	PLRMTYKAA	102	10	25	31						1532
NEF	PLRMTYKAA	102	10	25	39						1533
NEF	PLRMTYKAA	105	10	12	19						1534
NEF	PLRMTYKAA	105	10	12	19						1535
NEF	LYSKKRQEI	174	10	18	28						1536
NEF	SOKRDILDL	177	10	12	19						1537
NEF	DILDLVYIHT	185	10	12	19						1538
NEF	EILDLVYIHT	185	10	22	14						1539
NEF	EILDLVYIHT	185	10	11	17						1540
NEF	WQNYITGRT	204	10	18	29						1541
NEF	WQNYITGRT	204	10	21	33						1542
NEF	WQNYITGRT	204	10	11	17						1543
NEF	PLTGWCFKL	219	10	39	61	0.0350	0.0058	0.0021	0.0010	0.0400	1544
NEF	PLTGWCFKL	221	10	35	55	0.0170	0.0080	0.0540	0.0640	0.2000	1545
NEF	KLVPVDREV	228	10	11	17						1546
NEF	LLIHQCQIGM	257	10	10	16						1547
NEF	LLIHPCSGHGA	257	10	12	19						1548
NEF	RAEPAADGVA	32	11	01	17						1549
NEF	RAEPAADGVA	32	11	01	17						1550
NEF	RAEPAADGVA	32	11	01	17						1551
NEF	RTEPAAGVGA	32	11	01	17						1552
NEF	QAEPAAGVGA	33	11	01	17						1553
NEF	QAEPAAGVGA	33	11	01	17						1554
NEF	QAEPAAGVGA	33	11	01	17						1555
NEF	QAEPAAGVGA	33	11	01	17						1556
NEF	QAEPAAGVGA	33	11	01	17						1557
NEF	QAEPAAGVGA	33	11	01	17						1558
NEF	GAITSSTIAT	48	11	13	20						1559
NEF	ITSSNTAATN	64	11	12	19						1560
NEF	TAATNADCAWL	69	11	12	19						1561
NEF	TAATNADCAWL	71	11	12	19						1562
NEF	QAEPAAGVGA	83	11	17	22						1563
NEF	QAEPAAGVGA	83	11	17	22						1564
NEF	QAEPAAGVGA	83	11	47	73						1565
NEF	QAEPAAGVGA	100	11	20	31						1566
NEF	FLKEKGGLDL	117	11	26	41						1567
NEF	FLKEKGGLDL	117	11	29	45						1568
NEF	GLYSKKRQEI	173	11	18	28						1569
NEF	LYSKKRQEI	174	11	18	28						1570
NEF	YTGWRHRYPL	207	11	16	26						1571
NEF	YTGWRHRYPL	207	11	16	26						1572
NEF	YTGWRHRYPL	219	11	35	55						1573
NEF	PLTGWCFKL	219	11	10	16						1574
NEF	CLLHPMSQIGM	256	11	10	16						1575
POL	LAFPDGEA	6	8	12	19						1576
POL	LAFPDGEA	6	8	12	19						1577
POL	LAFPDGEA	6	8	16	25						1578
POL	QTRANSIT	21	8	14	22						1579
POL	PTSKRELV	35	8	01	33						1580
POL	PTSKRELV	35	8	01	33						1581
POL	PTSKRELV	36	8	01	33						1582
POL	PTSKRELV	36	8	01	33						1583
POL	GADQKQIV	70	8	01	20						1584

HIV_A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
POL	GTLCPOI	80	8	01	33						1579
POL	PTFNETOI	80	8	01	33						1580
POL	ITLWQREL	90	8	47	73						1581
POL	TLWQRLP	91	8	49	77						1582
POL	WQRLPYI	93	8	21	33						1583
POL	WQRLPYI	93	8	21	33						1584
POL	TKIGGQI	99	8	17	27						1585
POL	TKIGGQI	99	8	11	17						1586
POL	GQIEALL	104	8	10	16						1587
POL	GQIEALL	104	8	34	53						1588
POL	LIEALLDT	106	8	10	16						1589
POL	DTGADDTA	112	8	108	95						1590
POL	TVLFDNL	118	8	61	92						1591
POL	TVLFDNL	118	8	13	20						1592
POL	TVLFDNL	118	8	15	23						1593
POL	GIGGFKV	136	8	64	100						1594
POL	KRQYDQI	142	8	41	64						1595
POL	QYDQI	144	8	10	16						1596
POL	QYDQI	144	8	10	16						1597
POL	EICGRIKAI	152	8	19	30						1598
POL	EICGRIKAI	152	8	24	38						1599
POL	KAIGTVLV	157	8	48	75						1600
POL	GTVLVGP	160	8	60	94						1601
POL	GTVLVGP	160	8	53	83						1602
POL	NIGRNML	170	8	26	41						1603
POL	NIGRNML	170	8	31	48						1604
POL	IGRNMLT	171	8	26	41						1605
POL	IGRNMLT	171	8	30	47						1606
POL	LLTQGGT	176	8	21	33						1607
POL	LLTQGGT	176	8	18	28						1608
POL	LLTQGGT	176	8	16	25						1609
POL	LTQIGCTL	177	8	42	66						1610
POL	LTQIGCTL	177	8	15	23						1611
POL	PISPIETV	187	8	57	89						1612
POL	PVKLKPQM	195	8	56	88						1613
POL	KYVQPLT	207	8	49	77						1614
POL	KYVQPLT	207	8	58	92						1615
POL	KIKALTEI	217	8	28	44						1616
POL	KIKALVEI	217	8	15	23						1617
POL	KALTECT	219	8	12	19						1618
POL	KALVECT	219	8	15	24						1619
POL	KALVECT	219	8	15	24						1620
POL	EMERERK	220	8	42	66						1621
POL	AIKKKOST	251	8	59	92						1622
POL	STKWRKLV	257	8	59	92						1623
POL	KLVDFFEL	262	8	63	98						1624
POL	RTQDFWEV	272	8	55	86						1625
POL	QLGIHPHA	280	8	36	89						1626
POL	QLGIHPHA	280	8	36	89						1627
POL	GLKKKKSV	288	8	52	81						1628

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SIQ ID NO
POL	TVLDVGDA	296	8	58	91						1629
POL	DAFVSPL	302	8	55	86						1630
POL	TAFITSI	317	8	37	58						1631
POL	DAFVSPL	317	8	37	58						1632
POL	GHVQYAV	330	8	52	80						1633
POL	PAIFQSSMT	346	8	42	66						1634
POL	AFQSSMT	347	8	39	61						1635
POL	FOSSMIKI	349	8	38	59						1636
POL	KNTDVI	362	8	14	22						1637
POL	DVIQYM	366	8	18	28						1638
POL	DAFVSPL	366	8	24	38						1639
POL	DLVAGSD	375	8	38	66						1640
POL	YVGSDEI	377	8	58	91						1641
POL	ILLRWGFT	397	8	22	34						1642
POL	ILLRWGFT	397	8	25	39						1643
POL	LLKAWGFT	398	8	23	36						1644
POL	LLKAWGFT	398	8	24	38						1645
POL	LLKAWGFT	410	8	62	97						1646
POL	FLKAGVFL	410	8	61	95						1647
POL	ELIPIKWT	422	8	60	94						1648
POL	WTQPIQL	428	8	28	44						1649
POL	WTQPIVL	428	8	13	20						1650
POL	TVNDIQKL	442	8	62	97						1651
POL	IQKLVGKL	446	8	62	97						1652
POL	TVNDIQKL	446	8	61	95						1653
POL	KLWAGVFL	452	8	11	18						1654
POL	QIVPGIKV	458	8	27	43						1655
POL	QIVPGIKV	458	8	29	45						1656
POL	KVQQLCKL	464	8	19	30						1657
POL	KVRLCKL	464	8	25	40						1658
POL	KLIRGAKA	470	8	25	40						1659
POL	KLIRGAKA	470	8	24	38						1660
POL	LLIRGAKA	471	8	30	47						1661
POL	LLIRGAKA	471	8	24	38						1662
POL	GAKALTDI	474	8	25	39						1663
POL	GTRALTEV	474	8	19	30						1664
POL	ALTDIPL	477	8	21	33						1665
POL	ALTEVPL	477	8	16	25						1666
POL	ALTEVPL	477	8	16	25						1667
POL	LTVEVPL	478	8	24	38						1668
POL	IVPLTEA	481	8	13	20						1669
POL	VPLTEA	481	8	11	17						1670
POL	PLTEAEL	483	8	30	47						1671
POL	ELAENREI	491	8	57	89						1672
POL	LAENREI	492	8	57	89						1673
POL	KQGDQYMT	523	8	35	53						1674
POL	KQGDQYMT	523	8	35	53						1675
POL	YQDPKXIL	534	8	43	67						1676
POL	NKATGKYA	540	8	58	92						1677
POL	KTKQYAKM	542	8	19	30						1678

HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	KTKGYARM	542	8	13	21						1679
POL	RTAIINDV	550	8	11	17						1680
POL	HTNDVKOL	553	8	49	77						1681
POL	DYKQUTEA	556	8	33	52						1682
POL	ETAKYK	560	8	34	50						1683
POL	ETAKYK	560	8	17	13						1684
POL	KIATESIV	566	8	14	22						1685
POL	IATLSIVI	567	8	14	22						1686
POL	SIVIVGKT	571	8	42	66						1687
POL	KLPQKRET	582	8	20	31						1688
POL	KLPQKRET	582	8	16	24						1689
POL	IQENKREA	585	8	15	21						1690
POL	IQENKREA	585	8	27	42						1691
POL	IQENKREA	585	8	11	17						1692
POL	ETWEAWWT	588	8	22	34						1693
POL	ETWEAWWT	588	8	15	23						1694
POL	WTDYWQAT	594	8	4	6						1695
POL	WTDYWQAT	594	8	52	86						1696
POL	WTDYWQAT	594	8	54	86						1697
POL	FNSTPLLV	608	8	57	89						1698
POL	NTPLLVKL	610	8	58	91						1699
POL	LVKLWYQL	614	8	12	19						1700
POL	KLWYQLET	616	8	14	22						1701
POL	YQLKXDPH	619	8	11	17						1702
POL	YQLKXDPH	619	8	11	17						1703
POL	YQLKXDPH	619	8	16	25						1704
POL	QLEKEPHV	620	8	55	86						1705
POL	ETFYVDGA	630	8	30	47						1706
POL	AANRETKL	637	8	36	56						1707
POL	KLGKAGYV	643	8	36	56						1708
POL	KLGKAGYV	643	8	11	17						1709
POL	KVSLIETI	657	8	10	16						1710
POL	VVSLIDIT	658	8	11	17						1711
POL	VVSLIETI	658	8	55	86						1712
POL	TINQKTEL	664	8	22	36						1713
POL	NQKTELIA	666	8	42	66						1714
POL	ELQNIYLA	670	8	16	25						1715
POL	ELQNIYLA	670	8	12	19						1716
POL	LQAIHLAL	671	8	16	25						1717
POL	LQAIYIAL	671	8	12	19						1718
POL	LALQDSQL	676	8	27	42						1719
POL	LALQDSQL	676	8	25	39						1720
POL	LQDSGEIV	678	8	26	41						1721
POL	GLENIVIT	682	8	61	95						1722
POL	IVTDSQVA	687	8	59	92						1723
POL	VTDISQYAL	688	8	39	59						1724
POL	SOYALGII	691	8	24	38						1725
POL	NOHEQL	711	8	20	31						1726
POL	NOHEQL	711	8	20	31						1727
POL	SQUEQLI	711	8	20	31						1728

HIV A02 Super Nont Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
POL	QLIKKKY	716	8	28	44						1729
POL	WVPAIKGI	727	8	63	98						1730
POL	GIGGNFQV	733	8	59	92						1731
POL	QVQDKLNSA	739	8	16	25						1732
POL	SAGIRKVL	745	8	15	23						1733
POL	GIRAVLFL	747	8	51	80						1734
POL	KLILKLV	750	8	50	78						1735
POL	FLDGIKKA	753	8	55	86						1736
POL	AMASDPNL	773	8	45	70						1737
POL	IVAKKEV	782	8	26	41						1738
POL	PVVAKEIV	782	8	28	44						1739
POL	IVAKEIVA	783	8	26	41						1740
POL	IVAKKEIV	783	8	26	41						1741
POL	CDLKGKAM	795	8	51	83						1742
POL	QVQKSPGI	805	8	57	89						1743
POL	GIWQLDCT	811	8	59	92						1744
POL	WQLDCTIL	813	8	61	95						1745
POL	CHILEGKI	817	8	35	55						1746
POL	ILLEGKIV	817	8	36	56						1747
POL	ILLEGKIL	819	8	31	48						1748
POL	ILLEGKIL	819	8	23	36						1749
POL	ILVAVIV	824	8	30	47						1750
POL	ILVAVIV	824	8	24	38						1751
POL	ILVAVIVA	825	8	54	84						1752
POL	ILVAVIVA	825	8	54	84						1753
POL	PAEIGDET	842	8	58	91						1754
POL	GOEIAVYH	846	8	31	48						1755
POL	GQELAVFL	846	8	26	41						1756
POL	TAYTLKL	849	8	32	50						1757
POL	TAYTLKL	849	8	27	42						1758
POL	FTSAVKA	873	8	28	44						1759
POL	FTSTVKA	873	8	14	22						1760
POL	AACVWAGI	880	8	32	50						1761
POL	GKGEFGI	886	8	22	34						1762
POL	GKGEFGI	886	8	11	17						1763
POL	QKGEFGI	886	8	55	89						1764
POL	DQAEHLKT	919	8	44	73						1765
POL	QAEHLKT	919	8	13	20						1766
POL	QAEHLKTA	920	8	59	92						1767
POL	ILKTAVQM	923	8	57	89						1768
POL	KTAQVQAV	925	8	57	89						1769
POL	QAEHLKTA	925	8	40	67						1770
POL	RVQIAT	951	8	29	44						1771
POL	RVQIAT	951	8	12	19						1772
POL	IASDIQT	955	8	15	23						1773
POL	IATDIQT	955	8	41	64						1774
POL	LQKQIKI	965	8	13	20						1775
POL	LQKQIKI	965	8	26	46						1776
POL	LLWKGKGA	993	8	62	97						1777

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*001	A*0202	A*0203	A*0206	A*5802	SEQ ID NO
POL	VIQNSDI	1003	8	37	58						1779
POL	VIQNSDI	1003	8	12	9						1780
POL	VIQNSDI	1003	8	12	11						1781
POL	VIQNSDI	1003	8	11	17						1782
POL	VIQNSDI	1003	8	44	69						1783
POL	VIQNSDI	1003	8	44	69						1784
POL	VIQNSDI	1003	8	44	69						1785
POL	VIQNSDI	1003	8	44	69						1786
POL	VIQNSDI	1003	8	44	69						1787
POL	VIQNSDI	1003	8	44	69						1788
POL	VIQNSDI	1003	8	44	69						1789
POL	VIQNSDI	1003	8	44	69						1790
POL	VIQNSDI	1003	8	44	69						1791
POL	VIQNSDI	1003	8	44	69						1792
POL	VIQNSDI	1003	8	44	69						1793
POL	VIQNSDI	1003	8	44	69						1794
POL	VIQNSDI	1003	8	44	69						1795
POL	VIQNSDI	1003	8	44	69						1796
POL	VIQNSDI	1003	8	44	69						1797
POL	VIQNSDI	1003	8	44	69						1798
POL	VIQNSDI	1003	8	44	69						1799
POL	VIQNSDI	1003	8	44	69						1800
POL	VIQNSDI	1003	8	44	69						1801
POL	VIQNSDI	1003	8	44	69						1802
POL	VIQNSDI	1003	8	44	69						1803
POL	VIQNSDI	1003	8	44	69						1804
POL	VIQNSDI	1003	8	44	69						1805
POL	VIQNSDI	1003	8	44	69						1806
POL	VIQNSDI	1003	8	44	69						1807
POL	VIQNSDI	1003	8	44	69						1808
POL	VIQNSDI	1003	8	44	69						1809
POL	VIQNSDI	1003	8	44	69						1810
POL	VIQNSDI	1003	8	44	69						1811
POL	VIQNSDI	1003	8	44	69						1812
POL	VIQNSDI	1003	8	44	69						1813
POL	VIQNSDI	1003	8	44	69						1814
POL	VIQNSDI	1003	8	44	69						1815
POL	VIQNSDI	1003	8	44	69						1816
POL	VIQNSDI	1003	8	44	69						1817
POL	VIQNSDI	1003	8	44	69						1818
POL	VIQNSDI	1003	8	44	69						1819
POL	VIQNSDI	1003	8	44	69						1820
POL	VIQNSDI	1003	8	44	69						1821
POL	VIQNSDI	1003	8	44	69						1822
POL	VIQNSDI	1003	8	44	69						1823
POL	VIQNSDI	1003	8	44	69						1824
POL	VIQNSDI	1003	8	44	69						1825
POL	VIQNSDI	1003	8	44	69						1826
POL	VIQNSDI	1003	8	44	69						1827
POL	VIQNSDI	1003	8	44	69						1828

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SIQ ID NO
POL	FAIRKDDST	250	9	59	92						1829
POL	TDFPWEVOL	273	9	55	86						1830
POL	QLQHIFVA	279	9	44	77						1831
POL	GLVQVQVVA	280	9	46	77						1832
POL	VTYLDVQGA	295	9	57	89						1833
POL	DYGDVAFSV	299	9	54	84						1834
POL	YTAFTIPSI	316	9	37	58	0.0005	0.7100	1.1000	0.3300	2.4000	1835
POL	YTAFTIPST	316	9	13	20	0.1900					1836
POL	YTAFTIPST	316	9	17	20						1837
POL	THSNNET	320	9	11	22						1838
POL	THSNNET	320	9	11	22						1839
POL	STNNETPGI	323	9	32	50						1840
POL	STNNETPGI	323	9	11	17						1841
POL	GRYQVNVL	330	9	52	81	0.0001					1842
POL	PGWKGSPA	339	9	59	92						1843
POL	PAHQSSMT	346	9	39	61						1844
POL	PAHQSSMT	346	9	38	61						1845
POL	VTQYMDL	368	9	51	80	0.0004					1846
POL	YOYMDLIV	370	9	61	95						1847
POL	DLEIGQIRA	381	9	28	44						1848
POL	DLEIGQIRT	381	9	21	33						1849
POL	EGGIRAKI	383	9	26	41						1850
POL	EGGIRAKI	383	9	21	33						1851
POL	KIELRRIH	390	9	19	30						1852
POL	KIELRRIH	390	9	17	27	0.0001					1853
POL	HLKRWGFT	397	9	22	34						1854
POL	HLKRWGFTT	397	9	24	38						1855
POL	ELHPKRWTV	422	9	60	94	0.0001					1856
POL	ELHPKRWTV	422	9	13	20						1857
POL	VLEPKDWT	434	9	13	20						1858
POL	WTVNDQKL	441	9	62	97	0.0001					1859
POL	TVNDQKLV	442	9	61	95						1860
POL	DQKLQKLV	445	9	62	97	0.0001					1861
POL	KLQKLINVA	448	9	91	95	0.0040	0.3400	1.7000	0.0930	0.0130	1862
POL	KLQKLINVA	448	9	27	45	0.0020					1863
POL	WASQYPI	455	9	29	45						1864
POL	SOYAGIRV	457	9	27	42						1865
POL	SOYPIGVK	457	9	27	42						1866
POL	YAGRVKOL	460	9	18	28						1867
POL	KVKQLCKLL	464	9	28	44						1868
POL	KVKQLCKLL	464	9	18	28						1869
POL	QLCKLLRG	467	9	25	39						1870
POL	QLCKLLRG	467	9	21	33						1871
POL	KLIRGAKAL	470	9	25	40						1872
POL	KLIRGAKAL	470	9	24	38	0.0069					1873
POL	KLIRGAKALT	471	9	30	47						1874
POL	KLIRGAKALT	471	9	24	38						1875
POL	GAKALDIV	474	9	11	17						1876
POL	GTRALHEVI	474	9	11	17						1877
POL	KALTDIVPL	476	9	21	33						1878
POL	KALTDIVPL	476	9	16	25						1879

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ*0201	Δ*0202	Δ*0203	Δ*0206	Δ*Δ002	Seq-ID NO
POI	ALTDVPLT	477	9	21	33						1879
POI	ALTDVPLT	477	9	16	25						1880
POI	DVPLTEEA	480	9	13	20						1881
POI	EVPLTEEA	480	9	11	17						1882
POI	LYTEAELE	484	9	37	58						1883
POI	ELAEIREIL	491	9	57	89						1884
POI	ELAEIRNOV	498	9	41	64	0.0001					1885
POI	GLAEIRNOV	502	9	39	59	0.0035					1886
POI	GLAEIRNOV	523	9	25	39						1887
POI	CGQQTWYGI	523	9	25	39						1888
POI	YAKMRETAIT	546	9	10	16						1889
POI	YAKMRETAIT	546	9	13	20						1890
POI	YAKMRETAIT	546	9	13	20						1891
POI	ITRDYKQLT	553	9	43	67	0.0001					1892
POI	DVQLKTEAV	556	9	33	52	0.0007					1893
POI	ITRDYKQLT	556	9	34	57						1894
POI	ITRDYKQLT	560	9	14	22						1895
POI	VQKLTESI	564	9	14	22						1896
POI	KIATLSIVI	566	9	14	22						1897
POI	KTPKFLPI	577	9	17	27						1898
POI	KTPKFLPI	577	9	29	45						1899
POI	PKQETWEA	584	9	15	23						1900
POI	PKQETWEA	584	9	17	24						1901
POI	PLKVLKQL	613	9	54	84	0.0002					1902
POI	YGLEKEPIV	619	9	16	25						1903
POI	YVGAFTYV	626	9	28	44	0.0099					1904
POI	EIFYVDGAA	630	9	51	80						1905
POI	GAANKREKL	636	9	30	47	0.0002					1906
POI	YVIRHRSKY	649	9	30	46						1907
POI	KVVSUFTTI	657	9	11	17						1908
POI	LDTITNQKT	661	9	19	30						1909
POI	LDTITNQKT	661	9	25	39						1910
POI	EDTNQKTEL	663	9	26	41						1911
POI	EDTNQKTEL	663	9	29	45						1912
POI	EDTNQKTEL	666	9	12	19						1913
POI	NKTELQIAI	666	9	42	68						1914
POI	KTELQIAIHL	668	9	15	23						1915
POI	KTELQIAIYL	668	9	12	19						1916
POI	ELQAIIHAL	670	9	16	25	0.0001					1917
POI	ELQAIIHAL	670	9	12	19						1918
POI	ALQDSGSEV	675	9	23	38	0.0005					1919
POI	ALQDSGSEV	677	9	24	39	0.0083					1920
POI	ALQDSGSEV	677	9	25	39						1921
POI	NVITDSQYA	686	9	61	95						1922
POI	NVITDSQYAL	687	9	59	92	0.0024					1923
POI	LVNCHIEQL	709	9	19	30						1924
POI	LVNCHIEQL	709	9	19	30						1925
POI	LVNCHIEQL	713	9	15	24						1926
POI	LKVLKVVYL	717	9	35	55						1927
POI	KVYLAWPVA	722	9	20	32	0.0001					

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	EQVDLWSA	738	9	16	25						1929
POL	LYSGRRKY	743	9	15	23	0.0001					1930
POL	YSGRRKY	743	9	15	23						1931
POL	RAMASDNI	772	9	41	66	0.0230	0.0370	0.0004	0.0710	0.0130	1932
POL	PVAKREVA	782	9	25	39						1933
POL	PVAKREVA	782	9	25	39						1934
POL	VASCDKQL	789	9	43	67						1935
POL	VASCDKQL	789	9	43	67						1936
POL	QYVCSGHI	804	9	57	89						1937
POL	QYVCSGHI	804	9	57	89						1938
POL	CTHLSEKVI	817	9	22	41						1939
POL	CTHLSEKVI	817	9	22	41						1940
POL	HLEGRKILV	819	9	31	48	0.0010					1941
POL	HLEGRKILV	819	9	31	48						1942
POL	KILLVAVIV	823	9	30	47	0.0006					1943
POL	KILLVAVIV	823	9	30	47	0.0002					1944
POL	KILLVAVIV	823	9	30	47	0.0001					1945
POL	VILVAVIVA	824	9	20	36						1946
POL	VILVAVIVA	824	9	20	36						1947
POL	AVIVASCVI	828	9	53	83						1948
POL	IVASGVIEA	830	9	52	81						1949
POL	IVASGVIEA	830	9	52	81						1950
POL	IVASGVIEA	830	9	52	81						1951
POL	IVASGVIEA	830	9	52	81						1952
POL	PAETGQETFA	842	9	62	98						1953
POL	PAETGQETFA	842	9	62	98						1954
POL	GOETVYFL	846	9	31	48						1955
POL	GOETVYFL	846	9	31	48						1956
POL	QRETAVFLL	846	9	26	41						1957
POL	ETAYFLKL	848	9	31	48						1958
POL	ETAYFLKL	848	9	31	48						1959
POL	ETAYFLKL	848	9	31	48						1960
POL	ETAYFLKL	848	9	31	48						1961
POL	TAYFLKLA	849	9	22	40						1962
POL	TAYFLKLA	849	9	22	40						1963
POL	LAGRAPVVKY	856	9	14	22						1964
POL	LAGRAPVVKY	856	9	14	22						1965
POL	LAGRAPVVKY	856	9	14	22						1966
POL	ITDINGSNFT	866	9	49	77						1967
POL	ITDINGSNFT	866	9	49	77						1968
POL	ITDINGSNFT	866	9	49	77						1969
POL	ITDINGSNFT	866	9	49	77						1970
POL	FTSTVKA	873	9	11	22						1971
POL	FTSTVKA	873	9	11	22						1972
POL	AVKACACWA	877	9	32	50						1973
POL	AVKACACWA	877	9	32	50						1974
POL	KAACACWAGI	879	9	31	49	0.0180	0.0040	0.1200	0.0230	0.0150	1975
POL	KAACACWAGI	879	9	31	49						1976
POL	KAACACWAGI	879	9	31	49						1977
POL	KAACACWAGI	879	9	31	49						1978
POL	ELKIKIGOV	902	9	48	75						1979
POL	ELKIKIGOV	902	9	48	75						1980
POL	ELKIKIGOV	902	9	48	75						1981
POL	ELKIKIGOV	902	9	48	75						1982
POL	IGQVREDQA	913	9	44	69	0.0001					1983
POL	IGQVREDQA	913	9	44	69						1984
POL	IGQVREDQA	913	9	44	69						1985
POL	IGQVREDQA	913	9	44	69						1986
POL	QVRDJAHEL	916	9	13	20						1987
POL	QVRDJAHEL	916	9	13	20	0.0001					1988
POL	QVRDJAHEL	916	9	13	20						1989
POL	QVRDJAHEL	916	9	13	20						1990
POL	QVRDJAHEL	916	9	13	20						1991
POL	QVRDJAHEL	916	9	13	20						1992
POL	QVRDJAHEL	916	9	13	20						1993
POL	QVRDJAHEL	916	9	13	20						1994
POL	QVRDJAHEL	916	9	13	20						1995
POL	QVRDJAHEL	916	9	13	20						1996
POL	QVRDJAHEL	916	9	13	20						1997
POL	QVRDJAHEL	916	9	13	20						1998
POL	QVRDJAHEL	916	9	13	20						1999
POL	QVRDJAHEL	916	9	13	20						2000
POL	QVRDJAHEL	916	9	13	20						2001
POL	QVRDJAHEL	916	9	13	20						2002
POL	QVRDJAHEL	916	9	13	20						2003
POL	QVRDJAHEL	916	9	13	20						2004
POL	QVRDJAHEL	916	9	13	20						2005
POL	QVRDJAHEL	916	9	13	20						2006
POL	QVRDJAHEL	916	9	13	20						2007
POL	QVRDJAHEL	916	9	13	20						2008
POL	QVRDJAHEL	916	9	13	20						2009
POL	QVRDJAHEL	916	9	13	20						2010
POL	QVRDJAHEL	916	9	13	20						2011
POL	QVRDJAHEL	916	9	13	20						2012
POL	QVRDJAHEL	916	9	13	20						2013
POL	QVRDJAHEL	916	9	13	20						2014
POL	QVRDJAHEL	916	9	13	20						2015
POL	QVRDJAHEL	916	9	13	20						2016
POL	QVRDJAHEL	916	9	13	20						2017
POL	QVRDJAHEL	916	9	13	20						2018
POL	QVRDJAHEL	916	9	13	20						2019
POL	QVRDJAHEL	916	9	13	20						2020
POL	QVRDJAHEL	916	9	13	20						2021
POL	QVRDJAHEL	916	9	13	20						2022
POL	QVRDJAHEL	916	9	13	20						2023
POL	QVRDJAHEL	916	9	13	20						2024
POL	QVRDJAHEL	916	9	13	20						2025
POL	QVRDJAHEL	916	9	13	20						2026
POL	QVRDJAHEL	916	9	13	20						2027
POL	QVRDJAHEL	916	9	13	20						2028
POL	QVRDJAHEL	916	9	13	20						2029
POL	QVRDJAHEL	916	9	13	20						2030
POL	QVRDJAHEL	916	9	13	20						2031
POL	QVRDJAHEL	916	9	13	20						2032
POL	QVRDJAHEL	916	9	13	20						2033
POL	QVRDJAHEL	916	9	13	20						2034
POL	QVRDJAHEL	916	9	13	20						2035
POL	QVRDJAHEL	916	9	13	20						2036
POL	QVRDJAHEL	916	9	13	20						2037
POL	QVRDJAHEL	916	9	13	20						2038
POL	QVRDJAHEL	916	9	13	20						2039
POL	QVRDJAHEL	916	9	13	20						2040
POL	QVRDJAHEL	916	9	13	20						2041
POL	QVRDJAHEL	916	9	13	20						2042
POL	QVRDJAHEL	916	9	13	20						2043
POL	QVRDJAHEL	916	9	13	20						2044
POL	QVRDJAHEL	916	9	13	20						2045
POL	QVRDJAHEL	916	9	13	20						2046
POL	QVRDJAHEL	916	9	13	20						2047
POL	QVRDJAHEL	916	9	13	20						2048
POL	QVRDJAHEL	916	9	13	20						2049
POL	QVRDJAHEL	916	9	13	20						2050
POL	QVRDJAHEL	916	9	13	20						2051
POL	QVRDJAHEL	916	9	13	20						2052
POL	QVRDJAHEL	916	9	13	20						2053
POL	QVRDJAHEL	916	9	13	20						2054
POL	QVRDJAHEL	916	9	13	20						2055
POL	QVRDJAHEL	916	9	13	20						2056
POL	QVRDJAHEL	916	9	13	20						2057
POL	QVRDJAHEL	916	9	13	20						2058
POL	QVRDJAHEL	916	9	13	20						2059
POL	QVRDJAHEL	916	9	13	20						2060
POL	QVRDJAHEL	916	9	13	20						2061
POL	QVRDJAHEL	916	9	13	20						2062
POL	QVRDJAHEL	916	9	13	20						2063
POL	QVRDJAHEL	916	9	13	20						2064
POL	QVRDJAHEL	916	9	13	20						2065
POL	QVRDJAHEL	916	9	13	20						2066
POL	QVRDJAHEL	916	9	13	20						2067
POL	QVRDJAHEL	916	9	13	20						2068
POL	QVRDJAHEL	916	9	13	20						2069
POL	QVRDJAHEL	916	9	13	20						2070
POL	QVRDJAHEL	916	9	13	20						2071
POL	QVRDJAHEL	916	9	13	20						2072
POL	QVRDJAHEL	916	9	13	20						2073
POL	QVRDJAHEL	916	9	13	20						2074
POL	QVRDJAHEL	916	9	13	20						2075
POL	QVRDJAHEL	916	9	13	20						2076
POL	QVRDJAHEL	916	9	13	20						2077
POL	QVRDJAHEL	916	9	13	20						2078
POL	QVRDJAHEL	916	9	13	20						2079
POL	QVRDJAHEL	916	9	13	20						2080
POL	QVRDJAHEL	916	9	13							

Table VIII
HIV_A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SEQ ID NO
POL	IDIATDI	952	9	29	45						1979
POL	IVDIATDI	952	9	12	19						1980
POL	DIASDIQT	954	9	15	23						1981
POL	DIATDIQT	954	9	40	63						1982
POL	DIATDIQT	954	9	40	63						1983
POL	QTKELQKDI	961	9	46	72						1984
POL	ELQKQIKI	964	9	13	21						1985
POL	ELQKQIKI	964	9	34	54						1986
POL	IKIQNFRV	969	9	12	19						1987
POL	IKIQNFRV	969	9	36	57						1988
POL	IKIQNFRV	969	9	36	57						1989
POL	PLWKGFAKL	985	9	19	30						1990
POL	KLWKGEGA	992	9	60	94	0.0002					1991
POL	LLWKGEGA	993	9	62	97	0.0230					1992
POL	VVIDNSDI	1002	9	37	58	0.0001					1993
POL	VVIDNSDI	1002	9	38	59						1994
POL	IQDSEIKV	1004	9	38	59						1995
POL	IQDSEIKV	1004	9	38	59						1996
POL	VVPRKAKI	1012	9	51	80						1997
POL	VVPRKAKI	1012	9	11	17						1998
POL	IKIDYQDM	1030	9	50	71						1999
POL	IKIDYQDM	1030	9	50	71						2000
POL	KQAGDDCV	1036	9	44	69	0.0001					2001
POL	KQAGDDCV	1036	9	44	69						2002
POL	KAREFSSEQ	12	10	10	16						2003
POL	KAREFSSEQ	12	10	16	25						2004
POL	RANSPTRREL	26	10	16	25						2005
POL	RANSPTRREL	26	10	16	25						2006
POL	STNSPTSRRL	33	10	01	33						2007
POL	SQTRANSITT	34	10	01	33						2008
POL	RANSPSSREL	35	10	01	33						2009
POL	RANSPTRREL	37	10	01	50						2010
POL	GAASLSQIT	79	10	01	17						2011
POL	GAASLSQIT	79	10	01	17						2012
POL	AISLSQIT	80	10	01	33						2013
POL	GLNCPQITL	80	10	01	33						2014
POL	PTFNFPQITL	80	10	01	33						2015
POL	QITLLWQRL	88	10	47	73						2016
POL	QITLLWQRL	88	10	47	73						2017
POL	ITLWQRLVT	90	10	37	58						2018
POL	ITLWQRLVT	91	10	21	33						2019
POL	ITLWQRLVT	91	10	18	28						2020
POL	ITLWQRLVT	91	10	14	22						2021
POL	WQRLVTIKI	93	10	14	22						2022
POL	WQRLVTIKI	93	10	14	22						2023
POL	ITLWQRLVT	97	10	13	20						2024
POL	ITLWQRLVT	97	10	13	20						2025
POL	KIGGLKEAL	101	10	23	36	0.0002					2026
POL	QGLLEALLDT	104	10	10	16						2027
POL	QGLLEALLDT	104	10	34	53						2028
POL	QGLLEALLDT	106	10	10	16						2029
POL	LIBALLDTGA	106	10	10	16						2030
POL	LIBALLDTGA	106	10	10	16						2031
POL	LIBALLDTGA	110	10	63	98	0.0005					2032
POL	LLDTGADTV	110	10	63	98						2033

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	GADDTVLEDI	114	10	15	23						2029
POL	GADDTVLEDI	114	10	18	28						2030
POL	GADDTVLERM	114	10	17	55						2031
POL	NLPKWKPKPM	124	10	35	55						2032
POL	KMGIGTGFI	132	10	62	97						2033
POL	FIKVRQYDQI	140	10	41	64						2034
POL	KVRQYDQILI	142	10	20	31						2035
POL	KVRQYDQIMI	142	10	13	20	0.0290	0.0790	2.1000	0.0048	0.0120	2036
POL	KVRQYDQIMI	142	10	20	31						2037
POL	ROZGQHEI	144	10	12	19						2038
POL	LIIEICGKKA	149	10	13	20						2039
POL	LIIEICGKKA	150	10	10	16						2040
POL	LIIEICGKKA	150	10	13	20						2041
POL	LIIEICGKKA	152	10	19	30						2042
POL	EICGKKAIGT	152	10	24	38						2043
POL	EICGKKAIGT	158	10	52	81						2044
POL	GVLMVGPVIV	160	10	53	83						2045
POL	VLVGPVIVNI	162	10	52	81	0.0025					2046
POL	PVNIIGRNLL	163	10	26	41	0.0015					2047
POL	PVNIIGRNLL	168	10	26	41	0.0002					2048
POL	IGRNLLCTQI	171	10	21	33						2049
POL	IGRNLLCTQI	171	10	18	28						2050
POL	IGRNLLCTQI	171	10	11	17						2051
POL	NLLTQIGCTL	175	10	21	33	0.0007					2052
POL	NMLTQIGCTL	175	10	18	28						2053
POL	NMLTQIGCTL	175	10	10	16						2054
POL	QIGCTLNPII	179	10	41	64	0.0025					2055
POL	QIGCTLNPII	179	10	16	25						2056
POL	QIGCTLNPII	182	10	60	94	0.0340					2057
POL	PSPIPIIVIV	187	10	54	88	0.0002					2058
POL	PSPIPIIVIV	191	10	54	88						2059
POL	QWPLITEKI	209	10	56	88	0.0002					2060
POL	QWPLITEKI	212	10	54	84						2061
POL	QWPLITEKI	213	10	37	58						2062
POL	QWPLITEKI	213	10	15	23						2063
POL	QWPLITEKI	217	10	12	19						2064
POL	KIKALVICTI	219	10	15	24						2065
POL	KALVEICTEM	225	10	27	42						2066
POL	CTEMLEKGI	225	10	27	42						2067
POL	KIGPEVPYNT	238	10	50	78						2068
POL	RIGPENPYNT	238	10	10	16						2069
POL	QWPLITEKI	272	10	53	83						2070
POL	QWPLITEKI	272	10	54	84						2071
POL	QWPLITEKI	286	10	54	84						2072
POL	QWPLITEKI	286	10	50	78						2073
POL	QWPLITEKI	288	10	49	77	0.0002					2074
POL	SVTVLDVGDA	294	10	57	89						2075
POL	SVTVLDVGDA	308	10	30	50	0.0002					2076
POL	PLIKDRKRYT	319	10	30	50						2077
POL	PLIKDRKRYT	319	10	37	58						2078

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	FTHSTNNET	319	10	13	20						2079
POL	PQGWKGSFAL	339	10	59	92						2080
POL	AFQSSMTKIL	347	10	36	56	0.0007					2081
POL	QVQVQVQVQV	367	10	46	91	0.0001					2082
POL	DIYVGSDEL	375	10	58	91						2083
POL	GOIRAKIEEL	385	10	25	39						2084
POL	GOIRAKIEEL	385	10	20	31						2085
POL	KIEELRHILL	390	10	19	30						2086
POL	KIEELRHILL	390	10	17	27						2087
POL	PEKEDSWTV	410	10	12	19	0.0002					2088
POL	PEKEDSWTV	410	10	62	92						2089
POL	IQEPEPHLWM	410	10	19	30						2090
POL	IQEPEPHLWM	410	10	62	92						2091
POL	IQEPEPHLWM	410	10	13	20						2092
POL	IVLPEKDSWT	433	10	13	20						2093
POL	QLPEKDSWT	434	10	13	20	0.0056					2094
POL	QLPEKDSWT	434	10	13	20	0.0001					2095
POL	WLNWASVLA	452	10	41	55	0.0230	0.0011	0.0250	0.0006	0.0130	2096
POL	KLWVQVQLCL	462	10	28	44						2097
POL	GKVRQLCL	462	10	18	28						2098
POL	KQLCKLLRGA	466	10	12	19						2099
POL	KQLCKLLRGT	466	10	14	22						2100
POL	KLKGLKLL	466	10	13	22						2101
POL	KLKGLKLL	466	10	22	40						2102
POL	KLKGLKLL	466	10	24	38						2103
POL	KALTDVPLT	470	10	21	33						2104
POL	KALTDVPLT	476	10	16	25						2105
POL	KALTDVPLT	476	10	16	25						2106
POL	IVLPEEDEL	481	10	13	20						2107
POL	IVLPEEDEL	481	10	17	27						2108
POL	IVLPEEDEL	481	10	30	47						2109
POL	IVLPEEDEL	481	10	36	56						2110
POL	IVLPEEDEL	481	10	36	56						2111
POL	IVLPEEDEL	481	10	36	56						2112
POL	IVLPEEDEL	481	10	36	56						2113
POL	IVLPEEDEL	481	10	36	56						2114
POL	IVLPEEDEL	481	10	36	56						2115
POL	IVLPEEDEL	481	10	36	56						2116
POL	IVLPEEDEL	481	10	36	56						2117
POL	IVLPEEDEL	481	10	36	56						2118
POL	IVLPEEDEL	481	10	36	56						2119
POL	IVLPEEDEL	481	10	36	56						2120
POL	IVLPEEDEL	481	10	36	56						2121
POL	IVLPEEDEL	481	10	36	56						2122
POL	IVLPEEDEL	481	10	36	56						2123
POL	IVLPEEDEL	481	10	36	56						2124
POL	IVLPEEDEL	481	10	36	56						2125
POL	IVLPEEDEL	481	10	36	56						2126
POL	IVLPEEDEL	481	10	36	56						2127
POL	IVLPEEDEL	481	10	36	56						2128

Table VIII
HIV A02 Sugar-Modified Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	WTDVWQAQTWI	594	10	14	22						2129
POL	WTEVWQAQTWI	594	10	24	38						2130
POL	WTEVWQAQTWI	602	10	24	81	0.0013					2131
POL	WTEVWQAQTWI	602	10	30	81						2132
POL	FVNTPLVYKL	608	10	54	86	0.0002					2133
POL	LVKLVYQLET	614	10	11	17						2134
POL	PVGAETPVGA	620	10	16	25						2135
POL	QLEKEPVGA	625	10	28	44						2136
POL	GAETFYVGA	628	10	48	75						2137
POL	GVGAEVYV	633	10	35	55						2138
POL	ETKLGAQYV	641	10	35	55						2139
POL	VYDRGRQKV	649	10	29	45	0.0002					2140
POL	VYDRGRQKV	650	10	28	44						2141
POL	RQVYSLTET	655	10	10	16						2142
POL	SLTDITNQT	660	10	11	17						2143
POL	SLTETINQT	660	10	19	30						2144
POL	SLTETINQT	664	10	12	19						2145
POL	TLNQTEFLDA	664	10	42	66						2146
POL	KTELQAIYLA	668	10	15	23						2147
POL	KTELQAIYLA	668	10	12	19						2148
POL	LALQDSGLEV	676	10	27	42	0.0006					2149
POL	LALQDSGLEV	676	10	25	39						2150
POL	LQDSGLEVNI	678	10	27	42						2151
POL	LVSSGIRKYL	680	10	24	39						2152
POL	NVDSQYALGI	686	10	59	92	0.0004					2153
POL	VDSQYALGI	688	10	58	91						2154
POL	SVYALGIQA	691	10	58	91						2155
POL	AQPDKSESEL	700	10	36	56						2156
POL	ELVNIQHEQL	708	10	18	28						2157
POL	ELVNIQHEQL	708	10	19	30						2158
POL	ELVNIQHEQL	708	10	19	30						2159
POL	LVSSGIRKYL	709	10	19	30						2160
POL	QIKKEKXYVL	716	10	28	44	0.0006					2161
POL	LIRKEKXYLA	717	10	20	31						2162
POL	LAWVTAIRGI	725	10	22	34						2163
POL	QVDKLVSAGI	739	10	15	23						2164
POL	QVDKLVSAGI	739	10	15	23						2165
POL	QVDKLVSAGI	742	10	15	23	0.0074					2166
POL	KLVSAGIRKYL	742	10	26	41						2167
POL	LVSSGIRKYL	743	10	15	23	0.0002					2168
POL	LVSSGIRKYL	743	10	26	41						2169
POL	SAGIRKYLFL	745	10	15	23						2170
POL	VIFLDGIDKA	751	10	51	80	0.0007					2171
POL	LVSSGIRKYL	774	10	25	34						2172
POL	LVSSGIRKYL	774	10	25	34	0.0800	0.1900	0.1800	0.1100	2.2000	2173
POL	MLPPVAKEL	779	10	26	41						2174
POL	MLPPVAKEL	779	10	27	42	0.0007					2175
POL	IVASCDKCOL	788	10	43	62	0.0006					2176
POL	GIWQLDCTHL	811	10	59	92	0.0003					2177
POL	CTILLEGKHL	817	10	31	48						2178

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	CTILFGKVIL	817	10	23	36						2179
POL	ILEGKQILVA	819	10	21	36						2180
POL	ILEGKQILVA	819	10	21	36						2181
POL	KVILVAVIVA	823	10	30	47						2182
POL	KVILVAVIVA	823	10	22	34						2183
POL	VAVHVASGYI	827	10	53	83						2184
POL	VASGVIEAEV	831	10	52	81						2185
POL	VIPAEITQGET	840	10	58	91						2186
POL	ETGQETAYFL	844	10	31	48						2187
POL	ETAYFLIKLA	848	10	26	41						2188
POL	ETAYFLIKLA	848	10	27	48						2189
POL	ILKLAGRPVY	853	10	34	53						2190
POL	ILKLAGRPVY	853	10	25	39	0.0004					2191
POL	KLGRWPVTK	855	10	14	22						2192
POL	KLGRWPVTK	855	10	30	47						2193
POL	LAGRWPVVKI	856	10	13	20						2194
POL	LAGRWPVVKI	856	10	22	34						2195
POL	AAVKAACWVA	876	10	28	34						2196
POL	TTVKAACWVA	886	10	14	22						2197
POL	WAGIQEFGI	884	10	21	33						2198
POL	WAGIQEFGI	884	10	11	17						2199
POL	POSQGVNESH	897	10	53	83						2200
POL	GVESNMKEL	901	10	48	75						2201
POL	SMNRELKII	905	10	53	83						2202
POL	KIQGVYRQQA	912	10	43	67						2203
POL	KIQGVYRQQA	912	10	13	20						2204
POL	GGVYRQQAELL	915	10	44	70						2205
POL	GGVYRQQAELL	915	10	13	20						2206
POL	EQNEHLKFAV	919	10	46	72						2207
POL	EQNEHLKFAV	919	10	13	20						2208
POL	ILKTAQVMAV	923	10	57	89	0.0005					2209
POL	KTAQVMAVFI	925	10	56	88	0.0002					2210
POL	SAGERIDPH	947	10	41	64						2211
POL	SAGERIDPH	947	10	14	22						2212
POL	RIDIADSI	951	10	22	34						2213
POL	RIDIADSI	951	10	20	29						2214
POL	IASHUTIKEL	951	10	12	19						2215
POL	IASHUTIKEL	956	10	14	22						2216
POL	IATDITOKEL	956	10	35	55						2217
POL	IYKELQKQI	960	10	44	69						2218
POL	QTKELQKQI	961	10	10	16						2219
POL	QTKELQKQIT	961	10	32	50						2220
POL	QIKIQNFRV	968	10	12	19	0.0002					2221
POL	QIKIQNFRV	968	10	55	85						2222
POL	PIWAGFPACKL	983	10	35	55						2223
POL	PIWAGFPACKL	983	10	18	28						2224
POL	KLWKGEGAV	992	10	60	94	0.0006					2225
POL	KLWKGEGAV	992	10	60	94	0.0360					2226
POL	LLWKGEGAV	993	10	61	95						2227
POL	AVVICDSDSI	1000	10	37	58						2228

Table VIII
 HIV A02 Super-Motif Epitopes with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	AVVQDNSEI	1000	10	12	19						2229
POL	VIQDN-SDIK	1003	10	37	58						2230
POL	VIQDN-SEIK	1003	10	12	19						2231
POL	IQDNSEIKV	1004	10	38	59						2232
POL	IQDNSEIKVV	1004	10	39	60						2233
POL	IKVYPRKAA	1009	10	12	20						2234
POL	EIKVYPRKAA	1009	10	13	20						2235
POL	KVYPRKAKI	1011	10	51	80						2236
POL	KVYPRKVKI	1011	10	11	17						2237
POL	VVPRKAKII	1012	10	50	78						2238
POL	VVPRKVKII	1012	10	11	17						2239
POL	KIKDYGRQM	1019	10	10	17						2240
POL	KIKDYGRQMI	1019	10	50	78						2241
POL	IKDYGRKMA	1020	10	11	17						2242
POL	IKDYGRKMA	1020	10	49	77						2243
POL	KOMAGDDCVA	1026	10	44	69						2244
POL	GAISLSLNIQT	79	11	01	17						2245
POL	GAISLSLNIQT	80	11	01	33						2246
POL	QITLWQRPLV	88	11	01	33						2247
POL	QITLWQRPLV	89	11	37	58						2248
POL	ITLWQRPLV	90	11	19	30						2249
POL	ITLWQRPLV	90	11	18	28						2250
POL	PLVTTIKGGOL	96	11	13	20						2251
POL	TIKIGGQKEA	99	11	17	27						2252
POL	QIGGQKEALL	101	11	23	36						2253
POL	QIGGQKEALL	101	11	01	16						2254
POL	QIEALLDTGA	105	11	01	51						2255
POL	QIEALLDTGA	105	11	34	51						2256
POL	QIEALLDTGA	108	11	60	94						2257
POL	ALIDTGADDTV	109	11	61	95						2258
POL	LLDTGADDTV	110	11	61	95						2259
POL	NLPQKWKPKMI	124	11	35	55						2260
POL	MIGGGGPKV	133	11	62	37						2261
POL	FIKRGYDQIL	140	11	13	20						2262
POL	FIKRGYDQIL	140	11	02	30						2263
POL	LIUEGCKEKA	149	11	13	20						2264
POL	LIUEGCKEKA	149	11	19	30						2265
POL	EICGKKAIGTV	152	11	23	36						2266
POL	EICGKKAIGTV	152	11	48	75						2267
POL	KAIGTVLVGPT	161	11	53	83						2268
POL	TVLVGPTPNI	161	11	53	83						2269
POL	VLVGPITPNI	162	11	26	41						2270
POL	PTVNIIGNRML	166	11	24	38						2271
POL	PVNIIGNRMLT	168	11	26	41						2272
POL	PVNIIGNRMLT	168	11	23	36						2273
POL	NIIGNRMLTQI	170	11	21	33						2274
POL	NIIGNRMLTQI	170	11	18	28						2275
POL	NIIGNRMLTQI	170	11	11	17						2276
POL	QIQCCTLIINRPI	178	11	41	64						2277
POL	QIQCCTLIINRPI	178	11	15	23						2278
POL	TLNIFSPNET	183	11	54	86						2279

HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SIQ ID NO
POL	ETVPVKKFGM	192	11	51	80						2279
POL	KLKPGMDGPKV	197	11	47	73						2280
POL	PLTEERIKALV	212	11	35	55						2281
POL	PLTEERIKALV	212	11	35	55						2282
POL	PLTEERIKALV	212	11	35	55						2283
POL	PLTEERIKALV	212	11	35	55						2284
POL	PLTEERIKALV	212	11	35	55						2285
POL	PVEAFKKKDS	248	11	37	58						2286
POL	LVDRELNRIT	263	11	60	94						2287
POL	TQDFVEVLGI	273	11	55	86						2288
POL	VQLGHPFAGL	279	11	54	84						2289
POL	PLTEERIKALV	279	11	35	55						2290
POL	GLKKKSSVTI	288	11	49	77						2291
POL	VLDVGDAFVS	297	11	53	83	0.0150					2292
POL	DVGDGAFVPL	299	11	54	84						2293
POL	PLDKDTRKYA	308	11	19	30						2294
POL	ETPGIRYQYV	327	11	51	80						2295
POL	PLTEERIKALV	327	11	35	55						2296
POL	PAVEQSATKI	346	11	36	56						2297
POL	AFQSSATKI	347	11	36	56						2298
POL	DWVYQYMDL	366	11	18	28						2299
POL	EWYQYMDL	366	11	24	38						2300
POL	VWYQYMDL	368	11	51	80						2301
POL	VWYQYMDL	372	11	51	80						2302
POL	DLGQHRIKI	381	11	20	31						2303
POL	RAKIELREIL	388	11	13	20						2304
POL	RTKIELRQIL	388	11	14	22						2305
POL	RQILLEWGTI	395	11	12	19						2306
POL	PLTEERIKALV	432	11	35	55						2307
POL	PVLPKDSWT	433	11	13	20						2308
POL	PVLPKDSWT	433	11	13	20						2309
POL	IQKLVGKLNWA	443	11	13	20						2310
POL	IQKLVGKLNWA	446	11	61	95						2311
POL	VYGLHWASQI	449	11	60	94						2312
POL	WASQYVGVK	455	11	16	25						2313
POL	WASQYVGVK	455	11	22	41						2314
POL	QVAGIKVKOL	458	11	18	29						2315
POL	QVAGIKVKOL	458	11	11	17						2316
POL	QVAGIKVKOL	458	11	14	22						2317
POL	GKVKQLCKLL	462	11	27	42						2318
POL	QVAGIKVKOL	462	11	18	29						2319
POL	QVAGIKVKOL	462	11	24	38						2320
POL	QVAGIKVKOL	462	11	24	38						2321
POL	QVAGIKVKOL	462	11	24	38						2322
POL	LLRGAKALDI	471	11	22	34						2323
POL	LLRGAKALDI	471	11	18	28						2324
POL	GAKALTDVPL	474	11	17	27						2325
POL	QVAGIKVKOL	474	11	17	27						2326
POL	QVAGIKVKOL	474	11	13	20						2327
POL	LTEVRLTEEA	478	11	17	27						2328
POL	DVPLTEEAEL	480	11	13	20						2329

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1020	A*1023	A*1026	A*6802	SEQ ID NO
POL	GVVPIETDELA	480	11	11	17					2329
POL	ELBLAAGRELL	481	11	29	85					2330
POL	GVVYDPSKLL	508	11	31	48					2331
POL	ELQKQGGQWT	520	11	12	19					2332
POL	ELQKQGGQWT	520	11	15	23					2334
POL	ELQKQGGQWT	520	11	23	20					2335
POL	KVQYQEPKRL	531	11	35	63					2336
POL	KVQYQEPKRL	531	11	40	63					2337
POL	KTGKYAKMRFA	542	11	10	16					2338
POL	KTGKYARMRGA	542	11	13	21					2339
POL	GAITNDVQKLT	551	11	18	28					2340
POL	SAITNDVQKLT	551	11	12	19					2341
POL	SAITNDVQKLT	551	11	10	16					2342
POL	ITNDVQKLEA	553	11	32	50					2343
POL	KOLTEAVQKIA	558	11	24	38					2344
POL	QLEAVQKIA	559	11	11	17					2345
POL	EAQKIAIESI	562	11	10	16					2346
POL	AVQKIAIESI	563	11	10	16					2347
POL	AVQKIAIESI	563	11	4	22					2348
POL	ALIESIWIQKLT	568	11	16	27					2349
POL	VIWKGITKPKL	573	11	17	27					2350
POL	VIWKGITKPKL	573	11	29	45					2351
POL	RLPQKLETWET	582	11	18	28					2352
POL	IQKLETWEAWWT	585	11	11	17					2353
POL	ELQKQGGQWT	585	11	13	20					2354
POL	ETWTDYQWAT	590	11	10	16					2355
POL	QATWIPSEWET	599	11	51	81					2356
POL	KLWYQLEKDPH	616	11	14	22					2357
POL	KLWYQLEKDPH	616	11	31	48					2358
POL	KLWYQLEKDPH	616	11	11	17					2359
POL	KLWYQLEKDPH	616	11	16	27					2360
POL	GAETFYDGGAA	628	11	44	65					2361
POL	AANRE*KLKGA	637	11	30	47					2362
POL	ETKLGKAGYVT	641	11	35	55					2363
POL	VYTDGRGKQVY	649	11	27	42					2364
POL	RQKYSLSLETT	655	11	10	16					2365
POL	ELQKQGGQWT	655	11	19	30					2366
POL	LETTNQKTEL	661	11	25	39					2367
POL	LETTNQKTEL	663	11	25	39					2368
POL	ETTNQKTELIA	663	11	11	17					2369
POL	ETTNQKTELIA	663	11	17	27					2370
POL	ETTNQKTELIA	664	11	12	19					2371
POL	ETTNQKTELIA	664	11	42	96					2372
POL	NKSTELQAVL	666	11	12	19					2373
POL	NKSTELQAVL	666	11	12	19					2374
POL	KTELQAVLAL	668	11	15	23					2375
POL	KTELQAVLAL	668	11	12	19					2376
POL	AHLALQDISGL	673	11	15	23					2377
POL	AHLALQDISGL	675	11	15	23					2378

Table VIII
 HIV A02 Superficial Peptides With Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
POL	ALDPSGLIYNI	677	11	27	42						2379
POL	ALDPSGLIYNI	677	11	31	42						2380
POL	LDDSGLEVNIV	678	11	27	42						2381
POL	LDDSGLEVNIV	678	11	27	42						2382
POL	EVNIVTDSQYA	684	11	25	39						2383
POL	IVTDSQYALGI	687	11	58	91						2384
POL	IVTDSQYALGI	687	11	58	91						2385
POL	QAPDSSISSEL	699	11	36	56						2386
POL	QAPDSSISSEL	699	11	36	56						2387
POL	QAPDSSISSEL	700	11	36	56						2388
POL	ELVNQIEQLI	708	11	18	28						2389
POL	ELVNSQIEQLI	708	11	19	30						2390
POL	HEQLIRKEKV	713	11	28	44						2391
POL	HEQLIRKEKV	713	11	28	44						2392
POL	ELVNSQIEQLI	715	11	18	28						2393
POL	QLKKFKYLA	716	11	19	30						2394
POL	YLAWYPAHKG	724	11	22	34						2395
POL	YLSWYMIKGI	724	11	37	58						2396
POL	GIGGNLQVKK	733	11	58	91						2397
POL	EQYDKLNSGI	738	11	15	23						2398
POL	EQYDKLNSGI	738	11	15	23						2399
POL	KLVSSGIRKVL	742	11	25	41						2400
POL	KLVSSGIRKVL	742	11	26	41						2401
POL	GIRKVI FLNG	747	11	49	77						2402
POL	KVIFLGDGKA	750	11	48	75						2403
POL	KVIFLGDGKA	750	11	48	75						2404
POL	AMASDPLNPI	773	11	18	28						2405
POL	AMASDPLNPI	773	11	18	28						2406
POL	AMASDPLNPI	774	11	26	41						2407
POL	MASDPLNPIV	774	11	25	39						2408
POL	NLPPIVAKEIV	779	11	26	41						2409
POL	NLPPIVAKEIV	779	11	27	42						2410
POL	ELVNSQIEQLI	787	11	43	67						2411
POL	ELVNSQIEQLI	787	11	43	67						2412
POL	QVICSQGIWQL	806	11	56	88						2413
POL	QVICSQGIWQL	806	11	56	88						2414
POL	QVICSQGIWQL	814	11	33	52						2415
POL	QLDCTILEGRV	814	11	26	41						2416
POL	CTILEGRVILV	817	11	31	48						2417
POL	CTILEGRVILV	817	11	31	48						2418
POL	CTILEGRVILV	817	11	23	36						2419
POL	CTILEGRVILV	819	11	23	36						2420
POL	CTILEGRVILV	819	11	23	36						2421
POL	CTILEGRVILV	819	11	23	36						2422
POL	CTILEGRVILV	819	11	23	36						2423
POL	CTILEGRVILV	819	11	23	36						2424
POL	CTILEGRVILV	819	11	23	36						2425
POL	CTILEGRVILV	819	11	23	36						2426
POL	CTILEGRVILV	819	11	23	36						2427
POL	CTILEGRVILV	819	11	23	36						2428

Table VIII
 HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6002	SEQ ID NO
POL	FLKLGRWPV	852	11	25	39						2429
POL	KLGRWPVKTI	855	11	13	20						2430
POL	KLGRWPVKVI	855	11	22	34						2431
POL	VIHTDNGSNFT	864	11	13	20						2432
POL	VIHTDNGSNFT	864	11	33	36						2433
POL	VIHTDNGSNFT	864	11	33	52						2434
POL	VIHTDNGSNFT	866	11	11	17						2435
POL	VIHTDNGSNFT	866	11	11	17						2436
POL	SAVKAACWVA	875	11	28	44						2437
POL	STTVKAACWVA	875	11	14	22						2438
POL	AVKAACWVAGI	877	11	10	16						2439
POL	TVKAACWVAGI	877	11	20	31						2440
POL	GIYPNQSGV	892	11	25	38						2441
POL	QVQAACWVAGI	916	11	43	67						2442
POL	QVQAACWVAGI	916	11	15	20						2443
POL	QVQAACWVAGI	916	11	15	20						2444
POL	QVQAACWVAGI	916	11	57	89						2445
POL	QVQAACWVAGI	920	11	58	91						2446
POL	FIINFKAAGGI	933	11	58	91						2447
POL	GIYFYKAGGI	942	11	57	89						2448
POL	SAGERVDIA	947	11	40	32						2449
POL	SAGERVDIA	947	11	44	33						2450
POL	VIHTDNGSNFT	952	11	12	19						2451
POL	VIHTDNGSNFT	952	11	27	42						2452
POL	VIHTDNGSNFT	952	11	12	19						2453
POL	VIHTDNGSNFT	955	11	14	22						2454
POL	VIHTDNGSNFT	955	11	34	53						2455
POL	VIHTDNGSNFT	959	11	44	69						2456
POL	VIHTDNGSNFT	960	11	40	47						2457
POL	VIHTDNGSNFT	960	11	30	47						2458
POL	VIHTDNGSNFT	967	11	12	19						2459
POL	VIHTDNGSNFT	967	11	34	54						2460
POL	VIHTDNGSNFT	976	11	34	53						2461
POL	VIHTDNGSNFT	976	11	14	22						2462
POL	VIHTDNGSNFT	990	11	59	92						2463
POL	VIHTDNGSNFT	992	11	59	92						2464
POL	VIHTDNGSNFT	993	11	59	92						2465
POL	VIHTDNGSNFT	999	11	37	58						2466
POL	VIHTDNGSNFT	999	11	12	19						2467
POL	VIHTDNGSNFT	1002	11	37	58						2468
POL	VIHTDNGSNFT	1002	11	12	19						2469
POL	VIHTDNGSNFT	1003	11	37	58						2470
POL	VIHTDNGSNFT	1003	11	37	58						2471
POL	VIHTDNGSNFT	1003	11	50	78						2472
POL	VIHTDNGSNFT	1003	11	50	78						2473
POL	VIHTDNGSNFT	1003	11	50	78						2474
POL	VIHTDNGSNFT	1003	11	50	78						2475
POL	VIHTDNGSNFT	1003	11	50	78						2476
POL	VIHTDNGSNFT	1003	11	50	78						2477
POL	VIHTDNGSNFT	1003	11	50	78						2478
POL	VIHTDNGSNFT	1003	11	50	78						2479
POL	VIHTDNGSNFT	1003	11	50	78						2480
POL	VIHTDNGSNFT	1003	11	50	78						2481
POL	VIHTDNGSNFT	1003	11	50	78						2482
POL	VIHTDNGSNFT	1003	11	50	78						2483
POL	VIHTDNGSNFT	1003	11	50	78						2484
POL	VIHTDNGSNFT	1003	11	50	78						2485
POL	VIHTDNGSNFT	1003	11	50	78						2486
POL	VIHTDNGSNFT	1003	11	50	78						2487
POL	VIHTDNGSNFT	1003	11	50	78						2488
POL	VIHTDNGSNFT	1003	11	50	78						2489
POL	VIHTDNGSNFT	1003	11	50	78						2490
POL	VIHTDNGSNFT	1003	11	50	78						2491
POL	VIHTDNGSNFT	1003	11	50	78						2492
POL	VIHTDNGSNFT	1003	11	50	78						2493
POL	VIHTDNGSNFT	1003	11	50	78						2494
POL	VIHTDNGSNFT	1003	11	50	78						2495
POL	VIHTDNGSNFT	1003	11	50	78						2496
POL	VIHTDNGSNFT	1003	11	50	78						2497
POL	VIHTDNGSNFT	1003	11	50	78						2498
POL	VIHTDNGSNFT	1003	11	50	78						2499
POL	VIHTDNGSNFT	1003	11	50	78						2500
POL	VIHTDNGSNFT	1003	11	50	78						2501
POL	VIHTDNGSNFT	1003	11	50	78						2502
POL	VIHTDNGSNFT	1003	11	50	78						2503
POL	VIHTDNGSNFT	1003	11	50	78						2504
POL	VIHTDNGSNFT	1003	11	50	78						2505
POL	VIHTDNGSNFT	1003	11	50	78						2506
POL	VIHTDNGSNFT	1003	11	50	78						2507
POL	VIHTDNGSNFT	1003	11	50	78						2508
POL	VIHTDNGSNFT	1003	11	50	78						2509
POL	VIHTDNGSNFT	1003	11	50	78						2510
POL	VIHTDNGSNFT	1003	11	50	78						2511
POL	VIHTDNGSNFT	1003	11	50	78						2512
POL	VIHTDNGSNFT	1003	11	50	78						2513
POL	VIHTDNGSNFT	1003	11	50	78						2514
POL	VIHTDNGSNFT	1003	11	50	78						2515
POL	VIHTDNGSNFT	1003	11	50	78						2516
POL	VIHTDNGSNFT	1003	11	50	78						2517
POL	VIHTDNGSNFT	1003	11	50	78						2518
POL	VIHTDNGSNFT	1003	11	50	78						2519
POL	VIHTDNGSNFT	1003	11	50	78						2520
POL	VIHTDNGSNFT	1003	11	50	78						2521
POL	VIHTDNGSNFT	1003	11	50	78						2522
POL	VIHTDNGSNFT	1003	11	50	78						2523
POL	VIHTDNGSNFT	1003	11	50	78						2524
POL	VIHTDNGSNFT	1003	11	50	78						2525
POL	VIHTDNGSNFT	1003	11	50	78						2526
POL	VIHTDNGSNFT	1003	11	50	78						2527
POL	VIHTDNGSNFT	1003	11	50	78						2528
POL	VIHTDNGSNFT	1003	11	50	78						2529
POL	VIHTDNGSNFT	1003	11	50	78						2530
POL	VIHTDNGSNFT	1003	11	50	78						2531
POL	VIHTDNGSNFT	1003	11	50	78						2532
POL	VIHTDNGSNFT	1003	11	50	78						2533
POL	VIHTDNGSNFT	1003	11	50	78						2534
POL	VIHTDNGSNFT	1003	11	50	78						2535
POL	VIHTDNGSNFT	1003	11	50	78						2536
POL	VIHTDNGSNFT	1003	11	50	78						2537
POL	VIHTDNGSNFT	1003	11	50	78						2538
POL	VIHTDNGSNFT	1003	11	50	78						2539
POL	VIHTDNGSNFT	1003	11	50	78						2540
POL	VIHTDNGSNFT	1003	11	50	78						2541
POL	VIHTDNGSNFT	1003	11	50	78						2542
POL	VIHTDNGSNFT	1003	11	50	78						2543
POL	VIHTDNGSNFT	1003	11	50	78						2544
POL	VIHTDNGSNFT	1003	11	50	78						2545
POL	VIHTDNGSNFT	1003	11	50	78						2546
POL	VIHTDNGSNFT	1003	11	50	78						2547
POL	VIHTDNGSNFT	1003	11	50	78						2548
POL	VIHTDNGSNFT	1003	11	50	78						2549
POL	VIHTDNGSNFT	1003	11	50	78						2550
POL	VIHTDNGSNFT	1003	11	50	78						2551
POL	VIHTDNGSNFT	1003	11	50	78						2552
POL	VIHTDNGSNFT	1003	11	50	78						2553
POL	VIHTDNGSNFT	1003	11	50	78						2554
POL	VIHTDNGSNFT	1003	11	50	78						2555
POL	VIHTDNGSNFT	1003	11	50	78						2556
POL	VIHTDNGSNFT	1003	11	50	78						2557
POL	VIHTDNGSNFT	1003	11	50	78						2558
POL	VIHTDNGSNFT	1003	11	50	78						2559
POL	VIHTDNGSNFT	1003	11	50	78						2560
POL	VIHTDNGSNFT	1003	11	50	78						2561
POL	VIHTDNGSNFT	1003	11	50	78						2562
POL	VIHTDNGSNFT	1003	11	50	78						2563
POL	VIHTDNGSNFT	1003	11	50	78						2564
POL	VIHTDNGSNFT	1003	11	50	78						2565
POL	VIHTDNGSNFT	1003	11	50	78						2566
POL	VIHTDNGSNFT	1003	11	50	78						2567
POL	VIHTDNGSNFT	1003	11	50	78						2568
POL	VIHTDNGSNFT	1003	11	50	78						2569
POL	VIHTDNGSNFT	1003	11	50	78						2570
POL	VIHTDNGSNFT	1003	11	50	78						2571
POL	VIHTDNGSNFT	1003	11	50	78						2572
POL	VIHTDNGSNFT	1003	11	50	78						2573
POL	VIHTDNGSNFT	1003	11	50	78						2574
POL	VIHTDNGSNFT	1003	11	50	78						2575
POL	VIHTDNGSNFT	1003	11	50	78						2576
POL	VIHTDNGSNFT	1003	11	50	78						2577
POL	VIHTDNGSNFT	1003	11	50	78						2578
POL	VIHTDNGSNFT	1003	11	50							

Table V.II
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
REV	GTQDSQGT	97	8	10	16						2479
REV	PGHETGV	101	8	05	18						2480
REV	SGTETGV	101	8	05	18						2481
REV	SGTETGV	101	8	05	18						2482
REV	SGTETGV	101	8	05	18						2483
REV	SGTETGV	101	8	05	18						2484
REV	CLGRPAEV	67	9	10	16						2485
REV	PAEVPLOL	71	9	21	33						2486
REV	PAEVPLOL	71	9	21	33						2487
REV	SAEVPLOL	71	9	12	19						2488
REV	PAEVPLOL	71	9	11	17						2489
REV	PAEVPLOL	71	9	11	17						2490
REV	LOLPLERL	77	9	11	17						2491
REV	LOLPLERL	77	9	36	56						2492
REV	LOLPLERL	77	9	18	28						2493
REV	TOGVSQPI	98	9	11	18						2494
REV	TOGVSQPI	98	9	11	18						2495
REV	TOGVSQPI	98	9	11	18						2496
REV	TOGVSQPI	98	9	11	18						2497
REV	TOGVSQPI	98	9	11	18						2498
REV	TOGVSQPI	98	9	11	18						2499
REV	TOGVSQPI	98	9	11	18						2500
REV	TOGVSQPI	98	9	11	18						2501
REV	TOGVSQPI	98	9	11	18						2502
REV	TOGVSQPI	98	9	11	18						2503
REV	TOGVSQPI	98	9	11	18						2504
REV	TOGVSQPI	98	9	11	18						2505
REV	TOGVSQPI	98	9	11	18						2506
REV	TOGVSQPI	98	9	11	18						2507
REV	TOGVSQPI	98	9	11	18						2508
REV	TOGVSQPI	98	9	11	18						2509
REV	TOGVSQPI	98	9	11	18						2510
REV	TOGVSQPI	98	9	11	18						2511
REV	TOGVSQPI	98	9	11	18						2512
REV	TOGVSQPI	98	9	11	18						2513
REV	TOGVSQPI	98	9	11	18						2514
REV	TOGVSQPI	98	9	11	18						2515
REV	TOGVSQPI	98	9	11	18						2516
REV	TOGVSQPI	98	9	11	18						2517
REV	TOGVSQPI	98	9	11	18						2518
REV	TOGVSQPI	98	9	11	18						2519
REV	TOGVSQPI	98	9	11	18						2520
REV	TOGVSQPI	98	9	11	18						2521
REV	TOGVSQPI	98	9	11	18						2522
REV	TOGVSQPI	98	9	11	18						2523
REV	TOGVSQPI	98	9	11	18						2524
REV	TOGVSQPI	98	9	11	18						2525
REV	TOGVSQPI	98	9	11	18						2526
REV	TOGVSQPI	98	9	11	18						2527
REV	TOGVSQPI	98	9	11	18						2528

0.0001

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Consensus (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SEQ ID NO
VIF	GVSEWRRL	87	8	18	28						2539
VIF	STQIDPDL	100	8	12	19						2539
VIF	STQIDPGL	100	8	11	17						2531
VIF	TDQIDPLA	101	8	12	19						2532
VIF	TDQIDPLA	101	8	11	17						2533
VIF	TDQIDPLA	101	8	16	22						2534
VIF	LADQIHIL	107	8	25	39						2535
VIF	LADQIHIM	107	8	17	27						2536
VIF	SAIRKAIL	123	8	35	55						2537
VIF	SAIRKAIL	123	8	12	19						2538
VIF	SAIRKAIL	123	8	18	28						2539
VIF	KVGSLSDFL	146	8	52	81						2540
VIF	KVGSLSDFL	146	8	12	19						2541
VIF	SLQYLALA	149	8	31	48						2542
VIF	SLQYLALT	149	8	12	19						2543
VIF	LOYLALAA	150	8	11	17						2544
VIF	LOYLALAA	150	8	28	44						2545
VIF	YLALTAL	152	8	10	16						2546
VIF	ALIRPKKI	157	8	10	16						2547
VIF	PLPSVRKL	168	8	21	33						2548
VIF	PLPSVRKL	168	8	14	22						2549
VIF	WQVIMVTV	170	8	33	51						2550
VIF	WQVIMVTV	170	8	46	72						2551
VIF	QVDRMRIT	172	9	12	19						2552
VIF	QVDRMRIT	172	9	10	16						2553
VIF	QVDRMRIT	172	9	31	48						2554
VIF	KIRTNLSV	177	9	12	19						2555
VIF	KIRTNLSV	177	9	15	23						2556
VIF	KIRTNLSV	177	9	15	23						2557
VIF	SLVKHIMTV	213	9	19	30						2558
VIF	SLVKHIMTV	213	9	21	33						2559
VIF	EVHPLGDA	54	9	24	38						2560
VIF	EVHPLGDA	54	9	25	39						2561
VIF	EVHPLGDA	54	9	30	46						2562
VIF	HLPLGAIL	56	9	20	31						2563
VIF	PLGELRLVI	58	9	10	16						2564
VIF	LVRITYWGL	66	9	10	16						2565
VIF	LVRITYWGL	66	9	22	34						2566
VIF	LVRITYWGL	66	9	16	25						2567
VIF	HTGERDWIL	75	9	21	33						2568
VIF	HTGERDWIL	75	9	12	19						2569
VIF	STQIDPDLA	100	9	12	19						2570
VIF	STQIDPDLA	100	9	11	17						2571
VIF	DLADQIHL	106	9	18	28						2572
VIF	DLADQIHL	106	9	15	23						2573
VIF	KVGSLSQPLA	146	9	52	81						2574
VIF	SLQYLALAA	149	9	12	19						2575
VIF	SLQYLALAA	149	9	11	17						2576
VIF	SLQYLALTA	149	9	31	48						2577
VIF	LOYLALAL	150	9	12	19						2578

0.0031

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6002	SEQ ID NO
VIF	LQYLAKAL	150	9	11	17						2579
VIF	LQYLALAL	150	9	33	52						2580
VIF	KLKPLPSV	164	9	14	16						2581
VIF	PLPSVKLT	168	9	13	20						2582
VIF	VNIWQVDRM	7	10	44	69						2583
VIF	IVWQVDRMKI	9	10	12	19						2584
VIF	IVWQVDRMKI	9	10	47	73						2585
VIF	IVWQVDRMKI	9	10	12	19						2586
VIF	WQVDRMRIT	11	10	10	16						2587
VIF	WQVDRMRIT	11	10	10	16						2588
VIF	WQVDRMRIT	11	10	31	48						2589
VIF	RAMKIRIWNLSL	15	10	12	19						2590
VIF	RAMKIRIWNLSL	15	10	15	23						2591
VIF	RAMKIRIWNLSL	15	10	15	23						2592
VIF	RAMKIRIWNLSL	15	10	15	23						2593
VIF	KSSIVIHPL	50	10	19	32						2594
VIF	RUSSEVHIPL	50	10	13	20						2595
VIF	HIPLGDARLV	56	10	10	16						2596
VIF	HIPLGDARLV	56	10	19	30						2597
VIF	HIPLGDARLV	56	10	19	30						2598
VIF	VITTVANGLOT	65	10	16	25						2599
VIF	VITTVANGLOT	65	10	16	25						2600
VIF	LOITGERDWHL	74	10	12	19						2601
VIF	QIDPLADQL	102	10	10	16						2602
VIF	QVDPGLADQL	102	10	14	22						2603
VIF	IVSPREYQA	133	10	11	17						2604
VIF	IVSPREYQA	133	10	31	49						2605
VIF	KVGSLOYLAL	146	10	51	80						2606
VIF	SLOYLALAL	149	10	12	19						2607
VIF	SLOYLALAL	149	10	11	17						2608
VIF	SLOYLALAL	149	10	31	48						2609
VIF	SLOYLALAL	149	10	28	44						2610
VIF	QVMIWQVDRM	8	11	43	67						2611
VIF	QVMIWQVDRM	8	11	43	67						2612
VIF	RAMKIRIWNLSL	15	11	12	19						2613
VIF	RAMKIRIWNLSL	15	11	15	23						2614
VIF	RAMKIRIWNLSL	15	11	15	23						2615
VIF	RTWNSLAKIHM	19	11	24	38						2616
VIF	RTWNSLAKIHM	19	11	24	38						2617
VIF	EVHIPLGDARL	54	11	13	54						2618
VIF	EVHIPLGDARL	54	11	20	31						2619
VIF	HIPLGDARLV	56	11	10	16						2620
VIF	HIPLGDARLV	56	11	10	16						2621
VIF	GLITGERDWHL	76	11	21	33						2622
VIF	GLITGERDWHL	73	11	12	19						2623
VIF	GLITGERDWHL	73	11	10	16						2624
VIF	QIDPLADQL	101	11	13	20						2625
VIF	QIDPLADQL	101	11	13	20						2626
VIF	QIDPLADQL	101	11	10	16						2627
VIF	QIDPLADQL	101	11	10	16						2628
VIF	QVMIWQVDRM	8	11	38	59						2629

0.0008

Table VIII
HIV A02 Super Motif Peptides With Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*0802	SEQ ID NO
VIF	KVGSLOYLALA	146	11	12	19						2629
VIF	SLQYLAU	147	11	23	19						2630
VIF	SLQYLAU	149	11	27	42						2631
VIF	LIKPKKIKPPL	158	11	10	16						2632
VIF	KTKGIRGCSITM	188	11	15	23						2633
VPR	ALLELEEL	19	8	10	16						2634
VPR	LYLEEL	19	8	14	16						2635
VPR	AVRIEPR	30	8	14	16						2636
VPR	ETYGDTWA	48	8	16	25						2637
VPR	ETYGDTWT	48	8	11	17						2638
VPR	DTWAGVEA	52	8	16	25						2639
VPR	DTWAGVEA	52	8	23	36						2640
VPR	DTWAGVEA	54	8	23	36						2641
VPR	GVEAHR	54	8	34	53						2642
VPR	IRHLQQL	60	8	42	66						2643
VPR	ILQQLFL	63	8	37	58						2644
VPR	LLFPHRI	67	8	44	69						2645
VPR	LLFPHRI	67	8	42	66						2646
VPR	CONSIGI	77	8	45	70						2647
VPR	WALELEEL	18	9	09	15						2648
VPR	WTLLELEEL	18	9	42	69	0.0035					2649
VPR	LLLEELKNEA	22	9	17	27						2650
VPR	LLLEELKNEA	22	9	16	25						2651
VPR	LLLEELKNEA	22	9	16	25						2652
VPR	WHLGLQHH	38	9	20	31	0.0001					2653
VPR	HLVETYGDT	45	9	17	27						2654
VPR	HLVETYGDT	45	9	14	22						2655
VPR	HLVETYGDT	45	9	14	22						2656
VPR	HLVETYGDT	45	9	16	25						2657
VPR	DTWAGVEA	52	9	20	31						2658
VPR	GVEAHR	54	9	34	53						2659
VPR	HLRLQQL	59	9	39	61	0.0150	0.1900	0.2400	0.0960		2660
VPR	HLRLQQL	60	9	42	66	0.0004				0.0730	2661
VPR	LLQQLFL	62	9	46	66	0.2600	0.0028	0.0000	0.1000	0.0220	2662
VPR	QLLPHRI	66	9	46	66	0.0530	0.0002	0.0004	0.0123	0.0640	2663
VPR	RIGCQHSRI	74	9	47	73						2664
VPR	RIGCQHSRI	74	9	12	19						2665
VPR	CONSIGI	77	9	16	25						2666
VPR	CONSIGI	77	9	16	25						2667
VPR	CONSIGI	77	9	14	22						2668
VPR	ROHRAKGA	90	9	13	20						2669
VPR	POREYNEWT	10	10	29	45						2670
VPR	ELLEEKNEA	21	10	16	25						2671
VPR	ELLEEKNEA	21	10	16	25						2672
VPR	LLLEELKNEA	22	10	16	25						2673
VPR	LLLEELKNEA	22	10	16	25						2674
VPR	AVRIEPR	30	10	14	22						2675
VPR	AVRIEPR	30	10	34	53	0.0002					2676
VPR	ETYGDTWAGV	48	10	16	25	0.0009					2677
VPR	ETYGDTWAGV	48	10	11	17						2678

Table VII
HIV A12 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*4802	SEQ ID NO
VPR	NTYGDTWEGV	48	10	16	25						2679
VPR	DTWAGVEAII	52	10	16	25						2680
VPR	DTWAGVEAII	52	10	19	30						2681
VPR	WAGYEAIRI	54	10	15	23						2682
VPR	WAGYEAIRI	54	10	31	52						2683
VPR	AIHIIQQL	59	10	39	61						2684
VPR	QQLFHIFRI	65	10	44	69						2685
VPR	QQLFVIFRI	65	10	16	16						2686
VPR	PQREYNTWIL	10	11	29	45						2687
VPR	QQLFVIFRI	65	11	16	16						2688
VPR	ELFELISAV	71	11	16	25						2689
VPR	EAVRIIFRWL	29	11	14	22						2690
VPR	EAVRIIFRWL	29	11	34	53						2691
VPR	GQHITYTGDT	43	11	17	27						2692
VPR	GQHITYTGDT	43	11	13	20						2693
VPR	WAGYEAIRI	54	11	15	23						2694
VPR	WAGYEAIRI	54	11	15	23						2695
VPR	EAIIRIQLL	58	11	33	52						2696
VPR	IRIRIQLLFI	60	11	33	52						2697
VPR	LOQLFHIFRI	64	11	44	69						2698
VPR	LOQLFHIFRI	64	11	10	16						2699
VPR	LOQLFHIFRI	64	11	45	70						2700
VPR	RIGCRISRIH	74	11	11	17						2701
VPR	#LIGRGRNGA	85	11	01	50						2702
VPU	LAKVDYRI	5	8	01	25						2703
VPU	LAKVDYRI	5	8	01	25						2704
VPU	KVDYRI	7	8	01	33						2705
VPU	KVDYRI	7	8	01	33						2706
VPU	RIDYRI	7	8	01	33						2707
VPU	LAVALV	12	8	12	19						2708
VPU	LAVALV	12	8	12	20						2709
VPU	LAVALV	12	8	19	36						2710
VPU	LAVALV	12	8	23	36						2711
VPU	LAVALV	12	8	23	36						2712
VPU	LAVALV	12	8	23	36						2713
VPU	LAVALV	12	8	29	45						2714
VPU	LAVALV	12	8	15	23						2715
VPU	LAVALV	12	8	15	23						2716
VPU	LAVALV	12	8	15	23						2717
VPU	LAVALV	12	8	15	23						2718
VPU	LAVALV	12	8	15	23						2719
VPU	LAVALV	12	8	15	23						2720
VPU	LAVALV	12	8	15	23						2721
VPU	LAVALV	12	8	15	23						2722
VPU	LAVALV	12	8	15	23						2723
VPU	LAVALV	12	8	15	23						2724
VPU	LAVALV	12	8	15	23						2725
VPU	LAVALV	12	8	15	23						2726
VPU	LAVALV	12	8	15	23						2727
VPU	LAVALV	12	8	15	23						2728

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VP1	LIDRIERA	58	9	12	19						2729
VP1	DOHELSALV	79	9	11	18						2730
VP1	VTLSSSKL	94	9	01	26						2731
VP1	LAKVDYRVI	5	10	01	25						2732
VP1	LAKVDYRLGV	5	10	01	25						2733
VP1	KVDYRIVVA	7	10	01	33						2734
VP1	KVDYRIVVA	7	10	01	33						2735
VP1	KVDYRIVVA	7	10	01	33						2736
VP1	KVDYRIVVA	7	10	01	33						2737
VP1	ILQKQKIDRL	27	10	20	31						2738
VP1	ILQKQKIDRL	27	10	20	31						2739
VP1	ILQKQKIDRL	27	10	14	23						2740
VP1	ILQKQKIDRL	46	10	01	50						2741
VP1	LVTLSSSKL	91	10	01	25						2742
VP1	LAKVDYRIV	7	11	01	33						2743
VP1	KVDYRIVVA	7	11	01	33						2744
VP1	KVDYRIVVA	7	11	15	23						2745
VP1	ILQKQKIDRL	45	11	13	20						2746
VP1	ILQKQKIDRL	46	11	13	20						2747

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*100	A*101	A*102	A*103	A*104	SEQ ID NO
ENV	SLWQSLK	123	8	47	75						2746
ENV	QSLKPCV	127	8	48	75						2747
ENV	ATQACPK	244	8	14	22						2748
ENV	TTTQACPK	244	8	11	17						2749
ENV	TTTQACPK	244	8	17	27						2750
ENV	PAQYALK	266	8	15	21						2751
ENV	PAQYALK	266	8	15	21						2752
ENV	ALKCNCK	271	8	20	31						2753
ENV	ILKCNCK	271	8	12	19						2754
ENV	SVENCTR	340	8	13	20						2755
ENV	TTTQSSR	375	8	11	33						2756
ENV	TTTQSSR	375	8	11	33						2757
ENV	TTTQSSR	375	8	11	33						2758
ENV	ITLPCRK	483	8	26	41						2759
ENV	NMWQGVGK	494	8	15	23						2760
ENV	ITGLLLTR	520	8	37	58						2761
ENV	RSELYKPK	558	8	54	84						2762
ENV	PLGAPTR	571	8	26	41						2763
ENV	PLGAPTR	571	8	26	41						2764
ENV	GVAPTKAK	573	8	19	30						2765
ENV	VAPTKAK	574	8	19	30						2766
ENV	VISTRTIR	584	8	01	50						2767
ENV	STRTHREK	586	8	01	50						2768
ENV	STRTHREK	586	8	01	50						2769
ENV	RVVQREK	587	8	12	22						2770
ENV	RVVQREK	587	8	12	22						2771
ENV	ITLTVQAR	621	8	32	50						2772
ENV	EAQQHLIK	646	8	12	19						2773
ENV	KLTWGHK	653	8	13	20						2774
ENV	KLTWGHK	653	8	13	20						2775
ENV	CKLQLOK	667	8	26	41						2776
ENV	LAVERYLK	667	8	11	17						2777
ENV	LAVERYLK	667	8	11	17						2778
ENV	GIWGLSGK	680	8	52	81						2779
ENV	MTWMEWER	721	8	12	19						2780
ENV	MTWMEWER	721	8	12	19						2781
ENV	AVLSNKR	795	8	31	48						2782
ENV	LSVNRVR	797	8	38	59						2783
ENV	ALAWDDLK	851	8	25	39						2784
ENV	RVELLGR	878	8	22	34						2785
ENV	RVELLGR	878	8	22	34						2786
ENV	RVVQREK	889	8	12	22						2787
ENV	AVAGETDR	928	8	31	48						2788
ENV	RAIHPR	945	8	13	20						2789
ENV	RAIHPR	946	8	13	20						2790
ENV	RIRQZLER	953	8	44	69						2791
ENV	RVVQREK	953	8	12	22						2792
ENV	VTENFMWK	102	9	37	58						2793
ENV	ISLWQSLK	122	9	47	73						2794
ENV	SAITGACPK	243	9	14	22						2795
ENV	SVITQACPK	243	9	10	16						2796
ENV	SVITQACPK	243	9	17	27						2797

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0301	A*1101	A*3101	A*3101	A*6001	SEQ ID NO
ENV	FAIKCNQK	269	9	14	22	0.0002	0.0002	0.0004	0.0015	0.0027	2796
ENV	AIUKCNQK	270	9	12	19						2796
ENV	TVQCTIGK	290	9	28	44	0.0021	0.0460	0.0042	0.0017	0.0190	2798
ENV	TVQCTIGR	290	9	23	36	0.0008	0.0008	0.0880	0.0330	0.0130	2799
ENV	LAEEAVIR	312	9	12	19	0.0002	0.0002	0.0004	0.0007	0.0002	2800
ENV	TVQCTIGR	312	9	28	44						2801
ENV	TVQCTIGR	312	9	28	44						2802
ENV	TVQCTIGR	312	9	28	44						2803
ENV	TVQCTIGR	312	9	28	44						2804
ENV	TVQCTIGR	312	9	28	44						2805
ENV	TVQCTIGR	312	9	28	44						2806
ENV	TVQCTIGR	312	9	28	44						2807
ENV	TVQCTIGR	312	9	28	44						2808
ENV	TVQCTIGR	312	9	28	44						2809
ENV	TVQCTIGR	312	9	28	44						2810
ENV	TVQCTIGR	312	9	28	44						2811
ENV	TVQCTIGR	312	9	28	44						2812
ENV	TVQCTIGR	312	9	28	44						2813
ENV	TVQCTIGR	312	9	28	44						2814
ENV	TVQCTIGR	312	9	28	44						2815
ENV	TVQCTIGR	312	9	28	44						2816
ENV	TVQCTIGR	312	9	28	44						2817
ENV	TVQCTIGR	312	9	28	44						2818
ENV	TVQCTIGR	312	9	28	44						2819
ENV	TVQCTIGR	312	9	28	44						2820
ENV	TVQCTIGR	312	9	28	44						2821
ENV	TVQCTIGR	312	9	28	44						2822
ENV	TVQCTIGR	312	9	28	44						2823
ENV	TVQCTIGR	312	9	28	44						2824
ENV	TVQCTIGR	312	9	28	44						2825
ENV	TVQCTIGR	312	9	28	44						2826
ENV	TVQCTIGR	312	9	28	44						2827
ENV	TVQCTIGR	312	9	28	44						2828
ENV	TVQCTIGR	312	9	28	44						2829
ENV	TVQCTIGR	312	9	28	44						2830
ENV	TVQCTIGR	312	9	28	44						2831
ENV	TVQCTIGR	312	9	28	44						2832
ENV	TVQCTIGR	312	9	28	44						2833
ENV	TVQCTIGR	312	9	28	44						2834
ENV	TVQCTIGR	312	9	28	44						2835
ENV	TVQCTIGR	312	9	28	44						2836
ENV	TVQCTIGR	312	9	28	44						2837
ENV	TVQCTIGR	312	9	28	44						2838
ENV	TVQCTIGR	312	9	28	44						2839
ENV	TVQCTIGR	312	9	28	44						2840
ENV	TVQCTIGR	312	9	28	44						2841
ENV	TVQCTIGR	312	9	28	44						2842
ENV	TVQCTIGR	312	9	28	44						2843
ENV	TVQCTIGR	312	9	28	44						2844
ENV	TVQCTIGR	312	9	28	44						2845

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*4801	SEQ ID NO
ENV	SLAEYEVIR	311	10	12	19						2846
ENV	CTRENNTRK	345	10	22	34						2847
ENV	ATGDIQDIR	369	10	12	19						2848
ENV	ETITSPNCR	430	10	11	17						2849
ENV	GSBNQTEIR	532	10	12	19						2850
ENV	PLGVATIKK	571	10	10	13						2851
ENV	GVATTKARR	573	10	17	27						2852
ENV	VSTRTHREK	584	10	01	50						2853
ENV	ISTRTHREK	585	10	01	50						2854
ENV	STRTHREK	586	10	01	50						2855
ENV	ASTLTVOAR	619	10	28	44						2856
ENV	IVQQNNLLR	634	10	25	39	0.0024	0.0190	0.0130	0.0072	0.0035	2858
ENV	ALDAQHLLK	644	10	26	41						2859
ENV	LLKLTVMGK	651	10	12	19						2860
ENV	LLKLTVMGK	651	10	13	20	0.0055	0.0110				2861
ENV	MLQITVGRK	651	10	10	16						2862
ENV	RLAVERYLK	665	10	18	28						2863
ENV	RVLAVERYL	665	10	10	16						2865
ENV	LLGWGCSGR	678	10	50	78						2866
ENV	ALVQVQGR	702	10	16	46						2867
ENV	ALVQVQGR	702	10	31	46						2868
ENV	FLALAWDDR	849	10	25	39						2869
ENV	RSCLFSYIR	858	10	31	48						2870
ENV	GLRLGWELK	892	10	10	32						2871
ENV	LLQYWSQELK	906	10	12	19						2872
ENV	ALVQVQGR	946	10	11	16						2873
ENV	ALVQVQGR	946	10	12	19						2874
ENV	PTIRQQLER	951	10	12	19						2875
ENV	VTVYGVPPVK	47	11	41	64		4.1000				2876
ENV	KTLFCASDAK	60	11	12	19						2877
ENV	PTLTKASDAK	60	11	12	19						2878
ENV	NTSVAQCPK	241	11	38	59						2879
ENV	NTSVAQCPK	241	11	14	22						2880
ENV	NTSVITQCPK	241	11	13	20						2881
ENV	VSTVQCTIGIK	288	11	28	44						2882
ENV	VSTVQCTIGIR	288	11	23	36						2883
ENV	GSALVQVQGR	306	11	12	19						2884
ENV	VSTVQCTIGIR	306	11	12	19						2885
ENV	KLREIFQENK	405	11	01	25						2886
ENV	ITEGNTIQQK	478	11	01	50						2887
ENV	NANITPCRIK	478	11	01	50						2888
ENV	QHNMQVQGR	491	11	12	19						2889
ENV	QHNMQVQGR	491	11	12	19						2890
ENV	NTENKATIK	537	11	01	19						2891
ENV	NTGNATIEIR	537	11	01	17						2892
ENV	EIFRPGGDMR	544	11	15	23						2893
ENV	EIFRPGGDMR	544	11	20	31						2894
ENV	ESLYKYKVVK	558	11	29	45						2895

Table IX
HIV A03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*030	A*101	A*330	A*680	SEQ ID NO
ENV	KIEPLGVAPTK	568	11	15	24					2896
ENV	PIGVAPTKAR	571	11	19	30					2897
ENV	PIGVAPTKAR	572	11	19	30					2898
ENV	KACERVQEEK	579	11	13	20					2900
ENV	INNIITFHREK	584	11	01	50					2901
ENV	VISTFHREK	584	11	01	50					2902
ENV	AASTLTQAR	618	11	28	44					2903
ENV	GVQDQNNLLR	633	11	25	39					2904
ENV	GVQDQNNLLR	633	11	25	39					2905
ENV	ILLKLTWGHK	650	11	13	20					2906
ENV	ILLQLTYWGHK	650	11	34	53					2907
ENV	TVWGKQLQAR	655	11	48	75					2908
ENV	QLQARVLAVR	661	11	33	52					2909
ENV	QLQARVLAVR	661	11	33	52					2910
ENV	QLQARVLAVR	661	11	33	52					2911
ENV	LIIESQNQEEK	740	11	20	31					2912
ENV	IMVGLGLGR	781	11	34	54					2913
ENV	IFAVLSVNR	792	11	14	22					2914
ENV	IFAVLSVNR	792	11	17	27					2915
ENV	IFAVLSVNR	792	11	17	27					2916
ENV	GVGEGGEEGR	839	11	11	19					2917
ENV	NLCUSFYHLR	859	11	11	17					2918
ENV	SLCUSFYHLR	859	11	31	48					2919
ENV	LLGRRGWELK	882	11	09	15					2920
ENV	NLLQYWSQELK	905	11	12	19					2921
ENV	NLLQYWSQELK	905	11	12	19					2922
ENV	TAVAVGEGTR	925	11	21	33					2923
ENV	RAILHIREIR	945	11	12	19					2924
GAG	GARASILR	2	8	10	16					2925
GAG	ASVLSGGK	5	8	29	45					2926
GAG	WAKSGLGK	30	8	44	70					2927
GAG	WABEILR	31	8	48	75					2928
GAG	OTGSEELR	71	8	12	19					2929
GAG	TLYCVHQK	86	8	12	19					2930
GAG	TLYCVHQK	86	8	15	23					2931
GAG	RIEVDTRK	93	8	13	20					2932
GAG	RIEVDTRK	93	8	13	20					2933
GAG	DTKEALIK	98	8	12	19	0.0003	0.0001			2934
GAG	KIEEQNK	105	8	23	36					2935
GAG	FAAADKEK	123	8	01	50					2936
GAG	RTLMAWVK	171	8	63	98	0.0410	0.0560			2937
GAG	WAVVPEEK	176	8	39	63					2938
GAG	WVAVVPEEK	176	8	45	75					2939
GAG	QVAVVPEEK	176	8	31	48	0.0003	0.0001			2940
GAG	QVAVVPEEK	176	8	61	95					2941
GAG	PIAPGQMR	243	8	19	30					2942
GAG	PIAPGQMR	243	8	17	27					2943
GAG	PIAPGQMR	243	8	10	16					2944
GAG	PIAPGQMR	243	8	18	28					2945
GAG	PIAPGQMR	243	8	48	75					2946
GAG	PIAPGQMR	243	8	48	75	0.0003	0.0001			2947
GAG	WILLINK	289	8	8	8					2948

Table IX
HIV A03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	PTSLDR	303	8	12	19						2946
GAG	IVSLDR	303	8	16	25						2947
GAG	IVSLDR	303	8	25	38						2948
GAG	GVGGPHK	376	8	37	58	0.0012	0.0018				2949
GAG	GVGGPHK	376	8	23	36						2950
GAG	ASAQDLK	392	8	01	50						2951
GAG	ATAQDLK	392	8	01	50						2952
GAG	AAAIMQK	400	8	04	19						2953
GAG	AAAIMQK	400	8	01	19						2954
GAG	SATIMQK	405	8	01	22						2955
GAG	YIAVFMQK	405	8	02	50						2956
GAG	MMQGSFK	409	8	10	16						2957
GAG	MMQGSFK	409	8	10	16						2958
GAG	MMQGSFK	409	8	23	36						2959
GAG	MMQGSFK	409	8	49	77						2960
GAG	RASLSGK	425	8	29	45						2961
GAG	KIDAWKIR	4	9	16	25						2962
GAG	KIDAWKIR	12	9	10	16						2963
GAG	DAWEKIRL	14	9	17	27						2964
GAG	KIRLIPGK	18	9	44	69						2965
GAG	KIRLIPGK	18	9	14	27						2966
GAG	LLTSEGR	52	9	17	27						2967
GAG	ATLYCVHQK	85	9	12	19						2968
GAG	ATLYCVHQK	85	9	15	23	0.0150	0.7100				2969
GAG	MVIOAISPR	163	9	27	42	0.1809	0.0670	1.0000	2.1000	0.8400	2970
GAG	PPVGEYK	279	9	35	55	0.0002	0.0012	0.0006	0.0005	0.0003	2971
GAG	PPVGEYK	279	9	35	55	0.0008	0.0001	0.0032	0.0100	0.0004	2972
GAG	ILDFQGGK	306	9	19	30	0.0420	0.0048	0.0006	0.0006	0.0002	2973
GAG	ILDFQGGK	306	9	42	66						2974
GAG	NSATIMQK	404	9	01	33						2975
GAG	IMMQSNFK	408	9	10	16						2976
GAG	IMMQSNFK	408	9	10	16						2977
GAG	IMMQSNFK	408	9	11	31						2978
GAG	TKFCNCGK	422	9	11	31						2979
GAG	TKFCNCGK	422	9	17	17						2980
GAG	IAKNRAIR	434	9	18	29	0.0009	0.0003	0.0330	0.0500	0.0039	2981
GAG	IAKNRAIR	434	9	13	21						2982
GAG	IAKNRAIR	434	9	20	32						2983
GAG	KWPSNGK	472	9	22	32	0.0770	0.0005	0.4400	0.0087	0.0001	2984
GAG	KWPSNGK	472	9	13	21						2985
GAG	KWPSNGK	472	9	10	16						2986
GAG	TAPPEESR	496	9	15	23						2987
GAG	TAPPEESR	508	9	02	67						2988
GAG	KIRLIPGK	18	9	44	69						2989
GAG	KIRLIPGK	18	10	44	69	1.9000	0.0010	0.0008	0.0005	0.0001	2990
GAG	RLKILHWASR	31	10	13	20						2991
GAG	RLKILHWASR	31	10	17	27						2992
GAG	IWVASRELER	35	10	20	31	0.0099	0.0066				2993
GAG	IWVASRELER	35	10	26	41						2994
GAG	GLLETSEGR	51	10	16	25						2995

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SIQ ID NO
GAG	VATLYCVIQR	84	10	12	19						2996
GAG	VATLYCVIQR	84	10	15	23						2997
GAG	KIEERQNSK	105	10	15	23						2998
GAG	QNAVIQMSR	162	10	27	42	0.0250	0.0010	0.0740	0.1000	0.0430	2999
GAG	NAWKVIEER	174	10	29	45	0.0004	0.0002				3000
GAG	YAGVQAEER	244	10	30	47						3001
GAG	PIPVGEIYR	279	10	34	53	0.0003	0.0001	0.0009	0.0010	0.0005	3002
GAG	ILGLNKIVR	290	10	57	89	0.0003	0.0006	0.0110	0.0260	0.0073	3003
GAG	YSPYSILDR	301	10	12	19						3004
GAG	YSPYSILDR	301	10	16	25						3005
GAG	YSPYSILDR	301	10	24	38						3006
GAG	STLAKGQKR	305	10	40	63						3007
GAG	SILDIRGPK	320	10	27	42	0.3100	0.7100	0.0017	0.0020	0.0060	3008
GAG	YVDRFPYKLR	320	10	28	44	0.0003	0.0006				3009
GAG	RAEQMSQVK	329	10	12	19						3010
GAG	RAEQMSQVK	329	10	12	19						3011
GAG	RAEQATQDK	329	10	15	23						3012
GAG	LVQNDNDCK	346	10	59	92	0.0002	0.0110				3013
GAG	GVGGTGHKAR	376	10	37	58	0.0003	0.0001				3014
GAG	GVGGTGHKAR	376	10	22	34						3015
GAG	GVGGTGHKAR	376	10	22	34						3016
GAG	GVGGTGHKAR	376	10	22	34						3017
GAG	GVGGTGHKAR	376	10	22	34						3018
GAG	GVGGTGHKAR	376	10	22	34						3019
GAG	GVGGTGHKAR	376	10	22	34						3020
GAG	GVGGTGHKAR	376	10	22	34						3021
GAG	GVGGTGHKAR	376	10	22	34						3022
GAG	GVGGTGHKAR	376	10	22	34						3023
GAG	GVGGTGHKAR	376	10	22	34						3024
GAG	GVGGTGHKAR	376	10	22	34						3025
GAG	GVGGTGHKAR	376	10	22	34						3026
GAG	GVGGTGHKAR	376	10	22	34						3027
GAG	GVGGTGHKAR	376	10	22	34						3028
GAG	GVGGTGHKAR	376	10	22	34						3029
GAG	GVGGTGHKAR	376	10	22	34						3030
GAG	GVGGTGHKAR	376	10	22	34						3031
GAG	GVGGTGHKAR	376	10	22	34						3032
GAG	GVGGTGHKAR	376	10	22	34						3033
GAG	GVGGTGHKAR	376	10	22	34						3034
GAG	GVGGTGHKAR	376	10	22	34						3035
GAG	GVGGTGHKAR	376	10	22	34						3036
GAG	GVGGTGHKAR	376	10	22	34						3037
GAG	GVGGTGHKAR	376	10	22	34						3038
GAG	GVGGTGHKAR	376	10	22	34						3039
GAG	GVGGTGHKAR	376	10	22	34						3040
GAG	GVGGTGHKAR	376	10	22	34						3041
GAG	GVGGTGHKAR	376	10	22	34						3042
GAG	GVGGTGHKAR	376	10	22	34						3043
GAG	GVGGTGHKAR	376	10	22	34						3044
GAG	GVGGTGHKAR	376	10	22	34						3045

Table IX
 HIV AD3 Super Motif Peptides With Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.01$	$\Delta^*1.01$	$\Delta^*3.01$	$\Delta^*6.01$	SEQ ID NO
GAG	TVATLYCVHQK	83	11	12	19					3046
GAG	TVATLYCVIOR	83	11	14	22					3047
GAG	EVKDTEALDK	95	11	13	20					3048
GAG	ALDKTEHQNK	105	11	12	17					3049
GAG	ALDKTEHQNK	105	11	15	21					3050
GAG	PAAADKESK	123	11	01	50					3051
GAG	ISPRILNAWVK	168	11	36	56					3052
GAG	LSPRILNAWVK	168	11	17	27					3053
GAG	TINEEAEDWR	225	11	53	83					3054
GAG	HAGHAGQGMK	240	11	18	28					3055
GAG	HAGHPPQGMK	240	11	19	30					3056
GAG	PIPPQGMREK	243	11	17	27					3057
GAG	WILLGLNKIVR	289	11	57	89					3058
GAG	TSILDIRQGPK	304	11	12	19					3059
GAG	VSILDIRQGPK	304	11	16	25					3060
GAG	VSILDIRQGPK	304	11	25	39					3061
GAG	DIKQKKEPR	308	11	19	30					3062
GAG	DIKQKKEPR	308	11	41	64					3063
GAG	LLVQNAIDCK	345	11	58	91					3064
GAG	NANPDCKTILK	349	11	27	42					3065
GAG	NANPDCKTILK	349	11	18	28					3066
GAG	AAMMMQKSNFK	406	11	06	15					3067
GAG	ATIMMGRGNFR	406	11	11	28					3068
GAG	AMQKGRGNFR	406	11	15	25					3069
GAG	ILANCRAPRK	433	11	16	22					3070
GAG	ILANCRAPRK	433	11	13	20					3071
GAG	ILANCRAPRK	433	11	20	31					3072
GAG	ILANCRAPRK	434	11	14	22					3073
GAG	ILANCRAPRK	434	11	13	21					3074
GAG	LARNCRAPRK	434	11	19	30					3075
GAG	CLERQNHPRK	525	11	02	49					3076
GAG	AVSQDLQK	525	11	10	50					3077
NEF	AVSQDLQK	48	8	10	16					3078
NEF	AVSRDLEK	48	8	11	17					3079
NEF	PLRPATFK	102	8	10	16					3080
NEF	PLRPATFK	102	8	49	77	0.0010	0.0003			3081
NEF	LSFLFKK	114	8	22	34					3082
NEF	LSFLFKK	114	8	21	32					3083
NEF	LSFLFKK	113	8	21	36					3084
NEF	YTPGGR	207	8	20	31					3085
NEF	YTPGGR	207	8	21	33					3086
NEF	YTPGGR	207	8	12	19					3087
NEF	YTPGGR	207	8	39	61					3088
NEF	LTEGWCTK	221	8	11	17					3089
NEF	KLVPVDRK	238	8	11	22					3090
NEF	ELIIPGYK	324	8	22	34					3091
NEF	ELIIPGYK	324	8	22	34					3092
NEF	GAVSQDLQK	47	9	10	16					3093
NEF	GAVSQDLQK	47	9	11	17	0.0002	0.0004	0.0006	0.0001	3094
NEF	PVRPQVILR	95	9	48	75					3095

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consistency (%)	A*0301	A*1101	A*101	A*3301	A*6801	SEQ ID NO
NEF	AVDLSHFLK	111	9	14	22	0.0740	1.1000	0.0009	0.0008	0.0025	3096
NEF	DLSPFLKEK	113	9	22	34						3097
NEF	DLSPHLEK	113	9	27	42						3098
NEF	GLDGLYSK	125	9	16	25						3099
NEF	GLDGLYSK	125	9	16	25						3100
NEF	PLTGWGFK	219	9	39	61						3101
NEF	AADGAVGYSR	42	10	09	15						3102
NEF	QVPLRPMFK	100	10	10	16						3103
NEF	QVPLRPMFK	100	10	46	72						3104
NEF	GAFLDLSFLK	110	10	10	16	0.6100	0.6300	0.0008	0.0130	0.0600	3105
NEF	GAFLDLSFLK	110	10	10	16						3106
NEF	GVGAVSRDLK	125	10	16	25						3107
NEF	GVGAVSRDLK	125	10	16	25						3108
NEF	GVGAVSRDLK	125	10	16	25						3109
NEF	AVDLSHFLK	111	11	11	17						3110
NEF	GLDGLYSKSR	125	11	14	22						3111
NEF	MARELIPTFYK	321	11	10	16						3112
NEF	GLDGLYSKSR	125	11	16	22						3113
POL	RANSPFSR	26	8	17	27						3114
POL	RANSPFSR	32	8	01	33						3115
POL	RANSPFSR	35	8	01	33						3116
POL	RANSPFSR	37	8	01	50						3117
POL	LIETCOR	149	8	14	22						3118
POL	LIETCOR	150	8	14	22						3119
POL	LIETCOR	150	8	14	22						3120
POL	PIETVPVK	190	8	53	83						3121
POL	ETVPVAKL	192	8	53	83	0.0049	0.0001				3122
POL	GMGGRKVK	201	8	51	80	0.0007	0.0004				3123
POL	PLTEGRK	212	8	55	86						3124
POL	PLTEGRK	212	8	55	86						3125
POL	NTVFAIK	246	8	24	38						3126
POL	NTVFAIK	246	8	37	58	0.0003	0.0003				3127
POL	NTVFAIK	248	8	25	39						3128
POL	PFVFAIKK	248	8	37	58	0.0003	0.0001				3129
POL	PAGLKKKK	286	8	52	81						3130
POL	PAGLKKKK	286	8	52	81						3131
POL	NVLQGVK	316	8	9	100	0.0003	0.0012				3132
POL	KLEPPK	355	8	23	36						3133
POL	DLGEGQIR	381	8	52	81						3134
POL	EGQIRAK	383	8	27	42						3135
POL	EGQIRAK	383	8	22	34						3136
POL	RTKSELEK	388	8	16	25						3137
POL	ELREHLLK	393	8	17	27						3138
POL	ELRQHLK	393	8	15	23						3139
POL	WTVNDIQK	441	8	62	97	0.0003	0.0001				3140
POL	DIQGLVGR	445	8	62	97						3141
POL	ELREHLLK	393	8	15	23						3142
POL	GVGAVSRDLK	125	8	62	97						3143
POL	DLAEIQR	516	8	28	44						3144
POL	QIVQEPEK	532	8	41	64	0.0010	0.0013				3145

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*3001	A*1101	A*3101	A*6801	SEQ ID NO
POL	GAHTNDVK	551	8	19	30					3146
POL	TAINTNDVK	551	8	16	17					3147
POL	TAINTNDVK	551	8	11	17					3148
POL	QLTEAVQK	559	8	37	58					3149
POL	QLTEAVQK	559	8	11	17					3150
POL	LSIWIWTK	570	8	50	79					3151
POL	VWGKTKK	573	8	48	75					3152
POL	LSIWIWTK	573	8	16	72					3153
POL	YVDEANR	613	8	50	79					3154
POL	GAANREIK	636	8	45	70	0.0003	0.0001			3155
POL	KAGYVTR	646	8	42	66					3156
POL	VTDRGQRK	650	8	40	63	0.0090	0.0065			3157
POL	LDTTNRK	661	8	19	30					3158
POL	ITVNRK	661	8	10	17					3159
POL	ITVNRK	661	8	40	63					3160
POL	ITVNRK	661	8	16	25					3161
POL	ITVNRK	661	8	37	58					3162
POL	ITVNRK	661	8	37	58					3163
POL	ITVNRK	661	8	22	34					3164
POL	ITVNRK	661	8	22	34					3165
POL	ITVNRK	661	8	17	28					3166
POL	ITVNRK	661	8	17	28					3167
POL	ITVNRK	661	8	29	45					3168
POL	ITVNRK	661	8	16	25	0.0091	0.0054			3169
POL	ITVNRK	661	8	27	42					3170
POL	ITVNRK	661	8	27	42					3171
POL	ITVNRK	661	8	26	41					3172
POL	ITVNRK	661	8	26	41					3173
POL	ITVNRK	661	8	45	70					3174
POL	ITVNRK	661	8	31	48					3175
POL	ITVNRK	661	8	27	42					3176
POL	ITVNRK	661	8	27	42					3177
POL	ITVNRK	661	8	25	39					3178
POL	ITVNRK	661	8	50	78					3179
POL	ITVNRK	661	8	49	77					3180
POL	ITVNRK	661	8	53	83					3181
POL	ITVNRK	661	8	53	83					3182
POL	ITVNRK	661	8	53	83					3183
POL	ITVNRK	661	8	58	91					3184
POL	ITVNRK	661	8	14	22	0.0280	0.0380			3185
POL	ITVNRK	661	8	36	56					3186
POL	ITVNRK	661	8	13	21					3187
POL	ITVNRK	661	8	35	56					3188
POL	ITVNRK	661	8	35	56					3189
POL	ITVNRK	661	8	36	57					3190
POL	ITVNRK	661	8	58	91					3191
POL	ITVNRK	661	8	35	55					3192
POL	ITVNRK	661	8	14	22					3193
POL	ITVNRK	661	8	14	22					3194
POL	ITVNRK	661	8	36	56					3195
POL	ITVNRK	661	8	19	30					3196

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*2101	A*1301	A*4801	SEQ ID NO
POL	DIKVVPR	1009	8	48	75						3196
POL	ERKVVPR	1009	8	16	25						3197
POL	ELKVRK	1012	8	52	81		0.0001				3198
POL	VYPRK	1012	8	11	17						3199
POL	KIKDYK	1019	8	11	17						3200
POL	KIRDYK	1019	8	50	78						3201
POL	LAFOQEAR	6	9	12	19						3202
POL	LAFOQEAR	6	9	16	25						3203
POL	QTRANSFTR	21	9	15	24						3204
POL	PSRSFTSR	31	9	01	33						3205
POL	PSRSFTSR	39	9	01	33						3206
POL	PSRSFTSR	39	9	01	33						3207
POL	THKGGGLK	99	9	17	27	0.2700	0.0330	0.0010	0.0008	0.1100	3208
POL	DNLKGRWK	122	9	13	20						3209
POL	ENLKGKWK	122	9	13	19						3210
POL	NLKGKWK	124	9	36	56						3211
POL	GGGKVK	136	9	11	17						3212
POL	GGGKVK	136	9	15	24						3213
POL	QLEHCK	148	9	14	22	0.0008	0.0005	0.0062	0.0120	0.0001	3214
POL	ILIECGKK	149	9	14	22						3215
POL	PTPVNIGR	166	9	54	84	0.0008	0.0001	0.0007	0.0120	0.0002	3216
POL	CTEMEKEGK	225	9	28	44	0.0002	0.0001	0.0006	0.0006	0.0002	3217
POL	NTPIAKK	246	9	24	38						3218
POL	NTPIAKK	246	9	37	58	0.0330	0.0600	0.0006	0.0006	1.7000	3219
POL	AKKAKK	263	9	62	89	0.0017	0.0086	0.0018	0.0005	0.0001	3220
POL	LYDFELAK	263	9	62	89	0.0002	0.0000	0.0006	0.0006	0.0002	3221
POL	GHIFAGLK	282	9	56	89	0.2300	0.0650	0.0057	0.0005	0.0110	3222
POL	SVPLDKDFR	306	9	18	28						3223
POL	ALPQSSMTK	347	9	36	56	1.1000	0.9600	0.0076	0.0005	0.0230	3224
POL	MTKLEFFR	353	9	43	67	0.0008	0.0160	0.2200	0.4200	0.3100	3225
POL	TSQVKKQK	404	9	57	89	0.0002	0.0042	0.0021	0.0029	0.0053	3226
POL	ASQVPIK	456	9	23	43	0.0013	0.3400	0.0005	0.0018	0.0001	3227
POL	QIVAGIKVK	458	9	20	32						3228
POL	QIVAGIKVK	458	9	12	19						3229
POL	QIVAGIKVK	458	9	14	22						3230
POL	QIVAGIKVK	458	9	14	22						3231
POL	GRVQLQCK	462	9	28	44						3232
POL	GRVQLQCK	462	9	19	30						3233
POL	LAENELK	462	9	28	44						3234
POL	NIKTGKYAK	540	9	29	46	0.0002	0.0001	0.0004	0.0006	0.0001	3235
POL	NIKTGKYAK	540	9	29	46	0.0008	0.0001	0.0130	0.4400	0.0033	3236
POL	NIKTGKYAK	542	9	19	30						3237
POL	KTGKYAKMR	542	9	13	21						3238
POL	KTGKYAKMR	550	9	10	16						3239
POL	RSATINDVK	550	9	48	75	0.0850	0.3700	0.9900	0.3600	0.0330	3240
POL	RYNTRPK	572	9	44	86	0.0060	0.0600	0.0009	0.0099	0.0380	3241
POL	YVTRPK	572	9	39	66	0.0011	0.0010	0.0006	0.0006	0.0039	3242
POL	YVTRPK	609	9	11	17						3243
POL	SLTIDTNGK	660	9	21	33						3244
POL	SLTIDTNGK	660	9	21	33	0.0009	0.0400	0.0006	0.0005	0.0003	3245
POL	GHQAQPK	696	9	40	63						3246

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SHQ ID NO
POL	GHQAQPR	696	9	16	25						3246
POL	QHLELIKK	712	9	37	58	0.0091	0.1600	0.0006	0.0005	0.0120	3247
POL	YLAWVFAHK	724	9	22	34	0.0770	0.0570	0.0550	0.8800	4.0000	3248
POL	YLVFAHK	742	9	17	25						3249
POL	KLVSAGGRK	742	9	16	25	0.1300	0.0770	0.0017	0.0020	0.0001	3250
POL	KLVSAGGRK	742	9	27	42						3251
POL	VLEFLGDIK	751	9	51	80	0.0380	0.0320	0.0006	0.0006	0.0004	3252
POL	ASCDKCLQK	790	9	43	67	0.0027	0.0140	0.0020	0.0009	0.0001	3253
POL	KLAWRWPK	855	9	50	78	2.7000	0.0690	0.2100	0.0006	0.0002	3254
POL	AAACWAGIK	880	9	21	33	0.0130	0.0470	0.0023	0.0041	0.0014	3255
POL	ESLRELK	904	9	23	35						3256
POL	YLVFAHK	911	9	16	25	0.0170	0.1000	0.0480	0.0560	3.2000	3257
POL	AVFLINERK	911	9	62	97	0.1700	1.8000	3.5000	0.2700	1.9000	3258
POL	ILASHQITK	955	9	14	22						3259
POL	IATDIQIK	955	9	35	55	0.0250	0.0980	0.0007	0.0005	0.0002	3260
POL	DIQIKELQK	959	9	46	72	0.0099	0.0006	0.0006	0.0018	0.0001	3261
POL	QIKQPR	968	9	12	19						3262
POL	YLVFAHK	968	9	15	23	0.0021	0.0045	0.2400	0.0660	0.2600	3263
POL	VIDNSDIK	1003	9	37	58	0.0099	0.0068	0.0006	0.0005	0.0001	3264
POL	VIDNSDIK	1003	9	12	19						3265
POL	NSDIKVVPR	1007	9	40	63						3266
POL	NSDIKVVPR	1007	9	12	19						3267
POL	DIKVVPRK	1009	9	48	75	0.0002	0.0001	0.0006	0.0069	0.0065	3268
POL	DIKVVPRK	1009	9	15	23						3269
POL	KYPRKVK	1011	9	12	19	0.0290	0.0039	0.3100	0.0008	0.0002	3270
POL	KYPRKVK	1011	9	11	17						3271
POL	NLAFOQGEAR	5	10	16	25						3272
POL	NLAFOQGEAR	5	10	16	25						3273
POL	QTRAAQSPTR	21	10	11	18						3274
POL	QTRAAQSPTR	21	10	12	19						3275
POL	PSKANSPTSR	24	10	01	30						3276
POL	PSKANSPTSR	33	10	01	30						3277
POL	QTRAAQSPTR	35	10	01	33						3278
POL	VTIKIGQGLK	98	10	17	27						3279
POL	VLEEDNPGK	119	10	13	20	0.0370	0.2100	0.0017	0.0025	0.0640	3280
POL	VLEEDNPGK	119	10	12	19						3281
POL	MIGGGGIFK	133	10	62	97	0.0099	0.0550	0.0052	0.0012	0.3100	3282
POL	QLIEICQK	148	10	14	22	0.0033	0.0310	0.0017	0.0025	0.0001	3283
POL	KLVSAGGRK	188	10	53	83	0.0002	0.0001	0.0009	0.0009	0.0001	3284
POL	KLVSAGGRK	190	10	53	83	0.3900	0.0760	0.0009	0.0009	0.0003	3285
POL	KLKQMDGPK	197	10	49	77						3286
POL	LVEICTEMEK	221	10	15	24	0.0002	0.0120	0.0010	0.0013	0.0024	3287
POL	EMEKIGRISK	229	10	33	52	0.0004	0.0001	0.0009	0.0009	0.0003	3288
POL	NTPFAIKKK	246	10	24	38	0.0006	0.0046				3289
POL	NTPFAIKKK	246	10	37	58	0.0004	0.0002				3290
POL	PAKQDQSLK	260	10	62	97	0.1000	0.0960				3291
POL	KYPRKVK	263	10	60	94						3292
POL	LYPDELNRK	263	10	60	94						3293
POL	GHPHAGLKK	282	10	54	86	0.0110	0.1700	0.0009	0.0009	0.0007	3294
POL	DAVFSVFLDK	302	10	21	33						3295

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Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*2101	A*3301	A*5801	SEQ ID NO
POL	FSVLKDFR	305	10	18	28						3296
POL	SVLIDEDFR	306	10	18	28						3297
POL	SVLIDEDFR	307	10	18	28						3298
POL	SNINPEIR	323	10	11	17						3299
POL	PAFQSSMTK	346	10	36	56	0.0760	0.0930	0.0017	0.0025	0.0046	3300
POL	SMKLEPER	352	10	42	66	0.0004	0.0004				3301
POL	MTKLEPER	353	10	22	34	0.0150	0.0380	0.0150	0.0060	0.1100	3302
POL	GSLEIGQIR	379	10	52	81						3303
POL	DLFLEIQR	381	10	27	42						3304
POL	DLFLEIQR	381	10	27	42						3305
POL	FTIPDKHDK	403	10	51	80	0.0002	0.0150	0.0010	0.0013	0.0223	3306
POL	WMGVLEIPDK	418	10	60	94	0.0005	0.0004	0.0009	0.0016	0.0063	3307
POL	TVQIVLPEK	429	10	17	27						3308
POL	TVQIVLPEK	439	10	13	20	0.1040	5.6000				3309
POL	ESWIVLPEK	439	10	43	67	0.0007	0.0002				3310
POL	ESWIVLPEK	440	10	11	17						3311
POL	WASQIVAGIK	455	10	27	42						3312
POL	WASQIVAGIK	455	10	28	44						3313
POL	KVQLCKLLR	464	10	27	42						3314
POL	KVQLCKLLR	464	10	19	30						3315
POL	QVQLCKLLR	467	10	25	39						3316
POL	QVQLCKLLR	467	10	25	39						3317
POL	EAELEAFNR	487	10	51	83						3318
POL	ELAENREIK	491	10	54	84	0.0002	0.0003				3319
POL	ALTSIVWGK	568	10	19	30						3320
POL	ALTSIVWGK	571	10	42	66						3321
POL	SVINGKTRK	571	10	27	42						3322
POL	SVINGKTRK	573	10	27	42						3323
POL	SVINGKTRK	573	10	27	42						3324
POL	LVKLWVLEK	614	10	46	72	0.0360	0.0016	0.0075	0.0081	0.0097	3325
POL	AAANREPLK	637	10	30	47						3326
POL	KAGVIDRGR	646	10	39	61						3327
POL	VSLEDTNOK	659	10	20	31	0.0007	0.0370	0.0017	0.0025	0.0007	3328
POL	VSLEDTNOK	659	10	20	31	0.0004	0.0370	0.0017	0.0025	0.0007	3329
POL	VSLEDTNOK	659	10	20	31	0.0004	0.0370	0.0017	0.0025	0.0007	3330
POL	VSLEDTNOK	659	10	30	47	0.0005	0.0001	0.0009	0.0009	0.0003	3331
POL	IBQLKEIK	713	10	58	91						3332
POL	GHGNEQVOK	733	10	58	91						3333
POL	KVFLDGIK	750	10	48	75	0.3600	0.7800				3334
POL	VASCDICQIK	789	10	43	67	0.0004	0.0004				3335
POL	VASCDICQIK	789	10	60	95	0.0010	0.0003				3336
POL	GSNFTSVK	814	10	16	24						3337
POL	GSNFTSVK	870	10	16	24						3338
POL	KAACWVAGIK	879	10	20	32	0.0300	0.0740	0.0017	0.0025	0.0002	3339
POL	VVESNNKELK	902	10	48	75						3340
POL	ELKKIGQVR	909	10	56	88	0.0089	0.0093				3341
POL	QVRLKEIK	916	10	44	69						3342
POL	QVRLKEIK	916	10	44	69	0.6100	0.6400	0.0240	0.0083	0.0610	3343
POL	QVRLKEIK	916	10	60	94	0.0068	0.0083				3344
POL	MAVFIHNEK	930	10	60	94						3345
POL	AVFIHNEK	931	10	58	91	0.6600	0.8500	0.0010	0.0029	0.0003	3346
POL	GIGGYSAGER	942	10	58	91	0.0003	0.0001				3347

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Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*301	A*101	A*3101	A*4801	SEQ ID NO
POL	DHDSIQTK	954	10	14	22					3346
POL	DIATDIQTK	954	10	34	33				0.0170	3347
POL	KQNRVYVR	971	10	52	81	0.0056	0.0130	0.0025	0.0170	3348
POL	YVQNSQTK	1002	10	17	58	0.0005	0.0210	0.0080	0.0380	3349
POL	YVQNSQTK	1002	10	17	58	0.0005	0.0210	0.0013	0.0018	3350
POL	NSDKVYPR	1007	10	40	63	0.0007	0.0901		0.0018	3351
POL	NSDKVYPR	1007	10	12	19					3352
POL	KAKIRIDYGR	1017	10	41	64	0.0048	0.0018			3353
POL	MAGDCVAGR	1028	10	24	38					3354
POL	MAGDCVAGR	1028	10	24	38					3355
POL	NSPTRELOVR	37	11	40	31					3356
POL	NSPTRELOVR	37	11	40	31					3357
POL	NSPTRELOVR	37	11	50	50					3358
POL	NSPTRELOVR	39	11	01	50					3359
POL	FSPTQILWQR	85	11	14	22					3360
POL	TLWQRPLVTK	91	11	17	27					3361
POL	TLWQRPLVTK	91	11	13	20					3362
POL	TVLEENLQGR	91	11	13	20					3363
POL	TVLEENLQGR	118	11	13	20					3364
POL	TVLEENLQGR	118	11	12	19					3365
POL	DNLQGRWKPR	122	11	13	20					3366
POL	ENLQGRWKPR	122	11	12	19					3367
POL	ENLQGRWKPR	122	11	12	19					3368
POL	ENLQGRWKPR	122	11	52	87	2.3000	0.7000			3369
POL	ENLQGRWKPR	187	11	52	87					3370
POL	KVQWPLTEK	207	11	46	72	0.0750	0.0330			3371
POL	ALVELCTEMK	220	11	15	23					3372
POL	EICTEMEKEK	223	11	27	42					3373
POL	ARKKQSTKWR	251	11	57	89					3374
POL	ARKKQSTKWR	251	11	58	91					3375
POL	SLVDRELQGR	262	11	60	92					3376
POL	OLGPHIPAGLK	280	11	56	89					3377
POL	GHIPHAGLKK	282	11	53	84					3378
POL	FSVPLDKDFRK	305	11	18	28					3379
POL	FSNNETFOIR	322	11	31	48					3380
POL	FSNNETFOIR	322	11	31	48					3381
POL	SSMTKLEPR	352	11	32	50					3382
POL	SMTKLEPR	352	11	22	34					3383
POL	KIELREHLK	390	11	13	20					3384
POL	KIELREHLK	390	11	15	23					3385
POL	LLKRGFTTFDK	398	11	23	36					3386
POL	LLKRGFTTFDK	398	11	23	36					3387
POL	WTQVQPLFEK	428	11	13	20					3388
POL	WTQVQPLFEK	428	11	13	20					3389
POL	TVNDQKQLVGR	442	11	61	95	0.0011	0.0510			3390
POL	ASQYAGIKVK	456	11	20	32	0.0400	0.1700			3391
POL	ASQYAGIKVK	456	11	12	19					3392
POL	ASQYAGIKVK	456	11	18	26					3393
POL	YVIGYVQVCK	505	11	39	61					3394
POL	PVIGYVQVCK	505	11	25	39					3395
POL	PSKDLAEIQK	513	11	25	63	0.9200	0.0540			3396
POL	WTYQIQYQEK	529	11	40						3397

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	Δ^*1101	Δ^*3101	Δ^*3301	Δ^*6801	SEQ ID NO
POL	QVQGPFRKILK	532	11	40	63	0.2800	0.2900				3396
POL	NLKTGKYARIR	540	11	18	29						3397
POL	NLKTGKYARIR	540	11	13	21						3398
POL	BMRGATINDYK	548	11	12	19						3399
POL	DVKOLTEAVOK	556	11	33	22		0.0240				3400
POL	IATSVIWKVK	567	11	14	22						3401
POL	ESVIVWGRK	570	11	17	65						3402
POL	IVWKGKTKER	572	11	17	27						3403
POL	KTPKEFLPIQK	572	11	29	45						3404
POL	KTPKEFLPIQK	577	11	14	22						3405
POL	PLVKLWYQLEK	577	11	22	34						3406
POL	EFYVUGAANIR	630	11	45	70						3407
POL	EFYVUGAANIR	630	11	33	69						3408
POL	KLKGAQYVIR	643	11	30	47						3409
POL	VVSLTITTNQK	658	11	24	38						3410
POL	VVSLTITTNQK	658	11	11	17						3411
POL	ALGIQACPDK	694	11	39	21						3412
POL	LYNQIEQLIK	694	11	15	23						3413
POL	LYNQIEQLIK	709	11	18	28						3414
POL	VSDIQLIK	710	11	19	30						3415
POL	QHEQLIKK	712	11	30	47						3416
POL	KVYLAWVPPIK	722	11	20	32		2.3000				3417
POL	KVYLAWVPPIK	722	11	23	37						3418
POL	QVDELVSAGIR	739	11	5	5	8.6000					3419
POL	QVDELVSAGIR	739	11	29	45						3420
POL	QVDELVSAGIR	756	11	25	39						3421
POL	QVDELVSAGIR	756	11	14	22						3422
POL	QVDELVSAGIR	756	11	45	71						3423
POL	QVDELVSAGIR	756	11	45	71						3424
POL	QVDELVSAGIR	756	11	45	71						3425
POL	QVDELVSAGIR	756	11	45	71						3426
POL	QVDELVSAGIR	756	11	45	71						3427
POL	QVDELVSAGIR	756	11	45	71						3428
POL	QVDELVSAGIR	756	11	45	71						3429
POL	QVDELVSAGIR	756	11	45	71						3430
POL	QVDELVSAGIR	756	11	45	71						3431
POL	QVDELVSAGIR	756	11	45	71						3432
POL	QVDELVSAGIR	756	11	45	71						3433
POL	QVDELVSAGIR	756	11	45	71						3434
POL	QVDELVSAGIR	756	11	45	71						3435
POL	QVDELVSAGIR	756	11	45	71						3436
POL	QVDELVSAGIR	756	11	45	71						3437
POL	QVDELVSAGIR	756	11	45	71						3438
POL	QVDELVSAGIR	756	11	45	71						3439
POL	QVDELVSAGIR	756	11	45	71						3440
POL	QVDELVSAGIR	756	11	45	71						3441
POL	QVDELVSAGIR	756	11	45	71						3442
POL	QVDELVSAGIR	756	11	45	71						3443
POL	QVDELVSAGIR	756	11	45	71						3444
POL	QVDELVSAGIR	756	11	45	71						3445

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HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*6801	SEQ ID NO
POL	EIKVTRIRAK	1009	11	13	20					3446
POL	YVIRKIRAK	1010	11	24	36					3447
POL	QVIRKIRAK	1011	11	42	38					3448
POL	QVAGDCVAGR	1027	11	19	30					3449
REV	QVAGDCVAGR	1027	8	12	19					3450
REV	DSIDELLK	7	8	17	27					3451
REV	QARKNRNR	40	8	18	19					3452
REV	QARKNRNR	40	8	18	19					3453
REV	RAHQQRIR	20	8	12	19					3454
REV	RAHQQRIR	20	8	12	19					3455
REV	LSLTCGRK	103	8	06	19					3456
REV	LSLTCGRK	103	8	06	19					3457
REV	LLKTVRLK	12	9	10	16					3458
REV	GTRQARKNR	36	9	15	23					3459
REV	GTRQARKNR	36	9	15	23					3460
REV	GTRQARKNR	36	9	01	50					3461
REV	TTRQARKNR	37	9	16	25					3462
REV	QARKNRNR	40	9	38	59					3463
REV	QARKNRNR	40	9	38	59					3464
REV	ELSLTCLGR	62	9	12	19					3465
REV	PLQLPIER	76	9	11	17					3466
REV	PLQLPIER	76	9	35	55					3467
REV	PSPEGTQAR	31	10	13	20					3468
REV	GTRQARKNR	36	10	15	23					3469
REV	GTRQARKNR	36	10	34	53					3470
REV	QARKNRNR	37	10	01	50					3471
REV	TTRQARKNR	37	10	01	50					3472
REV	RSQSDDELLK	4	11	11	17					3473
REV	PSPEGTQAR	31	11	13	20					3474
REV	GTRQARKNR	36	11	34	53					3475
REV	GTRQARKNR	36	11	34	53					3476
REV	GTRQARKNR	37	11	01	50					3477
REV	GTRQARKNR	37	11	01	50					3478
REV	QARKNRNR	40	11	16	25					3479
REV	QARKNRNR	40	11	37	58					3480
REV	VPVQLPIPIER	74	11	11	17					3481
REV	VPVQLPIPIER	74	11	54	87					3482
TAT	GLGISYGR	47	8	58	91					3483
TAT	GLGISYGR	47	8	58	91					3484
TAT	ISYGRKSK	48	8	58	91					3485
TAT	PTGPKSK	88	8	20	31					3486
TAT	TACNNCYCK	23	9	17	27					3487
TAT	TACTNICYCK	23	9	10	16					3488
TAT	GLGISYGRK	47	9	57	89					3489
TAT	GLGISYGRK	47	9	57	89					3490
TAT	GLGISYGRK	48	9	46	72					3491
TAT	PTGPKSK	88	9	18	28					3492
TAT	ESKKVKVSK	93	9	12	19					3493
TAT	VPDPLPIPIK	3	10	11	17					3494
TAT	TACNNCYCKK	23	10	11	17					3495
TAT	GLGISYGRKK	45	10	35	57					3496
TAT	GLGISYGRKK	47	10	45	70					3497

Table IX
HIV A03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1301	A*1101	A*3101	A*1301	A*6801	SEQ ID NO
TAT	PTGPKSKKK	88	10	12	19						3496
TAT	KAGPGGYRR	101	10	01	50						3497
TAT	GLGISYGRKKR	45	11	54	86						3498
TAT	ISYGRGGRQR	48	11	39	61						3499
TAT	KLGLGKGRKK	01	11	10	16						3500
VIF	LMVQVDR	8	8	10	16						3501
VIF	MLVQVDR	8	8	46	72						3502
VIF	QVDEMRKR	12	8	13	20						3503
VIF	QVDEMRKR	12	8	34	53						3504
VIF	RMINTWK	15	8	10	16						3505
VIF	RTWNSLVK	15	8	15	23						3506
VIF	RTWNSLVK	15	8	15	23						3507
VIF	RTWNSLVK	19	8	27	42						3508
VIF	LIPLGDAR	56	8	13	20						3509
VIF	LIPLGEAR	56	8	20	31						3510
VIF	GVSEWRK	87	8	16	25						3511
VIF	GVSEWRK	87	8	16	25						3512
VIF	GVSEWRK	88	8	15	23						3513
VIF	GVSEWRK	88	8	15	23						3514
VIF	FSESARK	120	8	13	20						3515
VIF	FSESARK	120	8	14	22						3516
VIF	SLQYLAK	149	8	13	20						3517
VIF	SLQYLAK	153	8	16	25						3518
VIF	LALTALIK	153	8	16	25						3519
VIF	LALTALIK	155	8	13	20						3520
VIF	LALTALIK	155	8	13	20						3521
VIF	LKPKKIK	158	8	10	16						3522
VIF	LTEDRWK	178	8	31	48	0.0003	0.0045				3523
VIF	LVEDRWK	178	8	11	17						3524
VIF	VMVWQVDR	7	9	44	69	0.0034	0.0220	4.8000	5.5000	0.0010	3525
VIF	VMVWQVDR	9	9	12	20						3526
VIF	VMVWQVDR	9	9	42	72	0.0008	0.0007	0.4500	0.5600	0.0048	3527
VIF	GVSEWRK	87	9	14	22						3528
VIF	GVSEWRK	88	9	11	17						3529
VIF	GVSEWRK	88	9	11	17						3530
VIF	GVSEWRK	88	9	13	20						3531
VIF	GVSEWRK	88	9	16	25						3532
VIF	GVSEWRK	88	9	16	25						3533
VIF	GVSEWRK	88	9	16	25						3534
VIF	GVSEWRK	88	9	16	25						3535
VIF	GVSEWRK	88	9	16	25						3536
VIF	GVSEWRK	88	9	16	25						3537
VIF	GVSEWRK	88	9	16	25						3538
VIF	GVSEWRK	88	9	16	25						3539
VIF	GVSEWRK	88	9	16	25						3540
VIF	GVSEWRK	88	9	16	25						3541
VIF	GVSEWRK	88	9	16	25						3542
VIF	GVSEWRK	88	9	16	25						3543
VIF	GVSEWRK	88	9	16	25						3544
VIF	GVSEWRK	88	9	16	25						3545

Table IX
HIV A03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*030	A*101	A*301	A*680	SEQ ID NO
VIF	ALALIKPKK	154	10	11	17					3546
VIF	PSYKLTEDR	173	10	13	20					3547
VIF	WVQVDRMR	9	11	13	64					3548
VIF	WVQVDRMR	9	11	33	52					3549
VIF	QVDRMRITWK	12	11	10	16					3550
VIF	QVDRMRITWK	12	11	14	22					3551
VIF	SLVNIHMYSK	23	11	12	19					3552
VIF	SLVNIHMYSK	23	11	12	19					3553
VIF	SLVNIHMYSK	28	11	22	19					3554
VIF	ILCHGGSSEVR	83	11	22	34					3555
VIF	ILCHGGSSEVR	83	11	22	34					3556
VIF	ILCHGGSSEVR	83	11	25	39					3557
VIF	ILCHGGSSEVR	83	11	13	20					3558
VIF	LAALALIKPK	152	11	13	20					3559
VIF	LAALALIKPK	153	11	13	33					3560
VIF	LIEDRWKPKQK	178	11	21	17		0.0130			3561
VIF	LIEDRWKPKQK	178	11	17	16					3562
VIF	ELKSEAVR	25	8	17	27					3563
VIF	ELKSEAVR	25	8	16	25					3564
VIF	EAVRIHPR	29	8	59	92					3565
VIF	QLLEHIFR	66	8	44	69					3566
VIF	QLLEHIFR	66	8	10	16					3567
VIF	QLLEHIFR	66	8	10	16					3568
VIF	RIGTRISR	74	8	12	19					3569
VIF	ISRGHTR	79	8	10	16					3570
VIF	ISRGHTR	79	8	11	17					3571
VIF	ISRGHTR	81	8	10	16					3572
VIF	RIGTRISR	85	8	10	50					3573
VIF	RIGTRISR	85	8	10	30					3574
VIF	RANGASR	91	8	19	16					3575
VIF	ALLELEELK	19	9	10	16					3576
VIF	ALLELEELK	19	9	44	69					3577
VIF	WAGVEAIR	54	9	16	25					3578
VIF	WAGVEAIR	54	9	11	17					3579
VIF	FIHFRCGR	69	9	11	17					3580
VIF	FIHFRCGR	69	9	10	62					3581
VIF	QAVEDQDQK	3	10	39	15					3582
VIF	WALELEELK	18	10	09	15					3583
VIF	WALELEELK	18	10	42	69					3584
VIF	KSEAVRIHPR	27	10	14	22					3585
VIF	ISRGHTRQK	79	10	10	16					3586
VIF	ISRGHTRQK	79	10	17	21					3587
VIF	LELEKSEAVR	22	11	16	25					3588
VIF	DTWAGVEAIR	52	11	16	28					3589
VIF	DTWAGVEAIR	52	11	18	28					3590
VIF	ILQLLEHIFR	63	11	35	55					3591
VIF	ILLEHIFRCGR	11	11	11	17					3592
VIF	ILLEHIFRCGR	11	11	10	16					3593
VIF	ILLEHIFRCGR	11	11	10	16					3594
VIF	TVFIEYR	36	8	12	19					3595
VIF	LVQKQDKR	43	8	01	50					3596
VIF	KIDRLIDR	52	8	15	23					3597

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
VPU	LIDRRER	58	8	14	22						3596
VPU	VTLSSSK	94	8	01	16						3597
VPU	WTVVFIEYR	34	9	01	16						3598
VPU	LVQRKQDRR	46	9	01	50						3599
VPU	LVQRKQDRR	46	9	15	23						3600
VPU	LIDRRER	56	9	10	16						3601
VPU	VTLSSSK	91	9	01	50						3602
VPU	KILQRKQDR	45	10	15	23	0.0039	0.0001				3603
VPU	KIDRIDRR	52	10	10	16						3604
VPU	VVWTVVFIEYR	31	11	10	16						3605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	Nc. of Amino Acids	Sequence Frequency	Consensus (P)	A*2401	SFQ ID NO
ENV	LILGLVII	21	8	09	15		3606
ENV	KLWVTYYY	44	8	11	17		3607
ENV	NLWVTYYY	44	8	35	52		3608
ENV	DTESIVNW	49	8	55	86		3609
ENV	NTLENFM	75	8	19	30		3610
ENV	VLENFMNW	101	8	34	53		3611
ENV	SLKPCVKL	102	8	34	53		3612
ENV	LTPLCVTL	128	8	55	86		3613
ENV	HYCAPAGF	135	8	54	84		3614
ENV	HYCAPAGF	262	8	17	42		3615
ENV	CTPAGFAL	264	8	11	17		3616
ENV	TVQCTIGI	290	8	10	16		3617
ENV	PVYSTOLL	300	8	51	80		3618
ENV	VYSTOLL	301	8	60	94		3619
ENV	QLLNGSL	305	8	60	94		3620
ENV	NTRKSRI	351	8	57	89		3621
ENV	SLKPCVKL	351	8	10	17		3622
ENV	GIKGGITF	360	8	11	17		3623
ENV	SIGSGOAF	360	8	01	33		3624
ENV	I-YAIGDII	367	8	12	19		3625
ENV	KLRIHQF	405	8	01	25		3626
ENV	SPNCGGEF	437	8	01	25		3627
ENV	SPNCGGEF	447	8	36	56		3628
ENV	SPNCGGEF	447	8	16	28		3629
ENV	ITFEGTIL	478	8	21	31		3630
ENV	ITFEGTIL	478	8	01	50		3631
ENV	NTLPCRI	482	8	11	17		3632
ENV	TITLPCRI	482	8	14	22		3633
ENV	RIKQINM	488	8	30	47		3634
ENV	RIKQINM	488	8	12	17		3635
ENV	CHRCSSNI	512	8	01	17		3636
ENV	AVGIGIAF	537	8	25	39		3637
ENV	KVVKLEPI	565	8	11	17		3638
ENV	AVGIGIAF	595	8	11	17		3639
ENV	STMGAASI	614	8	39	61		3640
ENV	LTVOARQL	623	8	38	59		3641
ENV	LTVOARQL	624	8	36	41		3642
ENV	TVQQQNL	634	8	32	50		3643
ENV	TVQQQNL	634	8	32	50		3644
ENV	AVGIGIAF	644	8	49	77		3645
ENV	ILLKLTIV	650	8	13	20		3646
ENV	ILLKLTIV	650	8	34	53		3647
ENV	HMLQLTVW	650	8	10	16		3648
ENV	TVWGIKQL	655	8	59	86		3649
ENV	TVWGIKQL	665	8	33	53		3650
ENV	RYLKDQQL	671	8	34	53		3651
ENV	RYLKDQQL	671	8	30	47		3652
ENV	RYLKDQQL	671	8	18	28		3653
ENV	YLKDQQL	672	8	31	48	0.0001	3654
ENV	YLKDQQL	672	8	18	28		3655

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*3401	SEQ ID NO
ENV	WQCSGRL	681	8	48	75		3656
ENV	EWDMNTW	712	8	48	20		3657
ENV	EWDMNTW	716	8	13	20		3658
ENV	IWNMTWM	717	8	11	17		3659
ENV	IWNMTWM	717	8	17	27		3660
ENV	WNEWEREI	723	8	12	19		3661
ENV	DLLADKW	754	8	21	33		3662
ENV	ELDKWASI	757	8	11	11		3663
ENV	ELDKWASI	757	8	11	11		3664
ENV	ELDKWASI	757	8	18	28		3665
ENV	KWASLWNN	760	8	26	41		3666
ENV	SLWNWFDI	763	8	17	27		3667
ENV	WFDITNWL	767	8	10	16		3668
ENV	DIHFLVY	769	8	10	16		3669
ENV	INWNLWYI	770	8	16	23		3670
ENV	INWNLWYI	770	8	19	30		3671
ENV	KWLWYIKI	772	8	19	30		3672
ENV	NWLWYIKI	772	8	25	39		3673
ENV	NWLWYIKI	773	8	50	78		3674
ENV	WLWYIKFI	774	8	49	77		3675
ENV	WYIKFI	775	8	43	67		3676
ENV	YIKFI	776	8	43	67		3677
ENV	FINVGGI	780	8	44	69		3678
ENV	FINVGGI	781	8	35	56		3679
ENV	IVGGIIGL	783	8	42	66		3680
ENV	IVGGIIGL	783	8	10	16		3681
ENV	IVGGIIGL	783	8	16	23		3682
ENV	IVGGIIGL	787	8	16	25		3683
ENV	IVGGIIGL	787	8	29	45		3684
ENV	IVGGIIGL	787	8	15	23		3685
ENV	IVGGIIGL	792	8	20	31		3686
ENV	IVGGIIGL	792	8	10	16		3687
ENV	IVGGIIGL	809	8	13	20		3688
ENV	IVGGIIGL	812	8	13	20		3689
ENV	IVGGIIGL	842	8	14	22		3690
ENV	IVGGIIGL	845	8	19	30		3691
ENV	IVGGIIGL	845	8	20	31		3692
ENV	IVGGIIGL	853	8	20	31		3693
ENV	IVGGIIGL	856	8	17	27		3694
ENV	IVGGIIGL	856	8	42	66		3695
ENV	IVGGIIGL	864	8	18	28		3696
ENV	IVGGIIGL	864	8	23	36		3697
ENV	IVGGIIGL	867	8	13	20		3698
ENV	IVGGIIGL	881	8	09	15		3699
ENV	IVGGIIGL	881	8	23	37		3700
ENV	IVGGIIGL	881	8	12	19		3701
ENV	IVGGIIGL	896	8	12	19		3702
ENV	IVGGIIGL	902	8	15	23		3703
ENV	IVGGIIGL	903	8	15	23		3704
ENV	IVGGIIGL	920	8	14	22		3705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SHQ ID NO
ENV	ILIIIPRI	947	8	13	20		3706
ENV	PIRIQGL	951	8	12	19		3707
ENV	WVKEVAV	45	9	25	86		3708
ENV	VKKFATIL	55	9	22	84	0.0300	3709
ENV	PDIPNDEI	89	9	25	39		3710
ENV	NYTENFMW	101	9	34	53		3711
ENV	NFNWAKNDM	105	9	12	19		3712
ENV	NFNWAKNDM	105	9	18	28		3713
ENV	NFNWAKNDM	105	9	23	36		3714
ENV	NFNWAKNDM	105	9	23	36		3715
ENV	QAHLEDSI	116	9	22	59		3716
ENV	ISLWDSQL	121	9	38	37		3717
ENV	ISLWDSQL	121	9	10	16		3718
ENV	KLIPLCVIL	134	9	52	81		3719
ENV	PIKNSFNI	181	9	13	20		3720
ENV	PIKNSFNI	181	9	23	23		3721
ENV	WVKEVAV	232	9	35	47		3722
ENV	KVSEPIPI	254	9	31	48		3723
ENV	STFPIPII	271	9	12	19		3724
ENV	ILKCNDSKF	271	9	51	80		3725
ENV	STVQCTIIG	289	9	60	94		3726
ENV	PVYSTQLLL	300	9	13	20		3727
ENV	ILKCNDSKF	311	9	11	17		3728
ENV	PIKNSFNI	327	9	01	33		3729
ENV	GIQSQGFY	360	9	01	33		3730
ENV	SIQSQGFY	369	9	12	19		3731
ENV	ATIGRIDI	380	9	15	23		3732
ENV	DIQQAICNI	380	9	21	33		3733
ENV	PIKNSFNI	418	9	35	47		3734
ENV	SINCRGEFF	437	9	16	23		3735
ENV	FIYCNISGL	444	9	21	33		3736
ENV	FIYCNISGL	445	9	21	33		3737
ENV	FLPCRIQI	484	9	26	41		3738
ENV	PIKNSFNI	484	9	30	47		3739
ENV	PIKNSFNI	488	9	12	19		3740
ENV	MIQVGVQAM	495	9	15	23		3741
ENV	MIQVGVQAM	495	9	10	16		3742
ENV	PIRPGGDM	545	9	17	27		3743
ENV	PIRPGGDM	545	9	25	39		3744
ENV	PIRPGGDM	545	9	25	84		3745
ENV	LYKTKVVI	556	9	13	20	0.0200	3746
ENV	LYKTKVVI	561	9	29	45		3747
ENV	AVGGAVFL	595	9	11	17		3748
ENV	GIGAVFLGF	598	9	11	18		3749
ENV	MLGAMFLGF	599	9	04	36		3750
ENV	MLGAMFLGF	599	9	03	27		3751
ENV	FLGAGSIL	609	9	35	48		3752
ENV	TMGASITL	615	9	39	58		3753
ENV	TLTVQARQL	622	9	37	56		3754
ENV	TLTVQARQL	623	9	37	56		3755
ENV	GIQQQQNNL	633	9	26	41		3756

Table X
HIV-1 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	GIVQGSNL	633	9	32	50		3756
ENV	IVQGSNL	634	9	26	41		3757
ENV	IVQGSNL	635	9	26	41		3758
ENV	ALQAOHLL	644	9	48	75		3759
ENV	IKLITVWGI	651	9	13	20		3760
ENV	MLQLTYWGI	651	9	34	53		3761
ENV	MLQLTYWGI	651	9	10	16		3762
ENV	ITVWGRQL	654	9	59	92		3763
ENV	ITVWGRQL	654	9	59	92		3764
ENV	RYLQDQQL	671	9	29	45		3765
ENV	RYLQDQQL	671	9	17	27	0.7600	3766
ENV	GIWGCOSKL	680	9	48	75	0.2300	3767
ENV	IMTCSGKLI	681	9	48	75	0.0270	3768
ENV	LICTTAVW	688	9	19	30		3769
ENV	LICTTAVW	688	9	12	17		3770
ENV	LICTTAVW	688	9	12	17		3771
ENV	FWMEWERH	722	9	11	19		3772
ENV	EWEREIDNY	725	9	11	17		3773
ENV	ALDKWASLW	757	9	11	17		3774
ENV	ELDKWASLW	757	9	18	28		3775
ENV	WFTNANLW	760	9	26	41		3776
ENV	WFTNANLW	760	9	10	16		3777
ENV	WFTNANLW	760	9	10	16		3778
ENV	DFTNALWYI	769	9	16	25		3779
ENV	KWLWYKIF	772	9	25	39		3780
ENV	NWLWYKIF	772	9	49	77		3781
ENV	WLYWYKIF	773	9	53	67		3782
ENV	WYKIFIMI	775	9	43	62		3783
ENV	WYKIFIMI	775	9	41	64		3784
ENV	IFIMIVSGLI	779	9	35	55		3785
ENV	FMIVSGGLI	780	9	35	55		3786
ENV	FMIVSGGLI	782	9	36	56		3787
ENV	GLGLRIIF	786	9	15	23		3788
ENV	GLGLRIIF	786	9	17	25		3789
ENV	GLRIEAVL	789	9	28	44		3790
ENV	GLRIEAVL	789	9	28	44		3791
ENV	RIEFAVLSI	791	9	14	22		3792
ENV	RIVFAVLSI	791	9	19	30		3793
ENV	IVNVRQGY	799	9	38	59		3794
ENV	IVNVRQGY	799	9	35	56		3795
ENV	SIRLVNSGFL	842	9	13	20		3796
ENV	SIRLVNSGFL	842	9	13	20		3797
ENV	RLVNSGFLAL	844	9	12	19		3798
ENV	RLVNSGFLAL	844	9	12	19		3799
ENV	FLALNDLIL	849	9	25	39		3800
ENV	FLALNDLIL	849	9	13	22		3801
ENV	SVHRLDIL	864	9	12	19		3802
ENV	SVHRLDIL	864	9	12	19		3803
ENV	LIAMARTVEI	873	9	11	11		3804
ENV	SLKGLRLGW	889	9	11	18		3805
ENV	SLKGLRLGW	889	9	10	15		3806
ENV	SLRGLRQWGL	892	9	10	15		3807

Table X

HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RLGWGLKY	894	9	09	29		3806
ENV	KYWNLLQY	901	14	14	22		3807
ENV	YWNLLQY	902	9	15	25		3808
ENV	ELQWVQEL	906	9	16	25		3809
ENV	ELQWVQEL	910	9	10	16		3810
ENV	ELKNSASL	913	9	10	16		3811
ENV	ELKNSAVSL	913	9	12	19		3812
ENV	AVALGTDRI	928	9	16	25		3813
ENV	ALIIIPRI	946	9	12	19		3814
ENV	VTVYGVVW	947	10	12	19		3815
ENV	VWRLATITL	948	10	15	25		3816
ENV	VWRLATITL	955	10	22	34		3817
ENV	LFQASDAKAY	65	10	22	34	0.2700	3818
ENV	AYDTEVINW	73	10	42	66		3819
ENV	MWKNNAVEQ	108	10	18	28		3820
ENV	NVVEQMIEDI	112	10	35	55		3821
ENV	NVVEQMIEDI	113	10	20	31	0.0004	3822
ENV	QMIHEDISLW	116	10	23	45		3823
ENV	QMIHEDISLW	120	10	38	59		3824
ENV	DVSLWDSL	120	10	38	59		3825
ENV	RLNCHTSAL	236	10	15	24		3826
ENV	ITQACTKVSF	245	10	29	45		3827
ENV	PHIYCAPAGF	260	10	27	42		3828
ENV	PHIYCAPAGF	262	10	10	16		3829
ENV	ILYCAPAGFAL	262	10	27	42		3830
ENV	ILYCAPAGFAL	262	10	27	42		3831
ENV	ALIKCHDKKE	270	10	12	19		3832
ENV	GIRPVYSTQL	297	10	33	52		3833
ENV	GIRPVYSTQL	297	10	26	41		3834
ENV	STQLLNGSL	303	10	57	89		3835
ENV	NISPRVAY	376	10	31	51		3836
ENV	SPNGGGEFF	437	10	35	55		3837
ENV	SPNGGGEFF	437	10	16	25		3838
ENV	EFFYNTSGI	443	10	21	33		3839
ENV	FFYCNISGLF	444	10	21	33		3840
ENV	ITLPCRIKQI	483	10	25	39		3841
ENV	TLPCRIKQI	484	10	15	23		3842
ENV	NWQEVGKA	494	10	15	23	0.0001	3843
ENV	NWQEVGKA	495	10	15	23		3844
ENV	NWQEVGKA	495	10	15	23		3845
ENV	NTENKTEIF	537	10	01	17		3846
ENV	NTENKTEIF	537	10	01	17		3847
ENV	EIRPGGDM	544	10	17	27		3848
ENV	EIRPGGDM	544	10	21	33		3849
ENV	DMRDNRWSEL	552	10	17	27		3850
ENV	ELYKRYKVEI	560	10	25	39		3851
ENV	ELYKRYKVEI	560	10	25	39		3852
ENV	KYKVKLEPL	563	10	29	46		3853
ENV	GICAVFLGFL	598	10	11	18		3854
ENV	MLGAMFLGFL	599	10	04	36		3855

Table X
 HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	TIGAMFLGL	599	10	03	27		3856
ENV	STAGV	606	10	35	86		3857
ENV	STAGV	610	10	35	86		3858
ENV	FTLVQARQL	621	10	27	42		3859
ENV	TLTVQARQL	622	10	27	42		3860
ENV	GNQDQNNLL	633	10	26	55		3861
ENV	GNQDQNNLL	634	10	26	41		3862
ENV	ILLKLTWGI	650	10	12	20		3863
ENV	ILLQITWGI	650	10	34	53		3864
ENV	KLIVGKIKL	653	10	13	20		3865
ENV	KLIVGKIKL	653	10	14	69		3866
ENV	GIQIQKIKL	653	10	44	69		3867
ENV	YLDQDQLGI	672	10	27	42		3868
ENV	YLRDQQLGI	672	10	18	28		3869
ENV	GIWGCGLI	680	10	48	75		3870
ENV	GIWGCGLI	680	10	48	75		3871
ENV	KLICITVPW	687	10	17	27		3872
ENV	KLICITVPW	687	10	12	19		3873
ENV	TTNVPWSS	691	10	11	17		3874
ENV	TTNVPWSS	691	10	11	16		3875
ENV	MTNMEDE	721	10	11	17		3876
ENV	MTNMEDE	721	10	11	17		3877
ENV	LLLDKWSL	755	10	18	28		3878
ENV	WFDTNLW	767	10	10	16		3879
ENV	WFDTNLW	767	10	10	16		3880
ENV	HNWLWIKI	770	10	14	22		3881
ENV	KNLWYRKH	772	10	16	25		3882
ENV	KNLWYRKH	772	10	25	39		3883
ENV	KNLWYRKH	772	10	25	39		3884
ENV	KNLWYRKH	772	10	25	39		3885
ENV	KIPMIVGGL	778	10	38	59		3886
ENV	KIPMIVGGL	778	10	33	52		3887
ENV	IMYVGLLI	781	10	34	54		3888
ENV	IMYVGLLI	781	10	34	54		3889
ENV	SVNKRVRQY	798	10	36	56		3890
ENV	GVSLSPQTL	806	10	29	45		3891
ENV	LVSGTLALW	845	10	16	25		3892
ENV	LVSGTLALW	845	10	15	39		3893
ENV	ALWDLRSL	853	10	20	31		3894
ENV	AWDLRSLCL	853	10	20	31		3895
ENV	DLNRLCLFY	856	10	16	25		3896
ENV	DLNRLCLFY	856	10	15	35		3897
ENV	SLCLFSYHRL	859	10	31	48		3898
ENV	SLCLFSYHRL	859	10	31	48		3899
ENV	LFPSYHRLRF	862	10	18	28		3900
ENV	LFPSYHRLRF	862	10	22	34		3901
ENV	SYHLRDL	864	10	12	20		3902
ENV	SYHLRDL	864	10	12	20		3903
ENV	LIARTVELL	873	10	11	17		3904
ENV	IVELLGRGW	879	10	22	34		3905

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	LLGRGWEAL	882	10	09	15		3906
ENV	RLGWELKYL	894	10	09	29		3907
ENV	RYVWNLQY	901	10	14	22		3908
ENV	ELKNSVNSLL	905	10	16	25		3909
ENV	AVSLNATAI	918	10	10	16		3910
ENV	AVAEGLDRII	928	10	15	23		3912
ENV	AVAEGLDRII	928	10	14	22		3913
ENV	HFPRIRQQGL	949	10	13	21		3914
ENV	HFPRIRQQGL	949	10	11	19		3915
ENV	RIHQGLERAI	953	10	34	52		3916
ENV	WVTVTVGVFV	46	10	55	86		3917
ENV	PWKREATTLL	54	11	22	34		3918
ENV	TLFCASDAAK	64	11	40	63		3919
ENV	CYTDIPRQEI	87	11	25	39		3920
ENV	ELKNSVNSLL	905	11	32	44		3921
ENV	NKWSNNAYE	107	11	35	47		3922
ENV	NNVQGMIEHI	112	11	20	31		3923
ENV	SLKPCVKLTPL	128	11	54	84		3924
ENV	CVKLTPLCVI	132	11	52	81		3925
ENV	VITQCKPKYSF	244	11	14	22		3926
ENV	WVTVTVGVFV	46	11	55	86		3927
ENV	HYCAPAGAIL	262	11	22	42		3928
ENV	NYSTVQCIIGH	287	11	51	80		3929
ENV	GRIPVSTQLL	297	11	33	52		3930
ENV	GRIPVSTQLL	297	11	26	41		3931
ENV	PTAIGDHQDI	367	11	11	17		3932
ENV	ELKNSVNSLL	905	11	16	25		3933
ENV	THHSFNGGHE	432	11	10	16		3934
ENV	THHSFNGGHE	432	11	12	19		3935
ENV	VMHSFNGGGE	432	11	13	20		3936
ENV	EFFYCNSTGLF	443	11	21	33		3937
ENV	NTLCKRKHQI	482	11	11	17		3938
ENV	ELKNSVNSLL	905	11	16	25		3939
ENV	ITLPCRIHQI	483	11	15	23		3940
ENV	NWQVEGKKA	494	11	15	21		3941
ENV	EVGRKAMYAPH	498	11	18	28		3942
ENV	RVGGAMVAPP	498	11	10	16		3943
ENV	QKRCSSNITGL	512	11	11	17		3944
ENV	WVFEKRAVGI	588	11	17	28		3945
ENV	AVGIGAVFLGI	595	11	11	17		3946
ENV	STLTVOAARQL	620	11	27	42		3948
ENV	ITLTVOAARQL	621	11	27	42		3949
ENV	ITVQARQLLSGI	624	11	36	56		3950
ENV	ELKNSVNSLL	905	11	16	25		3951
ENV	ALFAQQHLHL	644	11	35	55		3952
ENV	ALFAQQHLHL	644	11	35	55		3953
ENV	AVERYLKIQQQ	668	11	23	36		3954
ENV	AVERYLRDQQQ	668	11	11	17		3955

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (P)	A*2401	SEQ ID NO
ENV	RYLKDQQLGL	671	11	25	39		3956
ENV	RYLKDQQLGL	672	11	27	37		3957
ENV	RYLKDQQLGL	673	11	27	41		3958
ENV	RYLKDQQLGL	674	11	18	28		3959
ENV	LLGWGCSGKL	678	46	46	72		3960
ENV	CTTNVWNS	690	11	11	17		3961
ENV	NMTWMEWER	720	11	12	19		3962
ENV	WMEWERDEIN	723	11	10	16		3963
ENV	LELLDKWAS	724	11	15	13		3964
ENV	LELLDKWAS	725	11	17	13		3965
ENV	LELLDKWAS	726	11	11	17		3966
ENV	LELLDKWAS	755	11	18	28		3967
ENV	ALDKWASLW	757	11	10	16		3968
ENV	ELDKWASLW	757	11	16	25		3969
ENV	KWASLWVWF	760	11	15	23		3970
ENV	WFDITNWLW	767	11	10	16		3971
ENV	TKWYKIFIM	770	11	12	27		3972
ENV	TKWYKIFIM	771	11	12	27		3973
ENV	KWYKIFIM	772	11	15	21		3974
ENV	NWYKIFIM	772	11	22	34		3975
ENV	WYKIFIM	773	11	43	67		3976
ENV	KIFIMVGGI	778	11	31	48		3977
ENV	FIMVGGI	780	11	34	53		3978
ENV	FIMVGGI	782	11	35	56		3979
ENV	WVGGI	783	11	16	19		3980
ENV	WVGGI	787	11	15	23		3981
ENV	LIGLRVAVL	787	11	20	31		3982
ENV	GLRIHFAVLS	789	11	14	22		3983
ENV	GLRIHFAVLS	789	11	19	30		3984
ENV	RVQGYSLF	802	11	47	73		3985
ENV	RVQGYSLF	842	11	16	25		3986
ENV	RVQGYSLF	842	11	16	25		3987
ENV	ADWDLRSICL	853	11	20	31		3988
ENV	CLFSYIURLDF	861	11	18	28		3989
ENV	CLFSYIURLDF	861	11	20	31		3990
ENV	LLSYIURLDF	862	11	13	20		3991
ENV	LLSYIURLDF	862	11	13	20		3992
ENV	LLSYIURLDF	878	11	22	34		3993
ENV	RIYELLGRIC	881	11	09	15		3994
ENV	ELIGRRGWEA	892	11	09	29		3995
ENV	GLRLGWEGKL	894	11	07	23		3996
ENV	GLRLGWEGKL	909	11	12	19		3997
ENV	AYVAAGTDRI	926	11	16	25		3998
ENV	AYVAAGTDRI	926	11	13	27		3999
GAG	SVLSGGKL	6	8	13	22		4000
GAG	SVLSGGKL	6	8	28	44		4001
GAG	SVLSGGKL	12	8	18	28		4002
GAG	KLDKWEKI	12	8	10	16		4003
GAG	IYVASREL	35	8	21	33		4004
GAG	IYVASREL	35	8	36	56		4005

Table X
HIV-A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	REALNTGL	45	8	20	31		4006
GAG	REAVNPL	45	8	16	25		4007
GAG	GTEELRSL	73	8	12	19		4008
GAG	LNTVATL	80	8	16	25		4009
GAG	LYNTVATL	80	8	22	34		4010
GAG	LYNCHIKI	87	8	17	28		4011
GAG	LYCHIQRI	87	8	13	28		4012
GAG	KYSONYPI	148	8	15	27		4013
GAG	QYSONYPI	148	8	27	48		4014
GAG	NYPIVQNL	152	8	31	48		4015
GAG	KYVEEKAF	178	8	24	38		4016
GAG	KYVEEKAF	178	8	28	44		4017
GAG	NYPIVQNL	189	8	46	48		4018
GAG	VYPIVQNL	189	8	12	22		4019
GAG	ATPDDLLNM	200	8	14	22		4020
GAG	DLNMLMLNI	204	8	12	19		4021
GAG	TLQEQJAW	263	8	12	19		4022
GAG	TLQEQJAW	263	8	27	42		4023
GAG	WMTNNPIPI	270	8	20	31		4024
GAG	WMTNNPIPI	270	8	16	25		4025
GAG	RPVVGDIY	279	8	11	17		4026
GAG	RPVVGDIY	279	8	35	55		4027
GAG	DIYKRWHI	284	8	17	27		4028
GAG	EYKRWHI	284	8	39	61		4029
GAG	YKRWHI	285	8	54	84		4030
GAG	ILGLNRI	290	8	57	89		4031
GAG	ILGLNRI	290	8	40	60		4032
GAG	RAYSPSIL	299	8	14	22		4033
GAG	RAYSPSIL	299	8	40	63		4034
GAG	MYSPSIL	300	8	14	22		4035
GAG	MYSPSIL	300	8	42	66		4036
GAG	ATQDVKNW	333	8	15	23		4037
GAG	ATQDVKNW	333	8	18	28		4038
GAG	WMTNNPIPI	339	8	16	25		4039
GAG	NWMTNPIPI	339	8	36	56		4040
GAG	ALGPAAIL	360	8	16	25		4041
GAG	ALGPGAIL	360	8	18	28		4042
GAG	IMMQKSNF	408	8	11	17		4043
GAG	IMMQKSNF	408	8	27	42		4044
GAG	CHERQANF	439	8	55	87		4045
GAG	CHERQANF	439	8	17	27		4046
GAG	EYPLTSL	543	8	14	22		4047
GAG	EYPLTSL	543	8	11	17		4048
GAG	PLASLSKSL	548	8	15	23		4049
GAG	PLTSLKSL	548	8	12	19		4050
GAG	PLTSLKSL	548	8	12	19		4051
GAG	LTSLSKSLF	549	8	13	20		4052
GAG	PLTSLKSLF	549	8	12	19		4053
GAG	SLEGSDDPL	554	8	12	19		4054
GAG	SLEGSDDPL	554	8	11	17		4055

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	KYRLKIIHW	29	9	10	16		4036
GAG	KYRLKILVW	29	9	16	25		4037
GAG	HIWASREL	34	9	21	33		4038
GAG	PEALNGELL	45	9	26	36		4039
GAG	PEALNGELL	45	9	26	36		4040
GAG	REAVHPGLL	45	9	16	25	0.0100	4061
GAG	ETSEGRQI	54	9	16	25		4062
GAG	ILGQLOPSL	62	9	11	17		4063
GAG	SLQTSSEL	69	9	14	22		4064
GAG	SLNTVATL	79	9	16	25		4065
GAG	SLNTVATL	79	9	16	25		4066
GAG	LENIVATLY	80	9	12	21		4067
GAG	LYNTVATLY	80	9	22	34		4068
GAG	LYCYVIQKI	86	9	12	19		4069
GAG	LYCYVIQRI	86	9	15	23		4070
GAG	IVKDKREAL	95	9	11	17		4071
GAG	IVKDKREAL	95	9	11	17		4072
GAG	IVKDKREAL	95	9	30	50		4073
GAG	DTKEALEKI	98	9	10	16		4074
GAG	IVONNAQQQM	155	9	21	33		4075
GAG	IVONNAQQQM	155	9	29	45		4076
GAG	ILNMAWYKVI	172	9	30	47		4077
GAG	ILNMAWYKVI	172	9	30	47		4078
GAG	EVIMPEFAL	188	9	46	72		4079
GAG	EVIMPEFAL	188	9	46	72		4080
GAG	ATPDQLNAM	200	9	12	19		4081
GAG	ATPDQLNAM	200	9	42	66		4082
GAG	IVGRIQAM	211	9	12	19		4083
GAG	IVGRIQAM	211	9	17	25		4084
GAG	AMQNLKETT	218	9	31	52		4085
GAG	AMQNLKETT	218	9	26	41		4086
GAG	TINEEAAEW	225	9	53	83		4087
GAG	DIAGTSTL	256	9	48	75		4088
GAG	TTSTLQEOI	260	9	45	71		4089
GAG	TTSTLQEOI	262	9	45	71		4090
GAG	STLQEQIWM	262	9	27	42		4091
GAG	TLQEQIWM	263	9	17	19		4092
GAG	TLQEQIWM	263	9	27	42		4093
GAG	GWMTNNPHI	269	9	18	28	0.0140	4094
GAG	GWMTNNPHI	269	9	10	16		4095
GAG	PVGDYKRW	281	9	18	28		4096
GAG	PVGDYKRW	281	9	18	28		4097
GAG	DIYKRWIL	284	9	10	27		4098
GAG	EYKRWIL	284	9	37	58		4099
GAG	WILLGLNKI	289	9	57	89		4100
GAG	GLNKIVRMV	293	9	60	94		4101
GAG	RMYSFTSL	299	9	14	22		4102
GAG	RMYSFTSL	299	9	40	66		4103
GAG	PERDYNDIE	316	9	60	98		4104
GAG	YVDIFFKTL	320	9	27	42		4105

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	YVIREYKTL	120	9	28	44		4106
GAG	ATQDVKNWM	333	9	15	23		4107
GAG	ATQEVKNWM	333	9	18	28		4108
GAG	NIMMORGNF	407	9	10	17		4109
GAG	NIMMORGNF	407	9	13	22		4110
GAG	CTERQANFL	459	9	26	31		4111
GAG	PTAPPAESF	495	9	15	23		4112
GAG	PTAPPAESF	495	9	15	23		4113
GAG	PTAPPAESF	507	9	02	67		4114
GAG	PTAPPAESF	507	9	01	33		4115
GAG	PIDKELYPL	534	9	12	19		4116
GAG	PIDKELYPL	538	9	01	25		4117
GAG	TIDKELYPL	538	9	01	25		4118
GAG	PLASLSLF	548	9	12	23		4119
GAG	PLASLSLF	548	9	12	19		4120
GAG	PLASLSLF	548	9	12	19		4121
GAG	PLASLSLF	548	9	12	19		4122
GAG	VLSEGLDIAW	7	10	15	23		4123
GAG	KLDAWEKRL	12	10	16	25		4124
GAG	KLDAWEKRL	12	10	10	16		4125
GAG	RLRPGKKKY	20	10	34	53		4126
GAG	YVASHLELRF	56	10	24	30		4127
GAG	YVASHLELRF	56	10	14	22		4128
GAG	YVASHLELRF	56	10	11	17		4129
GAG	QTLGQDLSL	61	10	12	19		4130
GAG	QTLGQDLSL	71	10	12	19		4131
GAG	SLFNIVATLY	79	10	15	23		4132
GAG	SLFNIVATLY	79	10	22	34		4133
GAG	ATLYCYVHQKI	85	10	12	19		4134
GAG	ATLYCYVHQKI	152	10	15	23		4135
GAG	PIVONIQGOM	154	10	21	33		4136
GAG	ASPRLLNAW	167	10	29	45		4137
GAG	ASPRLLNAW	167	10	10	16		4138
GAG	RTLNAAWVKVI	171	10	30	47		4139
GAG	WVKVIEKAF	176	10	28	38		4140
GAG	WVKVIEKAF	184	10	28	44		4141
GAG	ASPRVIMAF	184	10	50	78	0.0078	4142
GAG	ATPQDLNML	200	10	12	19		4143
GAG	ATPQDLNML	200	10	42	66		4144
GAG	NIVGGHQAAW	210	10	12	19		4145
GAG	NTVGGHQAAW	210	10	47	73		4146
GAG	DTINEEAAEW	224	10	31	38		4147
GAG	DTINEEAAEW	224	10	22	34		4148
GAG	RLIIPVIAQW	235	10	22	34		4149
GAG	RVIIPIVIAQW	235	10	14	22		4150
GAG	QMIREFGSDI	248	10	44	69		4151
GAG	QMIREFGSDI	259	10	45	70		4152
GAG	GTSTTLOEQI	262	10	12	19		4153
GAG	STLOEQIAWM	262	10	12	19		4154
GAG	STLOEQIAWM	262	10	12	19		4155
GAG	PQDIYKRWI	281	10	17	27		4156
GAG	PQDIYKRWI	281	10	17	27		4157
GAG	PQDIYKRWI	281	10	40	63		4158

Table X
HIV Δ24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IVKRWILGL	285	10	54	84	0.0140	4156
GAG	RWILGLNKL	288	10	56	88		4157
GAG	ILGLNKLVRM	291	40	57	89		4158
GAG	IVKRWISPTSI	297	10	58	90		4159
GAG	IVKRWISPTSI	297	10	46	63		4160
GAG	MYSPVSLID	300	10	13	20		4161
GAG	MYSPVSLID	300	10	40	63		4162
GAG	DIKQGPKEPT	308	10	19	30		4163
GAG	DIKQGPKEPT	308	10	41	64		4164
GAG	PERDYVDFEF	316	10	35	55		4165
GAG	PERDYVDFEF	316	10	41	64		4166
GAG	IVKRWISPTSI	319	10	28	42		4167
GAG	DYKRWITET	336	10	12	19	0.0010	4168
GAG	DYKRWITET	336	10	11	17		4169
GAG	EYKRWITET	336	10	25	39		4170
GAG	ATIMMORGNF	406	10	11	28		4171
GAG	CFNCGREGIII	425	10	11	28		4172
GAG	CFNCGREGIII	425	10	27	42		4173
GAG	TFNCGREGIII	522	10	09	45		4174
GAG	ETIDKLYPL	537	10	01	01		4175
GAG	RTENSLYPL	538	10	01	25		4176
GAG	LYPLASLKL	544	10	09	17		4177
GAG	SVLSGGKLLDA	6	15	15	23		4178
GAG	IVWASRELERP	35	11	15	23		4179
GAG	IVWASRELERP	35	11	03	05		4180
GAG	ELERFAVNPGL	42	11	25	39		4181
GAG	ELERFAVNPGL	42	11	14	22		4182
GAG	LIETSEGCROI	52	11	15	23		4183
GAG	RIEVKDTREAL	93	11	16	25		4184
GAG	NLOGQMVIIQA	158	11	12	19		4185
GAG	MVIQASPTSL	163	11	15	23		4186
GAG	IVWASRELERP	175	11	22	34		4187
GAG	AWVKVVEKA	175	11	24	38		4188
GAG	ALSEGAATPDL	195	11	28	44		4189
GAG	IVGGHQAAMQ	211	11	58	91		4190
GAG	TVGGHQAAMQ	211	11	11	17		4191
GAG	TISTLQEQIA	260	11	47	73		4192
GAG	TISTLQEQIA	260	11	11	17		4193
GAG	QIGWATSNPPI	267	11	18	29		4194
GAG	QIGWATSNPPI	267	11	18	29		4195
GAG	PIVGEYKRW	279	11	34	53		4196
GAG	PVGDYKRWII	281	11	17	27		4197
GAG	PVGEYKRWII	281	11	39	61		4198
GAG	DIYKRWILGL	284	11	17	27		4199
GAG	DIYKRWILGL	284	11	37	59		4200
GAG	ILGLNKIVRAY	291	11	56	88		4201
GAG	ILGLNKIVRAY	291	11	57	89		4202
GAG	KIVRMVSPFSI	296	11	14	22		4203
GAG	KIVRMVSPFSI	296	11	39	61		4204

Table X
HIV-A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IVRMVSPISIL	297	11	14	22		4206
GAG	IVRMVSPVSL	297	11	40	63		4207
GAG	RMVSPISILDI	299	11	13	20		4208
GAG	IVRMVSPVSL	299	11	38	59		4209
GAG	IVRMVSPVSL	336	11	12	19		4210
GAG	IVRMVSPVSL	336	11	11	17		4211
GAG	IVRMVSPVSL	336	11	11	19		4212
GAG	IVRMVSPVSL	336	11	25	39		4213
GAG	IVRMVSPVSL	336	11	16	25		4214
GAG	IVRMVSPVSL	336	11	16	25		4215
GAG	IVRMVSPVSL	336	11	17	27		4216
GAG	IVRMVSPVSL	336	11	17	27		4217
GAG	IVRMVSPVSL	336	11	46	72		4218
GAG	IVRMVSPVSL	336	11	16	22		4219
GAG	IVRMVSPVSL	336	11	14	22		4220
GAG	IVRMVSPVSL	336	11	02	67		4221
GAG	IVRMVSPVSL	336	11	01	33		4222
GAG	IVRMVSPVSL	336	11	09	17		4223
GAG	IVRMVSPVSL	336	11	12	22		4224
GAG	IVRMVSPVSL	336	11	12	22		4225
GAG	IVRMVSPVSL	336	11	12	22		4226
GAG	IVRMVSPVSL	336	11	48	75		4227
GAG	IVRMVSPVSL	336	11	12	19		4228
GAG	IVRMVSPVSL	336	11	12	19		4229
GAG	IVRMVSPVSL	336	11	18	28		4230
GAG	IVRMVSPVSL	336	11	17	27		4231
GAG	IVRMVSPVSL	336	11	15	23		4232
GAG	IVRMVSPVSL	336	11	56	88		4233
GAG	IVRMVSPVSL	336	11	20	31		4234
GAG	IVRMVSPVSL	336	11	33	52		4235
GAG	IVRMVSPVSL	336	11	13	20		4236
GAG	IVRMVSPVSL	336	11	21	33		4237
GAG	IVRMVSPVSL	336	11	21	33		4238
GAG	IVRMVSPVSL	336	11	21	33		4239
GAG	IVRMVSPVSL	336	11	17	27		4240
GAG	IVRMVSPVSL	336	11	36	56		4241
GAG	IVRMVSPVSL	336	11	20	31		4242
GAG	IVRMVSPVSL	336	11	13	20		4243
GAG	IVRMVSPVSL	336	11	20	31		4244
GAG	IVRMVSPVSL	336	11	27	43		4245
GAG	IVRMVSPVSL	336	11	43	67		4246
GAG	IVRMVSPVSL	336	11	40	63		4247
GAG	IVRMVSPVSL	336	11	11	17		4248
GAG	IVRMVSPVSL	336	11	21	33		4249
GAG	IVRMVSPVSL	336	11	21	33		4250
GAG	IVRMVSPVSL	336	11	17	27		4251
GAG	IVRMVSPVSL	336	11	10	16		4252
GAG	IVRMVSPVSL	336	11	46	72		4253
GAG	IVRMVSPVSL	336	11	12	19		4254
GAG	IVRMVSPVSL	336	11	12	19		4255

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FFREDLAF	1	8	15	23		4306
POL	FFRENLAQ	1	8	41	64		4307
POL	FTLNCAQ	80	8	01	33		4308
POL	FTFNFTQI	86	8	01	34		4309
POL	NFTQITLW	86	8	22	34		4310
POL	FTFNFTQI	90	8	22	36		4311
POL	FTFNFTQI	90	8	47	73		4312
POL	TKLGGQFL	99	8	17	27		4313
POL	TVKIGGQFL	99	8	11	17		4314
POL	TVLEDNL	118	8	13	20		4315
POL	TVLEENL	118	8	15	23		4316
POL	DNLNCKW	122	8	13	23		4317
POL	MLNCKW	132	8	12	19		4318
POL	MLNCKW	132	8	62	97		4319
POL	GFKVRQY	139	8	53	83		4320
POL	KVROYDQI	142	8	41	64		4321
POL	ELCHIKAI	152	8	19	30		4322
POL	ELCOKKAI	152	8	24	38		4323
POL	NIQRNLL	170	8	26	44		4324
POL	NIQRNLL	170	8	31	48		4325
POL	LIQIGCTL	177	8	42	66		4326
POL	LIQIGCTL	177	8	15	23		4327
POL	QIGCTLNF	179	8	41	64		4328
POL	QLGCTLNF	179	8	16	25		4329
POL	PVKLKPRM	195	8	36	58		4330
POL	KIKALTEI	217	8	25	44		4331
POL	NIQRNLL	221	8	15	23		4332
POL	LIQIGCTL	221	8	15	24		4333
POL	EMEKIEKI	229	8	42	66		4334
POL	KIGPENPY	238	8	51	80		4335
POL	RIGPENPY	238	8	11	17		4336
POL	KWKRLVDF	259	8	59	92		4337
POL	KLVDPRFL	262	8	62	98		4338
POL	KLVDPRFL	262	8	57	89		4339
POL	GHIPADGI	282	8	56	89		4340
POL	VLDVGDAY	297	8	60	94		4341
POL	SVPLDKDF	306	8	18	28		4342
POL	DFRYKYAF	312	8	42	66		4343
POL	GWKGSPIAI	341	8	59	92		4344
POL	MTALTEP	353	8	60	96		4345
POL	NIQRNLL	366	8	18	28		4346
POL	INQYMDLI	369	8	24	38		4347
POL	DLVYGSDL	375	8	61	93		4348
POL	YVGSDDL	377	8	63	98		4349
POL	FLWMGYEL	416	8	58	91		4350
POL	WTYQIQL	428	8	64	100		4351
POL	WTYQIQL	428	8	26	44		4352
POL	QLPEKDSW	434	8	13	20		4353
POL	VLPKDSW	434	8	13	20		4355

Table X
HIV A24 Superficial Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*2401	SEQ ID NO
POL	TVNDKQL	442	8	62	97		4356
POL	KLAWASQI	443	8	61	97		4357
POL	KLVQCLCK	452	8	61	95		4358
POL	KVRQLCKL	464	8	29	45		4359
POL	LLRGAKAL	464	8	19	30		4360
POL	LLRGAKAL	471	8	30	47		4361
POL	LLRGAKAL	471	8	24	38		4362
POL	LLRGAKAL	471	8	11	15		4363
POL	ALTEVPI	477	8	16	25		4364
POL	PLTEAEEL	483	8	30	47		4365
POL	ELAENREI	491	8	57	89		4366
POL	YYDPSKDL	510	8	43	67		4367
POL	KTKYAKIM	542	8	19	30		4368
POL	KTGKAKIM	542	8	13	18		4369
POL	KTGKAKIM	553	8	40	71		4370
POL	KTGKAKIM	553	8	34	53		4371
POL	LTEAVQKI	560	8	19	30		4372
POL	ALTEVPI	568	8	19	30		4373
POL	INWGPKEF	574	8	11	17		4374
POL	INWGPKEF	574	8	48	75		4375
POL	ETWQTDY	591	8	10	16		4376
POL	ETWQTDY	591	8	20	31		4377
POL	EYWOATWI	596	8	37	58		4378
POL	ETWQTDY	601	8	52	81		4379
POL	ETWQTDY	607	8	54	84		4380
POL	ETWQTDY	610	8	57	89		4381
POL	ETWQTDY	614	8	58	91		4382
POL	ETWQTDY	614	8	28	44		4383
POL	ETWQTDY	626	8	55	86		4384
POL	ETWQTDY	664	8	28	44		4385
POL	ETWQTDY	668	8	12	19		4386
POL	ETWQTDY	686	8	62	97		4387
POL	ETWQTDY	688	8	39	62		4388
POL	ETWQTDY	688	8	33	53		4389
POL	ETWQTDY	727	8	63	98		4390
POL	WVPAHKGI	747	8	51	80		4391
POL	KIRKVLFL	750	8	50	78		4392
POL	KVFLDGI	750	8	45	70		4393
POL	AMASDFNL	773	8	45	70		4394
POL	QVDSKGI	805	8	57	89		4395
POL	ETWQTDY	811	8	15	23		4396
POL	ETWQTDY	819	8	31	48		4397
POL	ETWQTDY	819	8	23	36		4398
POL	ETWQTDY	828	8	59	92		4399
POL	ETWQTDY	834	8	54	84		4400
POL	ETWQTDY	844	8	59	92		4401
POL	ETWQTDY	853	8	34	53		4402
POL	ETWQTDY	853	8	34	53		4403
POL	ETWQTDY	866	8	15	23		4404
POL	ETWQTDY	876	8	51	80		4405
POL	ETWQTDY	877	8	32	50		4406
POL	ETWQTDY	877	8	24	38		4407

Table X
HIV A24-Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	GKQEGG	886	8	22	34		4406
POL	GKQEGG	886	8	11	17		4407
POL	AVDMAGV	972	8	57	84		4408
POL	NFKRKG	936	8	60	84		4409
POL	GYSAGRI	945	8	57	89		4410
POL	QIRKQNF	968	8	12	19		4411
POL	QIRKQNF	968	8	35	55		4413
POL	QIRKQNF	968	8	35	55		4414
POL	QIRKQNF	968	8	32	36		4415
POL	QIRKQNF	968	8	32	36		4416
POL	QIRKQNF	968	8	32	36		4417
POL	QIRKQNF	968	8	32	36		4418
POL	QIRKQNF	968	8	32	36		4419
POL	QIRKQNF	968	8	32	36		4420
POL	QIRKQNF	968	8	32	36		4421
POL	QIRKQNF	968	8	32	36		4422
POL	QIRKQNF	968	8	32	36		4423
POL	QIRKQNF	968	8	32	36		4424
POL	QIRKQNF	968	8	32	36		4425
POL	QIRKQNF	968	8	32	36		4426
POL	QIRKQNF	968	8	32	36		4427
POL	QIRKQNF	968	8	32	36		4428
POL	QIRKQNF	968	8	32	36		4429
POL	QIRKQNF	968	8	32	36		4430
POL	QIRKQNF	968	8	32	36		4431
POL	QIRKQNF	968	8	32	36		4432
POL	QIRKQNF	968	8	32	36		4433
POL	QIRKQNF	968	8	32	36		4434
POL	QIRKQNF	968	8	32	36		4435
POL	QIRKQNF	968	8	32	36		4436
POL	QIRKQNF	968	8	32	36		4437
POL	QIRKQNF	968	8	32	36		4438
POL	QIRKQNF	968	8	32	36		4439
POL	QIRKQNF	968	8	32	36		4440
POL	QIRKQNF	968	8	32	36		4441
POL	QIRKQNF	968	8	32	36		4442
POL	QIRKQNF	968	8	32	36		4443
POL	QIRKQNF	968	8	32	36		4444
POL	QIRKQNF	968	8	32	36		4445
POL	QIRKQNF	968	8	32	36		4446
POL	QIRKQNF	968	8	32	36		4447
POL	QIRKQNF	968	8	32	36		4448
POL	QIRKQNF	968	8	32	36		4449
POL	QIRKQNF	968	8	32	36		4450
POL	QIRKQNF	968	8	32	36		4451
POL	QIRKQNF	968	8	32	36		4452
POL	QIRKQNF	968	8	32	36		4453
POL	QIRKQNF	968	8	32	36		4454
POL	QIRKQNF	968	8	32	36		4455

Table X
 HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SUI ID NO
POL	ETGIRYQV	327	9	52	81		4456
POL	GIRYQVNL	330	9	52	81		4457
POL	QNYVLPQW	334	9	63	98	0.0016	4458
POL	QNYVLPQW	341	9	63	98	0.0029	4459
POL	HSSMTKI	348	9	38	59	0.0110	4460
POL	SMTKLEPF	352	9	43	67		4461
POL	PERKQNDI	359	9	16	25		4462
POL	VYVOTMDDL	368	9	51	80		4463
POL	IYQYMDNL	369	9	61	95	0.0130	4464
POL	YVQYMDNL	371	9	58	91		4465
POL	YVQYMDNL	381	9	21	33		4466
POL	EGQIRAKI	383	9	21	33		4467
POL	EGQIRAKI	390	9	19	30		4468
POL	KHEUREHL	390	9	17	27		4469
POL	KHELRQIL	390	9	17	27		4470
POL	ELREHLKW	393	9	17	27		4471
POL	ELREHLKW	400	9	15	23		4472
POL	PEWAGYEL	415	9	60	94	0.0001	4473
POL	GVELIPIQW	420	9	60	94		4474
POL	KWTIVQIQL	427	9	28	44		4475
POL	KWTIVQIQL	427	9	12	19		4476
POL	IVIPEKDSW	433	9	13	20		4477
POL	YVQYMDNL	441	9	62	97		4478
POL	DIQKIYQKI	445	9	60	94		4479
POL	KLWASQIY	452	9	28	44		4480
POL	KVQLCKLL	464	9	19	30		4481
POL	KVQLCKLL	464	9	25	40		4482
POL	KLRGAKAL	470	9	25	40		4483
POL	KLRGAKAL	470	9	18	28		4484
POL	GTALATVI	474	9	11	18		4485
POL	LTEALTEL	484	9	37	58		4486
POL	FLAENREIL	491	9	57	89		4487
POL	VYDPSKDL	509	9	39	61	0.0004	4488
POL	YVDPKDLI	510	9	35	55	0.0006	4489
POL	YVDPKDLI	523	9	42	66	0.0220	4490
POL	IYQYMDNL	533	9	46	73		4491
POL	QUTEAVQKI	539	9	34	53		4492
POL	KIATESVI	566	9	14	22		4493
POL	VIVGKTPKF	573	9	47	73		4494
POL	KTRFKLPI	577	9	19	27		4495
POL	KTRFKLPI	582	9	29	45		4496
POL	KLRQKETW	582	9	26	41		4497
POL	RLHQKETW	582	9	10	16		4498
POL	TWETWVTDY	589	9	10	16		4499
POL	TWETWVTEY	589	9	10	16		4500
POL	WTDYWGATW	594	9	14	22		4501
POL	WTDYWGATW	594	9	24	38		4502
POL	ATPHREILW	600	9	57	89		4503
POL	NTPHVKLW	613	9	57	89		4504
POL	PLVKLWYQL	613	9	57	89		4505
POL	WYQLERDPI	618	9	14	22		4506

Table X
HIV A24 Super-Native Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*5401	SEQ ID NO
POL	WYQLEKEPI	618	9	31	48	0.0001	4506
POL	WYQLEKEPI	619	9	31	48		4507
POL	WYQLEKEPI	620	9	31	44		4508
POL	WYQLEKEPI	621	9	31	44		4509
POL	ETKLGKAGY	641	9	35	55		4510
POL	ETKLGKAGY	642	9	35	41		4511
POL	ETKLGKAGY	643	9	26	45		4512
POL	ETKLGKAGY	644	9	29	23		4513
POL	ETKLGKAGY	645	9	15	12		4514
POL	ETKLGKAGY	646	9	12	15		4515
POL	ETKLGKAGY	647	9	12	19		4516
POL	ETKLGKAGY	648	9	12	22		4517
POL	ETKLGKAGY	649	9	15	92		4518
POL	ETKLGKAGY	650	9	59	30		4519
POL	ETKLGKAGY	651	9	19	30		4520
POL	ETKLGKAGY	652	9	26	55		4521
POL	ETKLGKAGY	653	9	35	34		4522
POL	ETKLGKAGY	654	9	22	58		4523
POL	ETKLGKAGY	655	9	37	44		4524
POL	ETKLGKAGY	656	9	28	17		4525
POL	ETKLGKAGY	657	9	11	89	0.0016	4526
POL	ETKLGKAGY	658	9	44	89		4527
POL	ETKLGKAGY	659	9	57	92	0.0095	4528
POL	ETKLGKAGY	660	9	35	55		4529
POL	ETKLGKAGY	661	9	35	41		4530
POL	ETKLGKAGY	662	9	26	48		4531
POL	ETKLGKAGY	663	9	53	83		4532
POL	ETKLGKAGY	664	9	37	48		4533
POL	ETKLGKAGY	665	9	31	42		4534
POL	ETKLGKAGY	666	9	27	50		4535
POL	ETKLGKAGY	667	9	32	39		4536
POL	ETKLGKAGY	668	9	25	23		4537
POL	ETKLGKAGY	669	9	15	23		4538
POL	ETKLGKAGY	670	9	15	33		4539
POL	ETKLGKAGY	671	9	21	17	0.0120	4540
POL	ETKLGKAGY	672	9	11	88		4541
POL	ETKLGKAGY	673	9	48	75		4542
POL	ETKLGKAGY	674	9	53	83		4543
POL	ETKLGKAGY	675	9	48	75		4544
POL	ETKLGKAGY	676	9	53	83		4545
POL	ETKLGKAGY	677	9	53	83		4546
POL	ETKLGKAGY	678	9	60	94	0.0190	4547
POL	ETKLGKAGY	679	9	41	64		4548
POL	ETKLGKAGY	680	9	12	19		4549
POL	ETKLGKAGY	681	9	29	45		4550
POL	ETKLGKAGY	682	9	29	19		4551
POL	ETKLGKAGY	683	9	32	21		4552
POL	ETKLGKAGY	684	9	46	21		4553
POL	ETKLGKAGY	685	9	13	34		4554
POL	ETKLGKAGY	686	9	964	81		4555

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*2401	SEQ ID NO
POL	YVDSRDRI	978	9	34	53		4556
POL	YVDSRDPI	978	9	14	22		4557
POL	YVDSRDL	985	9	16	56		4558
POL	PLWKGPALK	985	9	36	30		4559
POL	PLWKGPALK	986	9	35	55		4560
POL	LWKGPALKL	986	9	18	28		4561
POL	VYIQDSDI	1002	9	37	58		4562
POL	VYIQDSDI	1002	9	37	58		4563
POL	VYPRRKAKI	1012	9	51	80		4564
POL	VYPRRKVKI	1012	9	51	17		4565
POL	IKDYDGKQM	1020	9	11	17		4566
POL	IKDYDGKQM	1020	9	50	78		4567
POL	APFQGAKEF	1020	9	10	16		4568
POL	APFQGAKEF	1020	9	10	16		4569
POL	GTINPQITL	80	10	01	33		4570
POL	PTFNFPQITL	80	10	01	33		4571
POL	STSPQITLW	84	10	13	20		4572
POL	TLWQPLVTI	91	10	21	33		4573
POL	LVTKIGGEQL	97	10	13	20		4574
POL	LVTKIGGEQL	97	10	13	20		4575
POL	NLFGKWKPKM	124	10	35	55		4576
POL	NLFGKWKPKM	124	10	35	55		4577
POL	KWKPKMIGGI	128	10	42	66		4578
POL	KWKPKMIGGI	128	10	17	27		4579
POL	KMIEGGIGGI	132	10	62	97	0.0001	4580
POL	FKYROYDOI	140	10	41	64		4581
POL	KYRQYDQILI	142	10	20	31		4582
POL	KYRQYDQILI	142	10	20	31		4583
POL	LIEICGKAI	150	10	16	16		4584
POL	LIEICGKAI	150	10	13	20		4585
POL	VLVGTPTVNI	162	10	53	83		4586
POL	LYGPIPVNI	163	10	52	81		4587
POL	PVNHGKALL	168	10	26	41		4588
POL	PVNHGKALL	168	10	26	41		4589
POL	IGRNALTOI	171	10	21	33		4590
POL	IGRNALTOI	171	10	18	28		4591
POL	IGRNALTOI	171	10	11	17		4592
POL	NLLTQGGCTL	175	10	21	33		4593
POL	NLLTQGGCTL	175	10	18	28		4594
POL	NLLTQGGCTL	175	10	18	28		4595
POL	LTOGLGCTLNE	177	10	41	64		4596
POL	LTOGLGCTLNE	177	10	15	23		4597
POL	QIGCTLNFPI	179	10	41	64		4598
POL	QIGCTLNFPI	179	10	16	25		4599
POL	CTLNFISPI	182	10	60	94		4600
POL	PLTEFEKAI	201	10	54	80		4601
POL	PLTEFEKAI	201	10	54	80		4602
POL	PLTEFEKAI	212	10	54	80		4603
POL	CTEMEKEGKI	225	10	27	42		4604
POL	AIKKKDKSTK	251	10	57	89		4605
POL	STKWRLKLVDF	257	10	58	91		4606

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Concomitancy (%)	A*2401	SEQ ID NO
POL	ELNKRTPQW	268	10	57	89		4606
POL	ELNKRTPQW	272	10	57	89		4607
POL	OLGHPHAGL	280	10	56	89		4608
POL	TVLVDVGDY	295	10	57	88		4609
POL	TVLVDVGDY	296	10	56	89		4610
POL	VFSVPLDKDF	304	10	18	29		4611
POL	DKRKYTAFT	312	10	42	66		4612
POL	DKRKYTAFT	313	10	37	66		4613
POL	AFQSSMTKL	347	10	36	56		4614
POL	AFQSSMTKL	348	10	38	59		4615
POL	IFGSSMTKL	348	10	36	56		4616
POL	IVIVQYMDLL	367	10	42	66	0.0002	4617
POL	VIVQYMDLL	368	10	51	80		4618
POL	DLVYGSLL	375	10	58	91		4619
POL	DLVYGSLL	376	10	59	91		4620
POL	KIEFLRQLL	390	10	17	27		4621
POL	POLPEKDSW	432	10	13	20		4622
POL	POLPEKDSW	432	10	13	20		4623
POL	SWTVNDIQKL	440	10	54	84		4624
POL	NWASQYAGH	454	10	27	42		4625
POL	NWASQYAGH	454	10	27	42		4626
POL	IYAGIKVQOL	459	10	18	28		4627
POL	IYAGIKVQOL	459	10	11	17		4628
POL	IYPIGKVRQL	459	10	15	23		4629
POL	GRKVKOLCKL	462	10	28	44		4630
POL	GRKVKOLCKL	462	10	18	28		4631
POL	GRKVKOLCKL	462	10	13	20		4632
POL	VPLTEAEEL	481	10	13	17		4633
POL	PLTEAEEL	483	10	30	47		4634
POL	ELLEAENREI	489	10	53	83		4635
POL	ILKEPVIGVY	498	10	40	63		4636
POL	GVYVDSKDL	508	10	38	59		4637
POL	GVYVDSKDL	508	10	38	59		4638
POL	EIOKGGQGW	520	10	13	20		4639
POL	EIOKGGQGW	520	10	15	23		4640
POL	WIVQVQEPF	539	10	42	66		4641
POL	QVQEPKRL	532	10	40	63	0.0150	4642
POL	PHENLKTKGY	537	10	45	70		4643
POL	PHENLKTKGY	537	10	45	70		4644
POL	NLKGKRYARM	540	10	13	21		4645
POL	AVQKATIESI	563	10	10	16		4646
POL	KIATESIVW	566	10	14	22		4647
POL	IIVWGTIKPF	572	10	47	73		4648
POL	IWGRTPKRL	574	10	17	27		4649
POL	PIQKETWEAW	584	10	15	23		4650
POL	PIQKETWEAW	584	10	27	42		4651
POL	ETWETWTD	588	10	10	16		4652
POL	ETWETWTE	588	10	10	16		4653
POL	ETWETWTDY	589	10	10	16		4654
POL	WTDTWQAT	593	10	14	22		4655

Table X
HIV A24 Super-Motif Peptides With Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	WVTEYVQAT	593	10	23	36		4656
POL	WTDYVQATW	594	10	14	22		4657
POL	WVTEYVQATW	595	10	14	38		4658
POL	WVTEYVQATW	597	10	52	81		4659
POL	EWETVNTPL	605	10	50	78	0.0660	4660
POL	FVNTPLVVL	608	10	54	86		4661
POL	NTPPLVVLWY	610	10	57	89		4662
POL	LWYQLEKDPH	617	10	14	22		4663
POL	LWYQLEKDPH	618	10	11	48		4664
POL	LWYQLEKDPH	617	10	11	17		4665
POL	LWYQLEKDPH	617	10	11	17		4666
POL	EVNVTDSQY	684	10	59	92		4667
POL	NVNTDSQVAL	686	10	59	92		4668
POL	VTDQVALGI	688	10	58	91		4669
POL	ELVNDQHEQL	708	10	18	28		4670
POL	ELVNDQHEQL	709	10	19	30		4671
POL	ELVNDQHEQL	709	10	19	30		4672
POL	LVSQHEQL	709	10	19	30		4673
POL	QLKKEKVVYL	716	10	28	44		4674
POL	QVDKLVASGI	739	10	15	23		4675
POL	QVDKLVASGI	739	10	29	45		4676
POL	LVSQHEKVL	743	10	15	23		4677
POL	LVSQHEKVL	743	10	15	23		4678
POL	NLPVVAKEI	779	10	26	41		4679
POL	NLPVVAKEI	779	10	27	42		4680
POL	IVASCDKCOL	788	10	43	67		4681
POL	GWQLDCTHL	811	10	59	92		4682
POL	GWQLDCTHL	811	10	31	48		4683
POL	CTULGKRVL	817	10	23	38		4684
POL	LVAIVIVASGY	826	10	53	83		4685
POL	ETGQETAYFI	844	10	31	48		4686
POL	ETGQETAYFI	844	10	26	41		4687
POL	YPIKLAKRW	851	10	31	48		4688
POL	YPIKLAKRW	851	10	31	48		4689
POL	THITDINGSN	864	10	15	27		4690
POL	VHTDINGSN	864	10	24	38		4691
POL	STTVKAACW	875	10	15	23		4692
POL	CWVAGIKQEF	882	10	21	33		4693
POL	CWVAGIKQEF	882	10	11	17		4694
POL	GWVAGIKQEF	886	10	12	34		4695
POL	GWVAGIKQEF	886	10	11	17		4696
POL	GWVAGIKQEF	886	10	11	17		4697
POL	SMNKLKELII	905	10	53	83		4698
POL	KTAQMAVFI	925	10	56	88		4699
POL	RIDHIASDI	951	10	12	19		4700
POL	RIDHIASDI	951	10	12	19		4701
POL	RIVDIAVDI	951	10	12	19		4702
POL	QTKELQKQH	961	10	12	19		4703
POL	IKIQNFRVY	969	10	12	19		4704
POL	ITKIQNFRVY	969	10	36	57		4705
POL	VYVRSRSDPI	977	10	34	53		4706

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	VYVDSRDPL	977	10	14	22		4706
POL	VYVDSRDPL	978	10	14	22		4707
POL	VYVDSRDPL	978	10	14	22		4708
POL	PWKGPALL	985	10	35	55		4709
POL	TLWKGPAKLL	985	10	18	28		4710
POL	IWKGPALLW	986	10	35	55		4711
POL	LWKGPALLW	986	10	18	28		4712
POL	LVKGPALLW	986	10	35	55		4713
POL	AVVQDSSEI	1000	10	32	54		4714
POL	AVVQDSSEI	1000	10	12	19		4715
POL	KVPRRKAKI	1011	10	51	80		4716
POL	KVPRRKAKI	1011	10	11	17		4717
POL	KVPRRKAKI	1012	10	50	78		4718
POL	KVPRRKAKI	1012	10	11	17		4719
POL	KVPRRKAKI	1019	10	11	17		4720
POL	KVPRRKAKI	1019	10	50	78		4721
POL	GTTLNFTQIF	79	10	01	01		4722
POL	AMSLSPQTL	80	11	01	33		4723
POL	GTTLNFTQIL	80	11	01	33		4724
POL	GTTLNFTQIL	80	11	01	33		4725
POL	ITLWQPLVTKI	92	11	14	22		4726
POL	ITLWQPLVTKI	92	11	14	22		4727
POL	LWQPLVTKI	92	11	12	19		4728
POL	PLVTKIGQQL	96	11	13	20		4729
POL	KGGQQLKEALL	101	11	23	36		4730
POL	PLVTKIGQQL	101	11	13	20		4731
POL	VLEEDNIPKRW	119	11	13	20		4732
POL	VLEEDNIPKRW	119	11	12	19		4733
POL	NLPGRKWKPKM	124	11	35	55		4734
POL	GIGGGRKVRQY	136	11	53	83		4735
POL	GIGGGRKVRQY	136	11	41	64		4736
POL	GIGGGRKVRQY	136	11	13	20		4737
POL	ELIHCGRKAL	149	11	13	20		4738
POL	TVLVGPTPVNI	161	11	53	83		4739
POL	TVLVGPTPVNI	161	11	51	80		4740
POL	TVLVGPTPVNI	166	11	26	41		4741
POL	PTVNIIGRNL	166	11	24	38		4742
POL	PTVNIIGRNL	166	11	18	28		4743
POL	NIGRNMALTOI	170	11	18	28		4744
POL	NIGRNMALTOI	170	11	11	17		4745
POL	LLTQIGCTLNE	176	11	21	33		4746
POL	MLTQIGCTLNE	176	11	17	27		4747
POL	MLTQIGCTLNE	176	11	10	16		4748
POL	MLTQIGCTLNE	229	11	32	50		4749
POL	EMFKGKSKSI	235	11	32	50		4750
POL	KISKIGPIENY	235	11	41	64		4751
POL	KISKIGPIENY	235	11	11	17		4752
POL	KWKLVDFRE	259	11	59	92		4753
POL	GLKKKKSIVT	288	11	49	77		4754
POL	SVTVLIDVGD	294	11	36	88		4755

Table X
HIV A4-Supernatant Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	VTVLDVGDAY	295	11	56	88		4756
POL	DVGDATSPV	299	11	54	84		4757
POL	SVPLDKPRK	306	11	18	28		4758
POL	SINNETGIRY	323	11	32	50		4760
POL	STNNETGIRY	323	11	11	17		4761
POL	RYQYVLPQG	332	11	63	98		4762
POL	AFQSSMTKIL	347	11	36	56		4763
POL	YVQVYVQVQ	366	11	18	28		4764
POL	DIVVQYMDLL	366	11	18	28		4765
POL	EIVVQYMDLL	366	11	24	38		4766
POL	IVVQYMDLL	367	11	42	66		4767
POL	YMDDLTVGSD	372	11	61	95		4768
POL	DLEIGQIRAKI	381	11	26	41		4769
POL	DLEIGQIRAKI	381	11	20	31		4770
POL	PLLEIGQIRAKI	382	11	14	22		4771
POL	LELEILLKVG	393	11	14	22		4772
POL	ELKQILLRWG	393	11	12	19		4773
POL	WMGVYELIPIK	418	11	60	94		4774
POL	DIQKLVGKLN	445	11	62	97		4775
POL	LVKLNWASQ	449	11	60	94		4776
POL	GVKLVWASQ	450	11	58	91		4777
POL	QVYGVKVKOL	458	11	11	17		4778
POL	QVYGVKVKOL	458	11	14	22		4779
POL	GKVKQKCKLL	462	11	27	42		4780
POL	GKVKQKCKLL	462	11	18	28		4781
POL	LLRGKALTDI	471	11	22	34		4782
POL	LVPLTEAEEL	480	11	11	17		4783
POL	DVPLTEAEEL	480	11	13	20		4784
POL	EVPLTEAEEL	480	11	11	17		4785
POL	ELELAENREIL	489	11	53	83		4786
POL	ELKEPVIGVY	497	11	40	63		4787
POL	ILKEPVIGVY	498	11	38	59		4788
POL	GVKLVWASQ	501	11	58	91		4789
POL	QVYGVKVKOL	528	11	42	66		4790
POL	SVVWGVKTKIK	571	11	41	64		4791
POL	VWGVKTKIK	573	11	17	27		4792
POL	VWGVKTKIK	573	11	29	45		4793
POL	KEPLPQKETW	580	11	20	31		4794
POL	KEPLPQKETW	580	11	26	41		4795
POL	PIKETWETW	584	11	38	59		4796
POL	PIKETWETW	584	11	27	42		4797
POL	ETWETWTD	588	11	10	16		4798
POL	TWWTYDWA	592	11	10	16		4799
POL	TWWTYDWA	592	11	12	19		4800
POL	WWTDYWAQI	593	11	14	22		4801
POL	WWTDYWAQI	593	11	22	34		4802
POL	EYWAQIWIPE	596	11	19	30		4803
POL	EYWAQIWIPE	596	11	33	52		4804
POL	EFVNTPLVKL	607	11	54	84		4805

Table X
HLV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*2401	SLCID NO
POL	FNPTPLVKL	608	11	54	86		4806
POL	KLWYQLEKDP	616	11	14	22		4807
POL	KLWYQLEKPH	616	11	31	48		4808
POL	KLWYQLETEH	616	11	11	17		4809
POL	LTDTINQKTE	661	11	19	30		4810
POL	LTDTINQKTH	661	11	15	25		4811
POL	TTNOKTELDAI	664	11	12	19		4812
POL	TTNOKTELQAI	664	11	42	66		4813
POL	KTELQAILAL	668	11	15	23		4814
POL	KTELQAILAL	668	11	12	19		4815
POL	MIILALQDSGL	673	11	15	23		4816
POL	ALQDSGLVNI	673	11	17	28		4817
POL	ALQDSGSEVNI	677	11	25	34		4818
POL	IVTDSQVALGI	687	11	58	91		4819
POL	VITDSQVALGI	688	11	58	91		4820
POL	ILVNOHIEQL	708	11	18	28		4821
POL	ILVNOHIEQL	708	11	19	30		4822
POL	ILVNOHIEQL	710	11	19	30		4823
POL	LIKKEKVLVSW	717	11	11	20		4824
POL	YLAWVPAIKG	724	11	22	34		4825
POL	YLSWVPAIKG	724	11	37	58		4826
POL	GIGGNFQVDKLL	733	11	58	91		4827
POL	GIGGNFQVDKLL	732	11	58	91		4828
POL	KLVSAGIRKVL	742	11	26	41		4829
POL	KLVSAGIRKVL	743	11	15	23		4830
POL	LVSGIRKVL	743	11	26	41		4831
POL	GIRKVLFDGI	747	11	49	77		4832
POL	AVKRAMASD	770	11	41	64		4833
POL	AVKRAMASD	770	11	41	64		4834
POL	EVASGDKCOL	787	11	43	67		4835
POL	QVDCSGIQW	805	11	56	88		4836
POL	QLDCTILLEGKI	814	11	33	52		4837
POL	ILVAVHVASGY	825	11	53	83		4838
POL	ILVAVHVASGY	826	11	47	73		4839
POL	ETGQETAYELL	844	11	27	41		4840
POL	ETGQETAYELL	844	11	26	41		4841
POL	AVFLKLAGR	850	11	31	48		4842
POL	AVFLKLAGR	850	11	25	39		4843
POL	KLAGRWPVKI	855	11	13	20		4844
POL	KLAGRWPVKI	855	11	13	20		4845
POL	KVHTIDINGSNF	863	11	21	33		4846
POL	FTSAVKAAC	873	11	27	42		4847
POL	FTSTVKAAC	873	11	14	22		4848
POL	AVKAACWVA	877	11	10	16		4849
POL	AVKAACWVA	877	11	20	31		4850
POL	WVAGQDIEG	883	11	11	17		4851
POL	WVAGQDIEG	883	11	11	17		4852
POL	HLKTAVOMAV	923	11	57	89		4853
POL	AVQNAVTHIN	927	11	60	94		4854
POL	ETHNFKRKGGI	933	11	58	91		4855

Table X
HIV A2.4-Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	NEKIKGEGGY	936	11	59	92		4856
POL	GGGYGAGRI	942	11	57	89		4857
POL	GYSAGRIUDI	945	11	40	63		4858
POL	YSDIKEL	945	11	14	22		4859
POL	YSDIKEL	945	11	34	53		4860
POL	DIOTKELOEI	959	11	44	69		4861
POL	QIKQNFVY	968	11	12	19		4862
POL	QIKQNFVY	968	11	35	55		4863
POL	IKQNFVY	969	11	12	19		4864
POL	IKQNFVY	969	11	32	55		4865
POL	IKQNFVY	969	11	34	53		4866
POL	RYVYRISLDP	976	11	14	22		4867
POL	VYVYRISLDP	977	11	34	53		4868
POL	VYVYRISLDP	977	11	14	22		4869
POL	VYVYRISLDP	977	11	14	22		4870
POL	WKGPXKLL	985	11	15	55		4871
POL	WKGPXKLL	985	11	15	55		4872
POL	LLWKGEGAVY	993	11	59	92		4873
POL	KVPRKAKII	1011	11	50	78		4874
POL	KVPRKAKII	1011	11	11	17		4875
REV	LLKTYRLI	12	8	11	17		4876
REV	LLKTYRLI	12	8	11	17		4877
REV	LLKTYRLI	12	8	23	42		4878
REV	LLKTYRLI	12	8	24	42		4879
REV	QLPPIERL	78	8	37	58		4880
REV	QLPPIERL	78	8	11	17		4881
REV	LVESPAVL	114	8	13	20		4882
REV	AVRIKILY	17	9	25	48		4883
REV	AVRIKILY	17	9	35	55		4884
REV	RWRARQRI	48	9	11	17		4885
REV	RWRARQRI	48	9	11	17		4886
REV	PVPLQLPPI	74	9	35	55		4887
REV	PVPLQLPPI	74	9	35	55		4888
REV	PVPLQLPPI	74	10	34	53		4889
REV	PVPLQLPPI	74	10	34	53		4890
REV	OLPPIERLTI	78	10	18	28		4891
REV	GTQCVGSTQI	97	10	11	18		4892
REV	IKILYOSNPY	20	11	18	28		4893
TAT	CYCKKCTT	38	8	11	17		4894
TAT	CYCKKCTT	38	8	11	17		4895
TAT	CFHCQVCT	34	8	11	17		4896
TAT	FLNKGGLI	41	8	14	22		4897
TAT	PVDRNLEPW	3	9	20	31		4898
TAT	PVDRNLEPW	3	9	14	22		4899
TAT	FLNKGGLI	41	9	14	22		4900
TAT	FLNKGGLI	41	10	14	22		4901
TAT	FLNKGGLI	41	11	14	22		4902
VIF	RWOVLVW	4	8	10	16		4903
VIF	RWOVLVW	4	8	43	67		4904
VIF	IKWQVDMR	9	8	59	92		4905
VIF	KIRWNSL	17	8	12	19		4906

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	RIRTKSL	17	8	15	21		4906
VIF	RIRTKSL	17	8	15	23		4907
VIF	SLVKKIMY	23	8	44	69		4908
VIF	SLVKKIMY	23	8	39	30		4909
VIF	SLVKKIMY	23	8	15	21		4910
VIF	KASSEVII	50	8	15	21		4911
VIF	KASSEVII	50	8	20	31		4912
VIF	RISSEVII	30	8	15	23		4913
VIF	RLVITTYW	65	8	12	19		4914
VIF	RLVITTYW	65	8	12	19		4915
VIF	RLVITTYW	65	8	10	16		4916
VIF	RLVITTYW	65	8	22	16		4917
VIF	VRTYWGIL	67	8	16	16		4918
VIF	VRTYWGIL	67	8	11	17		4919
VIF	VRTYWGIL	67	8	11	17		4920
VIF	ILHGQVSI	83	8	25	39		4921
VIF	ILHGQVSI	83	8	26	41		4922
VIF	ILHGQVSI	83	8	26	28		4923
VIF	STQVDPGL	100	8	11	17		4924
VIF	STQVDPGL	100	8	11	17		4925
VIF	QIMILYVF	110	8	14	22		4926
VIF	QIMILYVF	110	8	14	22		4927
VIF	ILYYFDKF	113	8	16	25		4928
VIF	ILYYFDKF	113	8	16	25		4929
VIF	IVSPKCLY	133	8	14	22		4930
VIF	KVGSQYVL	146	8	52	81		4931
VIF	QYLAALAL	151	8	12	19		4932
VIF	QYLAALAL	151	8	11	17		4933
VIF	QYLAALAL	151	8	33	52		4934
VIF	QYLAALAL	151	8	33	52		4935
VIF	ALJPKSKI	157	8	10	16		4936
VIF	PLJPSVKKL	168	8	21	33		4937
VIF	PLJPSVKKL	168	8	14	22		4938
VIF	MYWQVDRKM	8	9	46	72		4939
VIF	MYWQVDRKM	8	9	46	72		4940
VIF	MYWQVDRKM	8	9	13	20		4941
VIF	MYWQVDRKM	8	9	46	72		4942
VIF	SLVKKIMYI	23	9	19	30		4943
VIF	HLPLGDARL	56	9	13	20		4944
VIF	HLPLGDARL	56	9	20	31		4945
VIF	HLPLGDARL	56	9	10	16		4946
VIF	PLGEARLVI	58	9	10	16		4947
VIF	PLGEARLVI	58	9	10	16		4948
VIF	LVITTYWGIL	66	9	22	34		4949
VIF	GLHTIGERDOW	73	9	22	34		4950
VIF	GLHTIGERDOW	73	9	12	19		4951
VIF	ITHTGERDWHIL	75	9	21	33		4952
VIF	ITHTGERDWHIL	75	9	12	19		4953
VIF	ITHTGERDWHIL	75	9	12	19		4954
VIF	ITHTGERDWHIL	75	9	18	28		4955
VIF	DLADQLIIL	106	9	11	17		4956
VIF	GLADQLIIL	106	9	15	23		4957
VIF	QYLAALALI	151	9	28	44		4958
VIF	QYLAALALI	151	9	28	44		4959
VIF	MYWQVDRK	7	10	44	69		4960
VIF	IVWQVDRKSKI	9	10	12	19		4961

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SIQ ID NO
VIF	IVQVDRMR	9	10	47	73		4956
VIF	QVDRMRITW	12	10	12	19		4957
VIF	QVDRMRITW	12	10	10	16		4958
VIF	QVDRMRITW	12	10	31	48		4959
VIF	QVDRMRITW	12	10	12	19		4960
VIF	RMRTWKS	15	10	15	23		4961
VIF	RMRTWNSL	15	10	15	23		4962
VIF	TWKSLVKIII	20	10	16	25		4963
VIF	TWNSLVKIII	20	10	25	39		4964
VIF	QVDRMRITW	20	10	14	22		4965
VIF	QVDRMRITW	20	10	14	22		4966
VIF	QVDRMRITW	20	10	13	20		4967
VIF	KSSSEVHPL	50	10	13	20		4968
VIF	RLVITWGL	65	10	12	19		4969
VIF	DWILGIGVSI	81	10	21	33		4970
VIF	DWILGIGVSI	81	10	18	28		4971
VIF	DWILGIGVSI	81	10	25	39		4972
VIF	HLGGVSEW	83	10	24	41		4973
VIF	RYSVDFGL	98	10	10	16		4974
VIF	QIDPLADQL	102	10	10	16		4975
VIF	QVDRGLADQL	102	10	14	22		4976
VIF	LIHCYDFCF	111	10	16	25		4977
VIF	LIHCYDFCF	111	10	16	25		4978
VIF	YDFCSFSAI	116	10	28	44		4979
VIF	KVGSQYLAL	146	10	51	80		4980
VIF	SLOYLALAL	149	10	12	19		4981
VIF	SLOYLALAL	149	10	11	17		4982
VIF	SLOYLALAL	149	10	31	48		4983
VIF	SVMLADW	149	10	11	17		4984
VIF	OVIMVQVDR	6	11	43	67		4985
VIF	MIVVQVDRM	8	11	43	67		4986
VIF	RTWKSIVKIII	19	11	14	22		4987
VIF	RTWKSIVKIII	19	11	24	38		4988
VIF	RTWKSIVKIII	19	11	16	25		4989
VIF	TWNSLVKIII	20	11	22	34		4990
VIF	EVIIPLGDARL	54	11	13	20		4991
VIF	EVIIPLGEARL	54	11	20	31		4992
VIF	HIPLGEARLVI	56	11	10	16		4993
VIF	WGLTFGRD	71	11	32	50		4994
VIF	WGLTFGRD	71	11	12	19		4995
VIF	GLITGERDWH	73	11	12	19		4996
VIF	GLITGERDWH	73	11	10	16		4997
VIF	GVSEWRLLR	87	11	10	16		4998
VIF	QIDPLATQII	102	11	10	16		4999
VIF	QIDPLATQII	102	11	14	22		5000
VIF	GLADLHRI	106	11	13	20		5001
VIF	QLIIMHYDFCF	110	11	13	20		5002
VIF	YDFCSFSAI	115	11	14	22		5003
VIF	YDFCSFSAI	115	11	20	31		5004
VIF	CFSESARRKAI	119	11	10	16		5005
VIF	CFSESARRKAI	119	11	12	19		5006

Table X
HIV A24 Super-Modi Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	CFSSAIRNAI	119	11	12	19		5006
VIF	SLYALIALAI	149	11	27	42		5007
VIF	AKGKSGRI	158	11	10	15		5008
VIF	KTKGHSQIT	188	11	15	23		5009
VPR	ALLELEEL	19	8	10	16		5010
VPR	TLELELEL	19	8	44	69		5011
VPR	AVRIPIRI	30	8	14	22		5012
VPR	WVGGQY	38	8	11	17		5013
VPR	WVGGQY	38	8	16	25		5014
VPR	TWEGEAI	53	8	20	31		5015
VPR	GVEAIRI	56	8	34	53		5016
VPR	IRILQQL	60	8	42	66		5017
VPR	IRILQQLF	62	8	45	70		5018
VPR	IRILQQL	62	8	37	58		5019
VPR	LIIFIRI	67	8	67	100		5020
VPR	LIIFIRI	67	8	12	19		5021
VPR	PYNEWLLEL	14	9	30	47	0.1400	5022
VPR	WTLELEEL	18	9	42	69		5023
VPR	AVRIPIRI	30	9	14	22		5024
VPR	WVGGQY	38	9	14	22		5025
VPR	PWLHGLQY	37	9	17	26		5026
VPR	WVGGQY	38	9	20	31		5027
VPR	IVETVGDW	46	9	31	48		5028
VPR	IVETVGDW	46	9	18	28		5029
VPR	IVETVGDW	46	9	16	25		5030
VPR	DTWAGVEAI	52	9	10	16		5031
VPR	DTWAGVEAI	52	9	16	25		5032
VPR	TWEGEAI	53	9	19	30	0.0580	5033
VPR	GVEAIRIL	56	9	34	53		5034
VPR	IRILQQL	59	9	39	61		5035
VPR	IRILQQL	60	9	42	66		5036
VPR	IRILQQL	60	9	46	71		5037
VPR	OLLFIRI	66	9	48	69		5038
VPR	QLLFVIRI	66	9	40	16		5039
VPR	RGCQISRI	74	9	47	73		5040
VPR	RGCQISRI	74	9	12	19		5041
VPR	WTLELEEL	14	10	30	47		5042
VPR	WTLELEEL	14	10	17	28		5043
VPR	ELKNEAVRIF	25	10	17	27		5044
VPR	ELKNEAVRIF	25	10	15	23		5045
VPR	AVRIPIRI	30	10	14	22		5046
VPR	AVRIPIRI	30	10	34	53		5047
VPR	IRILQQL	33	10	10	16		5048
VPR	IRILQQL	33	10	10	16		5049
VPR	IRILQQL	33	10	12	19		5050
VPR	PWLHGLQY	37	10	20	31		5051
VPR	IVETVGDW	45	10	17	27		5052
VPR	IVETVGDW	45	10	14	22		5053
VPR	IVETVGDW	45	10	14	22		5054
VPR	DTWAGVEAI	52	10	16	25		5055

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VPR	DTWEGVEAI	52	10	19	30		5056
VPR	AIRRIQQLL	59	39	61			5057
VPR	IRRLQQLF	60	10	41	64		5058
VPR	IRRLQQLF	61	10	41	64		5059
VPR	PWHLGLGDI	37	11	15	19		5060
VPR	QVIVETGDT	44	11	14	22		5061
VPR	TWAGVEAIRI	53	11	15	23		5062
VPR	TWEGVEAIRI	53	11	14	22		5063
VPR	AIRRIQQLLF	59	11	38	59		5064
VPR	IRRLQQLF	60	11	33	53		5065
VPR	IRRLQQLF	62	11	34	53		5066
VPR	IRRLQQLF	62	11	34	53		5067
VPR	IRRLQQLF	62	11	44	69		5068
VPR	IRRLQQLF	62	11	11	17		5069
VPR	IRRLQQLF	62	11	45	70		5070
VPR	IRRLQQLF	62	11	11	17		5071
VPR	IRRLQQLF	62	11	11	17		5072
VPR	IRRLQQLF	62	11	11	17		5073
VPR	IRRLQQLF	62	11	15	23		5074
VPR	IRRLQQLF	62	11	15	23		5075
VPR	IRRLQQLF	62	11	12	19		5076
VPR	IRRLQQLF	62	11	12	19		5077
VPR	IRRLQQLF	62	11	12	19		5078
VPR	IRRLQQLF	62	11	12	19		5079
VPR	IRRLQQLF	62	11	12	19		5080
VPR	IRRLQQLF	62	11	12	19		5081
VPR	IRRLQQLF	62	11	12	19		5082
VPR	IRRLQQLF	62	11	12	19		5083
VPR	IRRLQQLF	62	11	12	19		5084
VPR	IRRLQQLF	62	11	12	19		5085
VPR	IRRLQQLF	62	11	12	19		5086
VPR	IRRLQQLF	62	11	12	19		5087
VPR	IRRLQQLF	62	11	12	19		5088
VPR	IRRLQQLF	62	11	12	19		5089
VPR	IRRLQQLF	62	11	12	19		5090
VPR	IRRLQQLF	62	11	12	19		5091
VPR	IRRLQQLF	62	11	12	19		5092
VPR	IRRLQQLF	62	11	12	19		5093
VPR	IRRLQQLF	62	11	12	19		5094
VPR	IRRLQQLF	62	11	12	19		5095
VPR	IRRLQQLF	62	11	12	19		5096
VPR	IRRLQQLF	62	11	12	19		5097
VPR	IRRLQQLF	62	11	12	19		5098
VPR	IRRLQQLF	62	11	12	19		5099
VPR	IRRLQQLF	62	11	12	19		5100
VPR	IRRLQQLF	62	11	12	19		5101
VPR	IRRLQQLF	62	11	12	19		5102
VPR	IRRLQQLF	62	11	12	19		5103
VPR	IRRLQQLF	62	11	12	19		5104
VPR	IRRLQQLF	62	11	12	19		5105

Table XI
HIV B97 Super Motif Peptides With Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	B*P002	SEQ ID NO.
ENV	DNPQEVV	91	8	13	20		5106
ENV	APAGFAIL	265	8	29	45		5107
ENV	KPVSTQL	269	8	34	53		5108
ENV	GRQGFIA	362	8	26	41		5109
ENV	GRQGFIA	362	8	26	41		5110
ENV	L'CRKQI	485	8	31	48		5111
ENV	SPSQTL	808	8	30	47		5112
ENV	GDPRPQI	822	8	15	23		5113
ENV	EDRPERI	823	8	01	33		5114
ENV	EDRPERI	823	8	01	33		5115
ENV	EDRPERI	823	8	01	33		5116
ENV	DNPQEVV	91	8	13	20	0.0002	5117
ENV	KPVSTQL	269	8	34	53	0.0350	5118
ENV	KPVSTQL	269	8	34	53	0.0001	5119
ENV	KPVSTQL	269	8	34	53	0.0001	5120
ENV	KPVSTQL	269	8	34	53	0.0130	5121
ENV	KPVSTQL	269	8	34	53	0.0001	5122
ENV	KPVSTQL	269	8	34	53	0.0001	5123
ENV	KPVSTQL	269	8	34	53	0.0001	5124
ENV	KPVSTQL	269	8	34	53	0.0019	5125
ENV	KPVSTQL	269	8	34	53	0.0002	5126
ENV	KPVSTQL	269	8	34	53	0.0001	5127
ENV	KPVSTQL	269	8	34	53	0.0001	5128
ENV	KPVSTQL	269	8	34	53	0.0011	5129
ENV	KPVSTQL	269	8	34	53	0.0002	5130
ENV	KPVSTQL	269	8	34	53	0.0002	5131
ENV	KPVSTQL	269	8	34	53	0.0002	5132
ENV	KPVSTQL	269	8	34	53	0.0002	5133
ENV	KPVSTQL	269	8	34	53	0.0002	5134
ENV	KPVSTQL	269	8	34	53	0.0002	5135
ENV	KPVSTQL	269	8	34	53	0.0002	5136
ENV	KPVSTQL	269	8	34	53	0.0008	5137
ENV	KPVSTQL	269	8	34	53	0.0038	5138
ENV	KPVSTQL	269	8	34	53	0.0005	5139
ENV	KPVSTQL	269	8	34	53	0.0005	5140
ENV	KPVSTQL	269	8	34	53	0.1200	5141
ENV	KPVSTQL	269	8	34	53	0.0002	5142
ENV	KPVSTQL	269	8	34	53	0.0002	5143
ENV	KPVSTQL	269	8	34	53	0.0004	5144
ENV	KPVSTQL	269	8	34	53	0.0004	5145
ENV	KPVSTQL	269	8	34	53	0.0004	5146
ENV	KPVSTQL	269	8	34	53	0.0004	5147
ENV	KPVSTQL	269	8	34	53	0.0004	5148
ENV	KPVSTQL	269	8	34	53	0.0004	5149
ENV	KPVSTQL	269	8	34	53	0.0004	5150
ENV	KPVSTQL	269	8	34	53	0.0004	5151
ENV	KPVSTQL	269	8	34	53	0.0004	5152
ENV	KPVSTQL	269	8	34	53	0.0004	5153
ENV	KPVSTQL	269	8	34	53	0.0004	5154
ENV	KPVSTQL	269	8	34	53	0.0004	5155

Table XI
HIV RT Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	I ⁰ /I ⁰ 2	SFQ ID NO.
GAG	RFQGGKRYRL	22	10	16	25		5206
GAG	RFQGGKRYRL	186	10	16	64	0.0002	5207
GAG	SFEVIMETA	186	10	15	50		5208
GAG	NIPHVGDY	277	10	10	16		5209
GAG	NIPVIGETV	277	10	34	54	0.0002	5210
GAG	IPVGDYKRW	280	10	11	17		5211
GAG	IPVGDYKRW	280	10	34	53	0.0002	5212
GAG	IPVGDYKRW	280	10	34	98	0.0002	5213
GAG	EPFEDYVDFE	315	10	62	31	0.0002	5214
GAG	EPFEDYVDFE	315	10	28	44	0.0002	5215
GAG	NPDCKTLKA	351	10	18	25		5216
GAG	NPDCKTLKA	351	10	18	25	0.0020	5217
GAG	GPAATLEEMM	362	10	16	28		5218
GAG	GPAATLEEMM	362	10	18	28		5219
GAG	GRGATLEEMM	362	10	35	55	0.0002	5220
GAG	GRGATLEEMM	362	10	35	50		5221
GAG	GRGATLEEMM	362	10	35	50		5222
GAG	PPAEPAPPA	491	10	01	31		5223
GAG	EPTAPVIESF	494	10	20	31	0.0002	5224
GAG	EPTAPVIESF	494	10	15	23		5225
GAG	EPTAPVIESF	494	10	01	50		5226
GAG	PPHSTREEL	510	10	01	31		5227
GAG	PPHSTREEL	510	10	01	31	0.0019	5228
GAG	EPDKELYPL	531	10	12	19	0.0019	5229
GAG	EPDKELYPL	531	10	08	17	0.0019	5230
GAG	YPLASLKSFL	545	10	07	15	0.0140	5231
GAG	YPLASLKSFL	545	10	04	24		5232
GAG	YPLASLKSFL	545	10	01	33		5233
GAG	YPLASLKSFL	547	10	01	33		5234
GAG	YPLASLKSFL	547	10	01	33		5235
GAG	QPSLOTTSEEL	67	11	13	20		5236
GAG	YFVONAQOQ	153	11	20	31		5237
GAG	YFVONAQOQ	153	11	29	45	0.0076	5238
GAG	SPRLNAAWK	160	11	55	64	0.0005	5239
GAG	SFEVIMFESAL	186	11	41	20	0.0004	5240
GAG	SFEVIMFETAL	186	11	13	70		5241
GAG	HPMSALSEGA	190	11	45	23		5242
GAG	HPMSALSEGA	190	11	15	23		5243
GAG	HPMSALSEGA	190	11	15	17		5244
GAG	IPVGDYKRWI	280	11	16	53	0.0001	5245
GAG	IPVGDYKRWI	280	11	34	55		5246
GAG	EPFEDYVDFEF	315	11	35	44	0.0001	5247
GAG	EPFEDYVDFEF	315	11	28	44	0.0001	5248
GAG	NPDCKTLKAL	351	11	18	28		5249
GAG	NPDCKTLKAL	351	11	18	28		5250
GAG	WFSNKGRTGN	474	11	14	22		5251
GAG	WFSNKGRTGN	474	11	11	17		5252
GAG	WFSNKGRTGN	474	11	11	33		5253
GAG	PPPIESRFEFA	510	11	01	33		5254
NEF	APTAAGKV	101	8	01	33		5255
NEF	VPLKPMIF	101	8	10	16		5256

Table XI
HIV B07 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO
NEF	VPLRMITY	101	8	46	73	0.0001	5256
NEF	RPMYKAA	104	8	23	36		5257
NEF	RPMYKGA	104	8	25	39		5258
NEF	TPGKIRK	208	8	17	27		5259
NEF	TPGKIRL	208	8	17	27		5260
NEF	GRGIRYL	210	8	12	20		5261
NEF	GRGIRFL	210	8	13	20		5262
NEF	VPLDPRV	230	8	11	17		5263
NEF	IPICQIGM	239	8	10	16		5264
NEF	IPMSQIGM	239	8	12	19		5265
NEF	IPMSQIGM	239	8	12	19		5266
NEF	IPMSQIGM	239	8	12	19		5267
NEF	PIAAQVGA	40	9	06	15		5268
NEF	PIVRFQVPL	94	9	48	75		5269
NEF	RQVPLPM	98	9	47	73		5270
NEF	RPMYKGA	104	9	12	19		5271
NEF	YPLTHKVC	217	9	17	27		5272
NEF	YPLTHKVC	217	9	24	33		5273
NEF	YPLTHKVC	217	9	24	33		5274
NEF	ETAAAGVGAV	40	10	04	15		5275
NEF	VPLRMITYKA	101	10	20	32		5276
NEF	TPGKIRYPL	208	10	16	25		5277
NEF	TPGKIRYPL	208	10	13	20		5278
NEF	TPGKIRYPL	208	10	13	20		5279
NEF	GRGIRYPL	210	10	13	20		5280
NEF	GRGIRYPL	210	10	13	20		5281
NEF	APFAAKGVGA	34	11	01	16		5282
NEF	RQVPLRPM	98	11	10	16		5283
NEF	RQVPLRPM	98	11	36	56		5284
NEF	RQVPLRPM	98	11	36	56		5285
NEF	RQVPLRPM	98	11	36	56		5286
NEF	RQVPLRPM	98	11	36	56		5287
NEF	RQVPLRPM	98	11	36	56		5288
NEF	RQVPLRPM	98	11	36	56		5289
NEF	RQVPLRPM	98	11	36	56		5290
NEF	RQVPLRPM	98	11	36	56		5291
NEF	RQVPLRPM	98	11	36	56		5292
NEF	RQVPLRPM	98	11	36	56		5293
NEF	RQVPLRPM	98	11	36	56		5294
NEF	RQVPLRPM	98	11	36	56		5295
NEF	RQVPLRPM	98	11	36	56		5296
NEF	RQVPLRPM	98	11	36	56		5297
NEF	RQVPLRPM	98	11	36	56		5298
NEF	RQVPLRPM	98	11	36	56		5299
NEF	RQVPLRPM	98	11	36	56		5300
NEF	RQVPLRPM	98	11	36	56		5301
NEF	RQVPLRPM	98	11	36	56		5302
NEF	RQVPLRPM	98	11	36	56		5303
NEF	RQVPLRPM	98	11	36	56		5304
NEF	RQVPLRPM	98	11	36	56		5305

Table XI
HIV B17 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*7012	SEQ ID NO.
POL	PPLVKLWY	612	8	57	89	0.0001	5306
POL	PIPVAKEL	781	8	27	42		5307
POL	PIPVAKEL	781	8	29	45	0.0001	5308
POL	PIPVAKEL	781	8	30	46	0.0001	5309
POL	PIPVAKEL	781	8	37	58	0.0001	5310
POL	PIPVAKEL	781	8	37	58		5311
POL	PIPVAKEL	781	8	15	23		5312
POL	PIPVAKEL	781	8	51	80	0.0018	5313
POL	PIPVAKEL	781	8	11	17		5314
POL	PIPVAKEL	781	8	10	16		5315
POL	PIPVAKEL	781	8	14	21	0.0210	5316
POL	PIPVAKEL	781	8	14	21		5317
POL	PIPVAKEL	781	8	01	33		5318
POL	PIPVAKEL	781	8	01	50		5319
POL	PIPVAKEL	781	8	01	17		5320
POL	PIPVAKEL	781	8	39	61	0.0038	5321
POL	PIPVAKEL	781	8	25	45	0.0003	5322
POL	PIPVAKEL	781	8	56	88	0.0003	5323
POL	PIPVAKEL	781	8	51	80	0.0002	5324
POL	PIPVAKEL	781	8	51	80	0.0150	5325
POL	PIPVAKEL	781	8	24	38		5326
POL	PIPVAKEL	781	8	37	58	0.0002	5327
POL	PIPVAKEL	781	8	37	58	0.0150	5328
POL	PIPVAKEL	781	8	17	27	0.0001	5329
POL	PIPVAKEL	781	8	23	36		5330
POL	PIPVAKEL	781	8	63	98	0.0001	5331
POL	PIPVAKEL	781	8	63	98	0.0001	5332
POL	PIPVAKEL	781	8	11	17		5333
POL	PIPVAKEL	781	8	11	17		5334
POL	PIPVAKEL	781	8	19	30		5335
POL	PIPVAKEL	781	8	57	89	0.0001	5336
POL	PIPVAKEL	781	8	21	33	0.0001	5337
POL	PIPVAKEL	781	8	37	58	0.0006	5338
POL	PIPVAKEL	781	8	37	58	0.0006	5339
POL	PIPVAKEL	781	8	28	44	0.0006	5340
POL	PIPVAKEL	781	8	26	41		5341
POL	PIPVAKEL	781	8	28	44	0.0001	5342
POL	PIPVAKEL	781	8	50	78	0.4800	5343
POL	PIPVAKEL	781	8	11	17		5344
POL	PIPVAKEL	781	8	11	17		5345
POL	PIPVAKEL	781	8	01	33	0.0025	5346
POL	PIPVAKEL	781	8	01	20		5347
POL	PIPVAKEL	781	8	39	61		5348
POL	PIPVAKEL	781	8	15	23	0.0002	5349
POL	PIPVAKEL	781	8	26	41	0.0003	5350
POL	PIPVAKEL	781	8	26	41	0.0003	5351
POL	PIPVAKEL	781	8	53	83	0.0028	5352
POL	PIPVAKEL	781	8	54	84	0.0018	5353
POL	PIPVAKEL	781	8	24	38		5354
POL	PIPVAKEL	781	8	38	59	0.0002	5355

Table XI
HIV B07-SupE-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO
POL	NPNTPEAI	243	10	24	38		5356
POL	NPNTPEAI	243	10	37	58	0.0034	5357
POL	VPDKDFRY	307	10	18	28	0.0002	5358
POL	TPGIRYQRY	328	10	51	80	0.0004	5359
POL	EPKPKNDPI	328	10	16	25	0.0002	5360
POL	EPKPKNDPI	358	10	16	25	0.0002	5361
POL	NPPIVIOYM	364	10	17	27	0.0005	5362
POL	NPEIVIOYM	364	10	23	36		5363
POL	PPFLWMGYEL	414	10	64	100	0.0002	5364
POL	TPDKXIYQPI	424	10	53	83	0.0012	5365
POL	TPDKXIYQPI	424	10	56	100	0.0002	5366
POL	LPDKETWEA	583	10	15	23	0.0002	5367
POL	PPLVKLWYCL	612	10	53	83	0.0002	5368
POL	EPVGAETFY	624	10	21	33	0.0002	5369
POL	GPDKSUSSELY	701	10	37	58	0.0002	5370
POL	LPPIVAKETV	780	10	26	41	0.0002	5371
POL	LPPIVAKETV	780	10	25	41	0.0002	5372
POL	PPVAKETVA	781	10	28	39	0.0002	5373
POL	PPVAKETVA	781	10	28	44		5374
POL	IPAEITQGETA	841	10	58	91	0.0066	5375
POL	IPYRPSQGV	893	10	63	98	0.0002	5376
POL	IPYRPSQGV	894	10	63	98	0.0023	5377
POL	IPYRPSQGV	894	10	63	98	0.0001	5378
POL	IPYRPSQGV	894	10	63	98	0.0001	5379
POL	VPYNSPQITL	79	11	01	17		5380
POL	PPQITLWQRP	87	11	40	63		5381
POL	KPKMIGGIGGF	130	11	60	94	0.0004	5382
POL	TPYNIQRNLL	167	11	26	41	0.0002	5383
POL	PPYNIQRNLL	167	11	26	41	0.0002	5384
POL	PPYNIQRNLL	167	11	26	41	0.0002	5385
POL	PPYNIQRNLL	167	11	26	41	0.0001	5386
POL	PPYNIQRNLL	167	11	26	41	0.0001	5387
POL	PPYNIQRNLL	167	11	26	41	0.0001	5388
POL	PPYNIQRNLL	167	11	26	41	0.0001	5389
POL	PPYNIQRNLL	167	11	26	41	0.0001	5390
POL	PPYNIQRNLL	167	11	26	41	0.0001	5391
POL	PPYNIQRNLL	167	11	26	41	0.0001	5392
POL	PPYNIQRNLL	167	11	26	41	0.0001	5393
POL	PPYNIQRNLL	167	11	26	41	0.0001	5394
POL	PPYNIQRNLL	167	11	26	41	0.0001	5395
POL	PPYNIQRNLL	167	11	26	41	0.0001	5396
POL	PPYNIQRNLL	167	11	26	41	0.0001	5397
POL	PPYNIQRNLL	167	11	26	41	0.0001	5398
POL	PPYNIQRNLL	167	11	26	41	0.0001	5399
POL	PPYNIQRNLL	167	11	26	41	0.0001	5400
POL	PPYNIQRNLL	167	11	26	41	0.0001	5401
POL	PPYNIQRNLL	167	11	26	41	0.0001	5402
POL	PPYNIQRNLL	167	11	26	41	0.0001	5403
POL	PPYNIQRNLL	167	11	26	41	0.0001	5404
POL	PPYNIQRNLL	167	11	26	41	0.0001	5405

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	LPVVAKEIVA	780	11	27	42		5406
POL	IPAEQGETAY	841	11	58	91	0.0001	5407
POL	IPNQSQGVY	893	11	59	92	0.0001	5408
POL	IPNQSQGVY	893	11	59	92	0.0001	5409
POL	DPNKGPAKL	984	11	34	53		5410
POL	DPNKGPAKL	984	11	14	22		5411
REV	SPETRQA	33	8	13	20		5412
REV	RPAEPVPL	70	8	31	31		5413
REV	VPLQHPH	75	8	17	17		5414
REV	VPLQHPH	75	8	36	51	0.0400	5415
REV	LPPLRLTL	80	8	19	30	0.0001	5416
REV	LPPLRLTL	80	8	19	30	0.3100	5417
REV	QPQGETGV	100	9	05	18		5418
REV	PPSPGTRQA	30	10	12	19		5419
REV	RPAEPVPL	70	10	20	31		5420
REV	PPSPGTRQA	30	10	11	18		5421
REV	EPVPLQPL	73	10	34	53	0.0023	5422
REV	PPSPGTRQA	29	11	12	19		5423
REV	VPLQHPH	75	11	11	17		5424
REV	VPLQHPH	75	11	34	53	0.0001	5425
TAT	IPGSPKTA	16	9	26	41	0.0007	5426
TAT	IPGSPKTA	16	9	26	41		5427
TAT	IPGSPKTA	16	9	26	41		5428
TAT	EPVPLQPL	90	9	13	20		5429
TAT	EPVPLQPL	2	10	14	22		5430
VIF	IPKISSEV	48	8	13	20	0.0001	5431
VIF	IPKISSEV	48	8	13	20		5432
VIF	IPKISSEV	48	8	13	20		5433
VIF	IPKISSEV	48	8	13	20		5434
VIF	IPKISSEV	48	8	13	20		5435
VIF	IPKISSEV	48	8	13	20		5436
VIF	IPKISSEV	48	8	13	20		5437
VIF	IPKISSEV	48	8	13	20		5438
VIF	IPKISSEV	48	8	13	20		5439
VIF	IPKISSEV	48	8	13	20		5440
VIF	IPKISSEV	48	8	13	20		5441
VIF	IPKISSEV	48	8	13	20		5442
VIF	IPKISSEV	48	8	13	20		5443
VIF	IPKISSEV	48	8	13	20		5444
VIF	IPKISSEV	48	8	13	20		5445
VIF	IPKISSEV	48	8	13	20		5446
VIF	IPKISSEV	48	8	13	20		5447
VIF	IPKISSEV	48	8	13	20	0.0330	5448
VIF	IPKISSEV	48	8	13	20		5449
VIF	IPKISSEV	48	8	13	20		5450
VIF	IPKISSEV	48	8	13	20		5451
VIF	IPKISSEV	48	8	13	20		5452
VIF	IPKISSEV	48	8	13	20		5453
VIF	IPKISSEV	48	8	13	20		5454
VIF	IPKISSEV	48	8	13	20		5455

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
VPR	EPYNEWTLLEL	13	10	29	45	0.0054	5456
VPR	RPWLIGLQY	36	10	10	16		5457
VPR	EPYNEWTLLEL	13	11	29	45		5458
VPR	RPWLIGLQYH	36	11	12	19		5459
VPU	APWDYDDL	99	8	12	19		5460

Table XII
HIV B27 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	SEQ ID NO.
ENV	EKLWTVL	9	8	01	50	5461
ENV	RLSWEL	9	8	01	50	5462
ENV	WRWGELF	15	8	01	50	5463
ENV	WRWGTMLL	15	8	01	50	5464
ENV	EKLWTVY	43	8	09	15	5465
ENV	WKEATTL	56	8	23	36	5466
ENV	MLIEDHSL	117	8	29	45	5467
ENV	WKEATTL	117	8	29	45	5468
ENV	PKASPEFI	251	8	30	47	5469
ENV	LACNDPKKF	272	8	13	20	5470
ENV	AKTIQVL	330	8	14	22	5471
ENV	QRGPGRF	360	8	01	33	5472
ENV	KKKKGTGI	374	8	01	50	5473
ENV	IKQVNMW	484	8	17	28	5474
ENV	IKQVNMW	489	8	33	57	5475
ENV	IKQVNMW	489	8	13	21	5476
ENV	QRVQGMV	497	8	11	17	5477
ENV	FRTPGGDM	546	8	43	67	5478
ENV	WRSELYKY	557	8	54	84	5479
ENV	YKCKVYHL	562	8	10	20	5480
ENV	YKCKVYHL	562	8	29	46	5481
ENV	ARQLLSGI	627	8	38	59	5482
ENV	VRQLLSGI	627	8	10	16	5483
ENV	LKLTVMGI	652	8	13	20	5484
ENV	EKNEODLL	749	8	17	27	5485
ENV	EKNEODLL	749	8	18	28	5486
ENV	YKCKVYHL	790	8	17	27	5487
ENV	LRIVAVL	803	8	28	44	5488
ENV	VRQGYSP	803	8	56	88	5489
ENV	IRLVNGL	843	8	11	17	5490
ENV	IRLVNGL	843	8	13	20	5491
ENV	YHRLRDTL	865	8	13	20	5492
ENV	YHRLRDTL	865	8	15	23	5493
ENV	HIRLDFIL	866	8	13	20	5494
ENV	HIRLDFIL	866	8	13	20	5495
ENV	GRIGWEAL	884	8	09	15	5496
ENV	LKGLRLGW	890	8	12	40	5497
ENV	LKGLRLGW	890	8	05	17	5498
ENV	LRIVAVL	890	8	10	20	5499
ENV	LKLVNLL	900	8	14	22	5500
ENV	LKLVNLL	900	8	14	22	5501
ENV	LKNSAIL	914	8	10	16	5502
ENV	LKNSAIL	914	8	10	16	5503
ENV	LKNSAVSL	914	8	13	20	5504
ENV	FRIRPGP	951	8	11	17	5505
ENV	FRIRPGP	951	8	26	41	5506
ENV	GKDLWTVY	42	9	01	33	5507
ENV	EKLWTVY	43	9	09	15	5508
ENV	WKEATTLF	56	9	23	36	5509
ENV	WKNNNVQDM	109	9	35	55	5510

Table XII
 HIV-1 p24 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO
ENV	MIEDISLW	117	9	29	45	5511
ENV	GKNEIDTY	218	9	01	20	5512
ENV	IIHYCATAGF	261	9	27	42	5513
ENV	IIHYCATAGF	261	9	10	16	5514
ENV	IPVASTOL	298	9	31	51	5515
ENV	IRPVSTOL	298	9	26	41	5516
ENV	CRKIQINM	487	9	30	47	5517
ENV	CRKQIVNM	487	9	12	19	5518
ENV	GKAMYAPPI	501	9	23	36	5519
ENV	GKAMYAPPI	501	9	12	20	5520
ENV	MRNWSLEL	553	9	25	62	5521
ENV	YKVKIKLEI	564	9	48	39	5522
ENV	EREKIAVGI	590	9	11	17	5523
ENV	QILLKLTW	649	9	13	20	5524
ENV	QILLQITW	649	9	34	53	5525
ENV	QILLQITW	649	9	10	16	5526
ENV	QIKQIARVI	659	9	40	62	5527
ENV	ARYLQVRY	664	9	33	52	5528
ENV	ERYLQDQL	670	9	30	47	5529
ENV	ERYLRDQL	670	9	18	28	5530
ENV	LKPDQLLG	673	9	27	42	5531
ENV	ERYLRDQL	673	9	19	30	5532
ENV	DKSWLWNV	759	9	26	41	5533
ENV	TKWLWYIKI	771	9	15	23	5534
ENV	LRNLCLFSY	857	9	16	25	5535
ENV	LRNLCLFSY	857	9	35	55	5536
ENV	YHRLRDPI	865	9	13	20	5537
ENV	YHRLRDPI	865	9	13	20	5538
ENV	YHRLDILL	866	9	11	17	5539
ENV	LKNSAVSLI	914	9	11	17	5540
ENV	IRQGLERL	954	9	34	53	5541
ENV	KKLWTLYLAM	9	10	01	50	5542
ENV	RRSWSLYLAM	9	10	01	50	5543
ENV	RRSWSLYLAM	9	10	01	50	5544
ENV	WNGTMTLGM	15	10	01	50	5545
ENV	GKDLWVTVY	42	10	01	33	5546
ENV	LKPKVKLPI	129	10	55	86	5547
ENV	VKLPLCVIL	133	10	52	81	5548
ENV	PKVSEPIPI	251	10	30	47	5549
ENV	PKVSEPIPI	251	10	31	47	5550
ENV	IPVASTOL	298	10	24	42	5551
ENV	MISENGGGEF	433	10	13	20	5552
ENV	TISENGGGEF	433	10	22	34	5553
ENV	TISENGGGEF	433	10	13	20	5554
ENV	CRKIQINM	487	10	30	47	5555
ENV	CRKIQINM	487	10	12	19	5556
ENV	IRCSNMITGL	513	10	40	63	5557
ENV	MRDNWISLEY	553	10	40	63	5558
ENV	KRAYGIGAVF	593	10	11	17	5559
ENV	LRATIAQQIIL	642	10	45	70	5560

Table XII
 SCMV B27 Super-NatF Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	ARLAVERYL	664	10	33	52	5561
ENV	LRDQQL	670	10	39	45	5562
ENV	LRDQQL	671	10	17	42	5563
ENV	LRDQQLGW	673	10	27	42	5564
ENV	LRDQQLGW	673	10	19	30	5565
ENV	LRDQQLGW	673	10	19	30	5566
ENV	LRDQQLGW	673	10	17	27	5567
ENV	LRDQQLGW	673	10	13	20	5568
ENV	LRDQQLGW	673	10	13	20	5569
ENV	LRDQQLGW	673	10	13	20	5570
ENV	LRDQQLGW	673	10	13	20	5571
ENV	LRDQQLGW	673	10	13	20	5572
ENV	LRDQQLGW	673	10	13	20	5573
ENV	LRDQQLGW	673	10	13	20	5574
ENV	LRDQQLGW	673	10	13	20	5575
ENV	LRDQQLGW	673	10	13	20	5576
ENV	LRDQQLGW	673	10	13	20	5577
ENV	LRDQQLGW	673	10	13	20	5578
ENV	LRDQQLGW	673	10	13	20	5579
ENV	LRDQQLGW	673	10	13	20	5580
ENV	LRDQQLGW	673	10	13	20	5581
ENV	LRDQQLGW	673	10	13	20	5582
ENV	LRDQQLGW	673	10	13	20	5583
ENV	LRDQQLGW	673	10	13	20	5584
ENV	LRDQQLGW	673	10	13	20	5585
ENV	LRDQQLGW	673	10	13	20	5586
ENV	LRDQQLGW	673	10	13	20	5587
ENV	LRDQQLGW	673	10	13	20	5588
ENV	LRDQQLGW	673	10	13	20	5589
ENV	LRDQQLGW	673	10	13	20	5590
ENV	LRDQQLGW	673	10	13	20	5591
ENV	LRDQQLGW	673	10	13	20	5592
ENV	LRDQQLGW	673	10	13	20	5593
ENV	LRDQQLGW	673	10	13	20	5594
ENV	LRDQQLGW	673	10	13	20	5595
ENV	LRDQQLGW	673	10	13	20	5596
ENV	LRDQQLGW	673	10	13	20	5597
ENV	LRDQQLGW	673	10	13	20	5598
ENV	LRDQQLGW	673	10	13	20	5599
ENV	LRDQQLGW	673	10	13	20	5600
ENV	LRDQQLGW	673	10	13	20	5601
ENV	LRDQQLGW	673	10	13	20	5602
ENV	LRDQQLGW	673	10	13	20	5603
ENV	LRDQQLGW	673	10	13	20	5604
ENV	LRDQQLGW	673	10	13	20	5605
ENV	LRDQQLGW	673	10	13	20	5606
ENV	LRDQQLGW	673	10	13	20	5607
ENV	LRDQQLGW	673	10	13	20	5608
ENV	LRDQQLGW	673	10	13	20	5609
ENV	LRDQQLGW	673	10	13	20	5610

Table XII
 HIV-1 p27 SuperMotif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SHO ID NO.
GAG	KKYRLKHI	28	8	10	16	5611
GAG	KKYRLKIL	28	8	16	25	5612
GAG	KKYRLKIV	30	8	17	20	5613
GAG	YRLKILYW	30	8	13	20	5614
GAG	CRQLGOL	39	8	15	23	5615
GAG	IKDTREAL	96	8	10	16	5616
GAG	VKDTREAL	96	8	33	52	5617
GAG	VRDTREAL	96	8	10	16	5618
GAG	KRLDTREAL	96	8	13	16	5619
GAG	TKKRLKIL	99	8	10	12	5620
GAG	TKKRLKIV	99	8	10	95	5621
GAG	GIQAAAMQM	214	8	61	86	5622
GAG	KRWILGL	287	8	55	86	5623
GAG	PKPEFRDY	313	8	63	98	5624
GAG	FRDYVDFE	317	8	64	100	5625
GAG	CKTILKAL	354	8	78	44	5626
GAG	CKTILKAL	354	8	78	44	5627
GAG	ARVLAELM	384	8	57	88	5628
GAG	IKGRGNGF	477	8	23	37	5629
GAG	NKGRGNGF	477	8	14	23	5630
GAG	SKGRGNGF	477	8	11	18	5631
GAG	EKKRPPL	535	8	01	25	5632
GAG	EKKRPPL	535	8	01	25	5633
GAG	EKKRGGLY	538	8	01	25	5634
GAG	GLDAWEKI	11	9	17	27	5635
GAG	LRPGKKKY	21	9	35	55	5636
GAG	KKKYRLKIL	27	9	13	20	5637
GAG	KKKYRLKIL	27	9	13	20	5638
GAG	KKKYRLKIL	27	9	13	20	5639
GAG	ERFVAVNGL	44	9	15	23	5640
GAG	VKVEEKAF	177	9	24	38	5641
GAG	VKVEEKAF	177	9	28	44	5642
GAG	ERKATSPVLI	182	9	48	75	5643
GAG	GIQAAAMQVL	214	9	61	86	5644
GAG	GIQAAAMQVL	214	9	61	86	5645
GAG	VHIVVIAPI	236	9	22	35	5646
GAG	MREPGRGSDI	249	9	44	69	5647
GAG	YKRWILGL	286	9	55	86	5648
GAG	VRMVSPTS	288	9	14	22	5649
GAG	FRDYVDFE	317	9	40	61	5650
GAG	IRQPKPEF	309	9	42	66	5651
GAG	FRDYVDFE	317	9	35	55	5652
GAG	FRDYVDFE	317	9	29	45	5653
GAG	VKNWMTDL	337	9	16	25	5654
GAG	VKNWMTDL	337	9	36	56	5655
GAG	VKNWMTDL	337	9	36	56	5656
GAG	IKGRGNGF	477	9	23	37	5657
GAG	NKGRGNGF	477	9	09	15	5658
GAG	RKEPIAPPL	492	9	01	50	5659
GAG	DNKELVPL	536	9	01	25	5660

Table XII
HIV B27 Super-Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	GKKYRLKHL	25	10	12	19	5661
GAG	KYRLKHLVW	28	10	10	16	5662
GAG	KYRLKHLVW	28	10	16	25	5663
GAG	KHLVWASREL	33	10	31	33	5664
GAG	KHLVWASREL	33	10	36	56	5665
GAG	EFALNPOLL	44	10	15	23	5666
GAG	EFALNPOLL	44	10	44	33	5667
GAG	VIOALSPTLL	164	10	27	42	5668
GAG	VIOALSPTLL	164	10	11	17	5669
GAG	VRMSPTSL	298	10	14	22	5670
GAG	VRMSPTSL	298	10	40	63	5671
GAG	VKNWMTDILL	337	10	16	25	5672
GAG	VKNWMTDILL	337	10	16	36	5673
GAG	IKARVLAEAM	338	10	16	25	5674
GAG	IKARVLAEAM	382	10	57	89	5675
GAG	CRAPRKGCW	438	10	53	83	5676
GAG	WRCCGKLGQIM	447	10	46	72	5677
GAG	ERQANFLGKI	464	10	54	84	5678
GAG	ERQANFLGKI	464	10	23	37	5679
GAG	TKKEPTAPL	497	10	50	80	5680
GAG	QKQEPIDKEL	530	10	12	19	5681
GAG	EKEFKGLYPL	538	10	01	25	5682
GAG	DKELYPLASL	541	10	13	21	5683
GAG	DKELYPLASL	541	10	10	16	5684
GAG	LKSLFGHLL	552	10	12	19	5685
GAG	ARASVLSGKLL	3	11	17	25	5686
GAG	GRLDWWEKRL	11	11	28	44	5687
GAG	IRLFGGKKKY	19	11	16	25	5688
GAG	IRLFGGKKKY	19	11	33	52	5689
GAG	LRPGGKKKYLL	21	11	10	16	5690
GAG	LRPGGKKKYLL	21	11	16	25	5691
GAG	KHLVWASREL	32	11	21	33	5692
GAG	KHLVWASREL	32	11	22	34	5693
GAG	KHLVWASREL	32	11	22	34	5694
GAG	LRSLNTVAIL	77	11	13	20	5695
GAG	VKDTKEALDKI	96	11	16	25	5696
GAG	PRTLNANWKVI	170	11	30	48	5697
GAG	GRLDWWEKRL	171	11	48	78	5698
GAG	DRILPVHAGPI	234	11	22	35	5699
GAG	DRILPVHAGPI	234	11	14	22	5700
GAG	VHAGPIAPQOM	239	11	17	27	5701
GAG	VHAGPIAPQOM	239	11	17	27	5702
GAG	KWILGLNKI	287	11	55	86	5703
GAG	KWILGLNKI	287	11	15	25	5704
GAG	SHKARVLAEAM	381	11	50	78	5705
GAG	SHKARVLAEAM	381	11	50	78	5706
GAG	MKDC'ERQANF	456	11	54	84	5707
GAG	ERQANFLGKI	464	11	12	19	5708
GAG	QKQEPIDKELY	530	11	01	25	5709
GAG	LKDKETPLASL	535	11	01	25	5710
GAG	ERTENSLYPLL	537	11	01	25	5711

Table XII
HIV-127 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensuety (%)	SEQ ID NO.
NEF	GRWKSMSI	3	8	18	28	5711
NEF	SKKRLDEL	4	8	21	31	5712
NEF	EKGGLDEL	121	8	26	41	5713
NEF	SKKRLDEL	177	8	34	53	5714
NEF	KRQQLDL	181	8	25	39	5715
NEF	KRQQLDL	181	8	18	28	5716
NEF	KRQQLDL	322	8	32	50	5717
NEF	ARELIPFY	322	8	11	17	5718
NEF	EKGGLDGL	121	9	24	38	5719
NEF	EKGGLDGL	121	9	23	36	5720
NEF	EKGGLDGL	121	9	27	42	5721
NEF	KRQQLDL	179	9	25	39	5722
NEF	KRQQLDL	179	9	12	19	5723
NEF	KRQQLDL	181	9	18	28	5724
NEF	KRQQLDL	181	9	32	50	5725
NEF	RYPLTGW	214	9	13	20	5726
NEF	TRPLTGW	214	9	12	19	5727
NEF	LIPPCQHG	258	9	10	16	5728
NEF	LIPPCQHG	258	9	12	19	5729
NEF	ARELIPFY	322	9	11	17	5730
NEF	ARELIPFY	322	9	21	33	5731
NEF	ARELIPFY	322	9	14	22	5732
NEF	SDLESLGAI	50	10	14	22	5733
NEF	VRPQVLRPM	97	10	47	73	5734
NEF	LRPM1YKGF	103	10	12	19	5735
NEF	SIPLKKGGL	115	10	29	45	5736
NEF	SIPLKKGGL	115	10	26	42	5737
NEF	LKEKGGDLGL	118	10	21	33	5738
NEF	EKGGLDGL	121	10	19	30	5739
NEF	EKGGLDGL	121	10	19	30	5740
NEF	SKKRLDL	177	10	25	39	5741
NEF	KRQQLDL	179	10	25	39	5742
NEF	KRQQLDL	179	10	12	19	5743
NEF	YITGQYFDW	193	10	25	39	5744
NEF	GRWKSMSI	3	11	18	28	5745
NEF	LKEKGGDLGL	118	11	23	37	5746
NEF	LKEKGGDLGL	118	11	24	39	5747
NEF	SKKRLDL	177	11	25	39	5748
NEF	KRQQLDL	181	11	16	25	5749
NEF	KRQQLDL	181	11	29	44	5750
NEF	KRQQLDL	181	11	20	33	5751
NEF	TRPLTGWCF	214	11	10	16	5752
POL	TRRELQW	43	8	13	20	5753
POL	GRWKPAMI	127	8	41	64	5754
POL	GRWKPAMI	127	8	16	25	5755
POL	GRWKPAMI	127	8	14	22	5756
POL	IKKQDL	156	8	20	33	5757
POL	KKAGTIVL	156	8	29	45	5758
POL	GRNLTQI	173	8	21	33	5759
POL	GRNLTQI	173	8	19	30	5760
POL	GRNLTQI	173	8	11	17	5761

Table XII
HIV-1227 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PKVKQWPL	206	8	51	80	5761
POL	KKKDTKW	253	8	57	89	5762
POL	NKRTQDFW	270	8	57	89	5763
POL	KKRSYTVL	311	8	60	78	5764
POL	IRYKAVL	314	8	62	97	5765
POL	IRYDYNAL	331	8	53	83	5766
POL	WKGSPAF	342	8	59	92	5767
POL	FRKQNPDI	360	8	16	25	5768
POL	IRAKIEEL	387	8	26	41	5769
POL	IRTKIEEL	387	8	22	34	5770
POL	LRHILKKW	394	8	17	23	5771
POL	LRQILKKW	394	8	15	23	5772
POL	ELRLKGEF	396	8	14	22	5773
POL	QILLRWGF	396	8	12	19	5774
POL	KIQKLEPF	409	8	62	97	5775
POL	QKEPHLW	411	8	63	98	5776
POL	DKWTVQPI	426	8	54	84	5777
POL	VKQLCKLL	465	8	18	24	5778
POL	KKQKCKLL	465	8	19	30	5779
POL	TKLTVL	475	8	11	17	5780
POL	SKDLIAE	514	8	27	42	5781
POL	QKQGFQDQW	522	8	16	25	5782
POL	QKQGFQDQW	522	8	24	38	5783
POL	OKIATLSI	565	8	14	22	5784
POL	GKTKPKLL	576	8	17	23	5785
POL	QKQKCKLL	586	8	30	47	5786
POL	QKQKCKLL	586	8	15	23	5787
POL	QKQKCKLL	586	8	27	42	5788
POL	TKGKAGY	642	8	10	16	5789
POL	TRLGKAGY	642	8	36	56	5790
POL	GROKYSVL	654	8	14	38	5791
POL	QKTELHAI	667	8	12	18	5792
POL	QKTELHAI	667	8	42	66	5793
POL	IKSEKYYL	718	8	35	55	5794
POL	DKLVASGI	741	8	16	25	5795
POL	DKLVSSGI	741	8	29	45	5796
POL	YIINWRAM	767	8	10	16	5797
POL	YIINWRAM	767	8	39	61	5798
POL	WRAMASDF	815	8	33	55	5799
POL	YIINWRAM	818	8	35	55	5800
POL	TULGKVI	818	8	26	41	5801
POL	VHVASGYI	829	8	53	83	5802
POL	GRWPVKTI	858	8	13	21	5803
POL	GRWPVKVI	858	8	22	35	5804
POL	NKELKKII	907	8	48	79	5805
POL	VRDQAEIIL	917	8	13	20	5806
POL	VRDQAEIIL	917	8	13	20	5807
POL	RKQEGEY	939	8	59	92	5808
POL	TKELQKI	962	8	47	75	5809
POL	YRDSRDP	979	8	35	55	5810

Table XII
HW-127 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO
POL	VERSDRPL	979	8	14	22	5811
POL	WKGPAKLL	987	8	59	92	5812
POL	PRKAKII	1014	8	50	78	5813
POL	PRKCKII	1014	8	11	17	5814
POL	IKKCKAM	1021	8	11	17	5815
POL	IRDYGKGM	1021	8	50	78	5816
POL	QRPLVTIKI	94	9	14	22	5817
POL	QRPLVTIKI	94	9	12	19	5818
POL	WPKPMIGGI	129	9	60	94	5819
POL	IKVQYQYQI	141	9	41	64	5820
POL	VRQYQYQI	141	9	10	16	5821
POL	VRQYQYQI	143	9	11	30	5822
POL	GIIKKAIGTVL	155	9	20	31	5823
POL	GIIKKAIGTVL	155	9	29	45	5824
POL	EKKALTEI	216	9	28	44	5825
POL	EKKALTEI	216	9	15	23	5826
POL	IKKKAIGTVL	216	9	16	26	5827
POL	SKIGPENTY	237	9	41	66	5828
POL	SKIGPENTY	237	9	11	17	5829
POL	IKKKDSTKW	252	9	57	89	5830
POL	TKWRKLVDIF	258	9	59	92	5831
POL	KLKLPHREL	261	9	63	98	5832
POL	KKASGKAL	261	9	60	98	5833
POL	FRKYAFETI	313	9	61	97	5834
POL	RKQNDIVI	361	9	14	22	5835
POL	QIRKAKEEL	386	9	26	41	5836
POL	QIRKAKEEL	386	9	22	34	5837
POL	KIKIQKEPP	408	9	60	94	5838
POL	KIKIQKEPP	408	9	62	97	5839
POL	QKPEPLWN	411	9	62	97	5840
POL	OKLVGKLNW	447	9	62	97	5841
POL	GKLNWASQI	451	9	61	95	5842
POL	IKVKQLCKL	463	9	29	45	5843
POL	IKVKQLCKL	463	9	18	28	5844
POL	IKVKQLCKL	463	9	45	78	5845
POL	FNKLTKGY	538	9	10	16	5846
POL	YKNLTKGY	538	9	10	16	5847
POL	LKTKGYAKM	541	9	19	30	5848
POL	LKTKGYAKM	541	9	13	20	5849
POL	QKTEIWMW	552	9	46	72	5850
POL	QKTEIWMW	552	9	5	8	5851
POL	QKTEIWMW	586	9	22	42	5852
POL	QKTELQNI	667	9	12	19	5853
POL	KREKVYLSW	719	9	20	32	5854
POL	KREKVYLSW	719	9	13	21	5855
POL	IKKVLDTGI	749	9	50	78	5856
POL	IKKVLDTGI	749	9	10	16	5857
POL	IEHETVSNW	763	9	20	31	5858
POL	IEHETVSNW	763	9	13	20	5859
POL	THLEGGIIL	818	9	31	48	5860

Table XII
HIV-B27 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO.
POL	THLEKGVIL	818	9	23	36	5861
POL	IHTDGSNF	865	9	42	66	5862
POL	IKCEIPIOM	887	9	26	41	5863
POL	EDKGGGGM	927	9	26	41	5864
POL	KRKGIGGY	938	9	59	92	5865
POL	TKELQKQI	962	9	10	16	5866
POL	IKQIFRVY	970	9	12	19	5867
POL	TKQNFVRY	970	9	37	58	5868
POL	IKQNFVRY	970	9	35	55	5869
POL	IKQNFVRY	970	9	35	55	5870
POL	YKQNFVRY	970	9	14	22	5871
POL	YKQNFVRY	970	9	59	92	5872
POL	WKGDAKLV	987	9	61	95	5873
POL	WKGDAKLV	987	9	61	95	5874
POL	WKGDAKLV	987	9	61	95	5875
POL	WKGDAKLV	987	9	61	95	5876
POL	WKGDAKLV	987	9	61	95	5877
POL	WKGDAKLV	987	9	61	95	5878
POL	WKGDAKLV	987	9	61	95	5879
POL	WKGDAKLV	987	9	61	95	5880
POL	WKGDAKLV	987	9	61	95	5881
POL	WKGDAKLV	987	9	61	95	5882
POL	WKGDAKLV	987	9	61	95	5883
POL	WKGDAKLV	987	9	61	95	5884
POL	WKGDAKLV	987	9	61	95	5885
POL	WKGDAKLV	987	9	61	95	5886
POL	WKGDAKLV	987	9	61	95	5887
POL	WKGDAKLV	987	9	61	95	5888
POL	WKGDAKLV	987	9	61	95	5889
POL	WKGDAKLV	987	9	61	95	5890
POL	WKGDAKLV	987	9	61	95	5891
POL	WKGDAKLV	987	9	61	95	5892
POL	WKGDAKLV	987	9	61	95	5893
POL	WKGDAKLV	987	9	61	95	5894
POL	WKGDAKLV	987	9	61	95	5895
POL	WKGDAKLV	987	9	61	95	5896
POL	WKGDAKLV	987	9	61	95	5897
POL	WKGDAKLV	987	9	61	95	5898
POL	WKGDAKLV	987	9	61	95	5899
POL	WKGDAKLV	987	9	61	95	5900
POL	WKGDAKLV	987	9	61	95	5901
POL	WKGDAKLV	987	9	61	95	5902
POL	WKGDAKLV	987	9	61	95	5903
POL	WKGDAKLV	987	9	61	95	5904
POL	WKGDAKLV	987	9	61	95	5905
POL	WKGDAKLV	987	9	61	95	5906
POL	WKGDAKLV	987	9	61	95	5907
POL	WKGDAKLV	987	9	61	95	5908
POL	WKGDAKLV	987	9	61	95	5909
POL	WKGDAKLV	987	9	61	95	5910

Table XII
HIV-D27 Super-Native Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	IIILALQDSGL	674	10	15	23	5911
POL	IKKRYVLSW	718	10	20	31	5912
POL	IKKRYVLSW	718	10	20	31	5913
POL	IKKRYVLSW	718	10	20	31	5914
POL	DKAQEELHY	758	10	25	39	5915
POL	DKAQEELHY	758	10	15	23	5916
POL	EKYLISNWRAM	765	10	28	44	5917
POL	EKYLISNWRAM	765	10	10	16	5918
POL	WRAMASDFNL	771	10	41	64	5919
POL	DKQQLKGEAM	793	10	44	69	5920
POL	WRAMASDFNL	793	10	11	21	5921
POL	LKTAQMAVF	824	10	57	89	5922
POL	IIINFERKGGI	934	10	58	91	5923
POL	FKRKGGGIGY	937	10	59	92	5924
POL	QKQIKIQNF	966	10	12	19	5925
POL	QKQIKIQNF	966	10	34	53	5926
POL	IKQNFVYVY	970	10	12	19	5927
POL	IKQNFVYVY	970	10	37	58	5928
POL	BRKAKIRBY	1015	10	41	64	5929
POL	TRANSPTREL	22	11	11	17	5930
POL	ERAIISATREL	25	11	01	50	5931
POL	SRANSPTSDOL	25	11	01	50	5932
POL	TRANSPTREL	34	11	01	33	5933
POL	TRANSPTREL	36	11	01	33	5934
POL	TRANSPTREL	127	11	10	20	5935
POL	GRWKPKMGGI	127	11	41	64	5936
POL	GRWKPKMGGI	127	11	16	25	5937
POL	PKMGGIGGFI	131	11	62	97	5938
POL	IKVRYQDQLI	141	11	20	31	5939
POL	IKVRYQDQPI	141	11	13	20	5940
POL	VRQYDQDLIEI	143	11	10	16	5941
POL	VRQYDQDLIEI	143	11	11	17	5942
POL	VRQYDQDLIEI	143	11	12	18	5943
POL	VKGWPLTEKI	208	11	52	81	5944
POL	IKALVECTEM	218	11	15	23	5945
POL	KKKDKSTKWRKL	253	11	57	89	5946
POL	FRELNRQTDF	266	11	57	89	5947
POL	KRTQDHWVQL	271	11	52	81	5948
POL	KKKQVPSI	314	11	17	28	5949
POL	KKKQVPSI	314	11	14	22	5950
POL	AKIEELREHL	389	11	13	20	5951
POL	TKIFELRQIHL	389	11	14	22	5952
POL	DKKIQKEPPEL	407	11	60	94	5953
POL	KKHQKEPPELW	408	11	60	94	5954
POL	KHQKEPPELWM	409	11	62	97	5955
POL	QKEPPELWMGY	411	11	63	98	5956
POL	QKEPPELWMGY	411	11	51	80	5957
POL	LRTKAKATEVI	472	11	11	17	5958
POL	VKQLEAVOKI	557	11	30	47	5959
POL	QKIATESVIW	565	11	14	22	5960
POL	EKEPVGAEIF	622	11	16	25	5961

Table XII
HIV-B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	NRETKLGKAGY	639	11	28	44	5961
POL	DKSIELVNOI	703	11	18	28	5962
POL	DKSELSVNOI	703	11	19	30	5963
POL	MUGQVDCSPGI	802	11	32	81	5964
POL	LKTAVQMAVFI	854	11	26	88	5965
POL	ERVDIATDI	950	11	12	19	5966
POL	ERVDIATDI	950	11	29	45	5967
POL	TKELQKQIKI	962	11	11	17	5968
POL	TKELQKQIKI	962	11	10	16	5969
POL	IKVPRRKAKI	1010	11	31	49	5970
POL	IKVPRRKAKI	1010	11	31	49	5971
POL	IKVPRRKAKI	1010	11	41	17	5972
POL	IKVPRRKAKI	1018	11	41	64	5973
POL	AKVPRRKAKI	1018	11	42	66	5974
REV	AKVPRRKAKI	1018	8	18	28	5975
REV	AKVPRRKAKI	1018	8	18	28	5976
REV	AKVPRRKAKI	1018	8	21	33	5977
REV	AKVPRRKAKI	1018	8	40	63	5978
REV	AKVPRRKAKI	1018	8	36	55	5979
REV	AKVPRRKAKI	1018	8	11	17	5980
REV	AKVPRRKAKI	1018	9	18	28	5981
REV	AKVPRRKAKI	1018	9	39	61	5982
REV	AKVPRRKAKI	1018	9	10	16	5983
REV	AKVPRRKAKI	1018	9	20	31	5984
REV	AKVPRRKAKI	1018	9	12	17	5985
REV	AKVPRRKAKI	1018	10	17	27	5986
REV	AKVPRRKAKI	1018	10	25	39	5987
REV	AKVPRRKAKI	1018	10	34	53	5988
REV	AKVPRRKAKI	1018	10	11	17	5989
REV	AKVPRRKAKI	1018	11	16	25	5990
REV	AKVPRRKAKI	1018	11	34	53	5991
REV	AKVPRRKAKI	1018	11	11	17	5992
REV	AKVPRRKAKI	1018	11	10	16	5993
REV	AKVPRRKAKI	1018	11	20	31	5994
REV	AKVPRRKAKI	1018	11	12	19	5995
REV	AKVPRRKAKI	1018	11	15	23	5996
REV	AKVPRRKAKI	1018	11	14	22	5997
REV	AKVPRRKAKI	1018	11	19	30	5998
REV	AKVPRRKAKI	1018	11	12	16	5999
REV	AKVPRRKAKI	1018	11	16	27	6000
REV	AKVPRRKAKI	1018	11	32	50	6001
REV	AKVPRRKAKI	1018	11	22	34	6002
REV	AKVPRRKAKI	1018	11	22	34	6003
REV	AKVPRRKAKI	1018	11	31	48	6004
REV	AKVPRRKAKI	1018	11	47	73	6005
REV	AKVPRRKAKI	1018	11	47	73	6006
REV	AKVPRRKAKI	1018	11	19	30	6007
REV	AKVPRRKAKI	1018	11	13	21	6008
REV	AKVPRRKAKI	1018	11	25	39	6009
REV	AKVPRRKAKI	1018	11	10	16	6010

Table XII
HIV-1 p27 Super-Nuif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	NRQVMIVW	3	9	42	66	6011
VIF	MRIRWNSL	16	9	12	19	6012
VIF	MIRTWKSL	16	9	15	23	6013
VIF	WKSIVKSL	21	9	16	24	6014
VIF	WKSIVKHM	21	9	18	28	6015
VIF	WKSIVKHM	21	9	10	16	6016
VIF	PKISSEVH	49	9	15	23	6017
VIF	PKISSEVH	49	9	20	31	6018
VIF	PKISSEVH	49	9	15	23	6019
VIF	ARLVITYW	64	9	11	17	6020
VIF	ARLVITYW	64	9	23	36	6021
VIF	WILGQVSI	82	9	26	41	6022
VIF	WILGQVSI	82	9	16	25	6023
VIF	ILLYYDFC	112	9	15	23	6024
VIF	ILMYDFCF	112	9	15	23	6025
VIF	NRVGLQYL	145	9	47	75	6026
VIF	VKSLTEDRW	175	9	13	20	6027
VIF	WKSIVKHM	21	10	18	28	6028
VIF	WKSIVKHM	21	10	10	16	6029
VIF	VIRPGEARL	55	10	13	20	6030
VIF	VIRPGEARL	55	10	20	31	6031
VIF	LITGERDWIL	74	10	21	33	6032
VIF	GHGVSEWR	85	10	15	23	6033
VIF	GHGVSEWR	85	10	15	23	6034
VIF	GHGVSEWR	85	10	16	24	6035
VIF	IRPKRIEPL	139	10	18	28	6036
VIF	IRPKRIEPL	139	10	12	19	6037
VIF	DRMRITWKS	14	11	15	23	6038
VIF	DRMRITWKS	14	11	15	23	6039
VIF	DRMRITWKS	14	11	15	23	6040
VIF	WKSIVKHM	21	11	11	17	6041
VIF	IRPKVSEVH	47	11	16	25	6042
VIF	IRPKVSEVH	47	11	14	22	6043
VIF	IRPKVSEVH	47	11	15	23	6044
VIF	IRPKVSEVH	47	11	13	20	6045
VIF	ARLVITYWGL	64	11	11	17	6046
VIF	WILGHGVSEW	82	11	23	36	6047
VIF	WILGHGVSEW	82	11	26	41	6048
VIF	WILGHGVSEW	82	11	26	41	6049
VIF	GHGVSEWR	85	11	47	73	6050
VIF	NRVGLQYL	145	11	38	59	6051
VIF	NRVGLQYL	145	11	14	22	6052
VIF	VIRPGEARL	55	8	14	22	6053
VIF	VIRPGEARL	55	8	34	53	6054
VIF	VIRPGEARL	55	8	14	22	6055
VIF	IRPKVSEVH	47	8	14	22	6056
VIF	IRPKVSEVH	47	8	34	53	6057
VIF	IRPKVSEVH	47	8	14	22	6058
VIF	IRPKVSEVH	47	8	34	53	6059
VIF	IRPKVSEVH	47	8	14	22	6060
VIF	IRPKVSEVH	47	8	34	53	6061
VIF	IRPKVSEVH	47	8	14	22	6062
VIF	IRPKVSEVH	47	8	34	53	6063
VIF	IRPKVSEVH	47	8	14	22	6064
VIF	IRPKVSEVH	47	8	34	53	6065
VIF	IRPKVSEVH	47	8	14	22	6066
VIF	IRPKVSEVH	47	8	34	53	6067
VIF	IRPKVSEVH	47	8	14	22	6068
VIF	IRPKVSEVH	47	8	34	53	6069
VIF	IRPKVSEVH	47	8	14	22	6070
VIF	IRPKVSEVH	47	8	34	53	6071
VIF	IRPKVSEVH	47	8	14	22	6072
VIF	IRPKVSEVH	47	8	34	53	6073
VIF	IRPKVSEVH	47	8	14	22	6074
VIF	IRPKVSEVH	47	8	34	53	6075
VIF	IRPKVSEVH	47	8	14	22	6076
VIF	IRPKVSEVH	47	8	34	53	6077
VIF	IRPKVSEVH	47	8	14	22	6078
VIF	IRPKVSEVH	47	8	34	53	6079
VIF	IRPKVSEVH	47	8	14	22	6080
VIF	IRPKVSEVH	47	8	34	53	6081
VIF	IRPKVSEVH	47	8	14	22	6082
VIF	IRPKVSEVH	47	8	34	53	6083
VIF	IRPKVSEVH	47	8	14	22	6084
VIF	IRPKVSEVH	47	8	34	53	6085
VIF	IRPKVSEVH	47	8	14	22	6086
VIF	IRPKVSEVH	47	8	34	53	6087
VIF	IRPKVSEVH	47	8	14	22	6088
VIF	IRPKVSEVH	47	8	34	53	6089
VIF	IRPKVSEVH	47	8	14	22	6090
VIF	IRPKVSEVH	47	8	34	53	6091
VIF	IRPKVSEVH	47	8	14	22	6092
VIF	IRPKVSEVH	47	8	34	53	6093
VIF	IRPKVSEVH	47	8	14	22	6094
VIF	IRPKVSEVH	47	8	34	53	6095
VIF	IRPKVSEVH	47	8	14	22	6096
VIF	IRPKVSEVH	47	8	34	53	6097
VIF	IRPKVSEVH	47	8	14	22	6098
VIF	IRPKVSEVH	47	8	34	53	6099
VIF	IRPKVSEVH	47	8	14	22	6100
VIF	IRPKVSEVH	47	8	34	53	6101
VIF	IRPKVSEVH	47	8	14	22	6102
VIF	IRPKVSEVH	47	8	34	53	6103
VIF	IRPKVSEVH	47	8	14	22	6104
VIF	IRPKVSEVH	47	8	34	53	6105
VIF	IRPKVSEVH	47	8	14	22	6106
VIF	IRPKVSEVH	47	8	34	53	6107
VIF	IRPKVSEVH	47	8	14	22	6108
VIF	IRPKVSEVH	47	8	34	53	6109
VIF	IRPKVSEVH	47	8	14	22	6110
VIF	IRPKVSEVH	47	8	34	53	6111
VIF	IRPKVSEVH	47	8	14	22	6112
VIF	IRPKVSEVH	47	8	34	53	6113
VIF	IRPKVSEVH	47	8	14	22	6114
VIF	IRPKVSEVH	47	8	34	53	6115
VIF	IRPKVSEVH	47	8	14	22	6116
VIF	IRPKVSEVH	47	8	34	53	6117
VIF	IRPKVSEVH	47	8	14	22	6118
VIF	IRPKVSEVH	47	8	34	53	6119
VIF	IRPKVSEVH	47	8	14	22	6120
VIF	IRPKVSEVH	47	8	34	53	6121
VIF	IRPKVSEVH	47	8	14	22	6122
VIF	IRPKVSEVH	47	8	34	53	6123
VIF	IRPKVSEVH	47	8	14	22	6124
VIF	IRPKVSEVH	47	8	34	53	6125
VIF	IRPKVSEVH	47	8	14	22	6126
VIF	IRPKVSEVH	47	8	34	53	6127
VIF	IRPKVSEVH	47	8	14	22	6128
VIF	IRPKVSEVH	47	8	34	53	6129
VIF	IRPKVSEVH	47	8	14	22	6130
VIF	IRPKVSEVH	47	8	34	53	6131
VIF	IRPKVSEVH	47	8	14	22	6132
VIF	IRPKVSEVH	47	8	34	53	6133
VIF	IRPKVSEVH	47	8	14	22	6134
VIF	IRPKVSEVH	47	8	34	53	6135
VIF	IRPKVSEVH	47	8	14	22	6136
VIF	IRPKVSEVH	47	8	34	53	6137
VIF	IRPKVSEVH	47	8	14	22	6138
VIF	IRPKVSEVH	47	8	34	53	6139
VIF	IRPKVSEVH	47	8	14	22	6140
VIF	IRPKVSEVH	47	8	34	53	6141
VIF	IRPKVSEVH	47	8	14	22	6142
VIF	IRPKVSEVH	47	8	34	53	6143
VIF	IRPKVSEVH	47	8	14	22	6144
VIF	IRPKVSEVH	47	8	34	53	6145
VIF	IRPKVSEVH	47	8	14	22	6146
VIF	IRPKVSEVH	47	8	34	53	6147
VIF	IRPKVSEVH	47	8	14	22	6148
VIF	IRPKVSEVH	47	8	34	53	6149
VIF	IRPKVSEVH	47	8	14	22	6150
VIF	IRPKVSEVH	47	8	34	53	6151
VIF	IRPKVSEVH	47	8	14	22	6152
VIF	IRPKVSEVH	47	8	34	53	6153
VIF	IRPKVSEVH	47	8	14	22	6154
VIF	IRPKVSEVH	47	8	34	53	6155
VIF	IRPKVSEVH	47	8	14	22	6156
VIF	IRPKVSEVH	47	8	34	53	6157
VIF	IRPKVSEVH	47	8	14	22	6158
VIF	IRPKVSEVH	47	8	34	53	6159
VIF	IRPKVSEVH	47	8	14	22	6160
VIF	IRPKVSEVH	47	8	34	53	6161
VIF	IRPKVSEVH	47	8	14	22	6162
VIF	IRPKVSEVH	47	8	34	53	6163
VIF	IRPKVSEVH	47	8	14	22	6164
VIF	IRPKVSEVH	47	8	34	53	6165
VIF	IRPKVSEVH	47	8	14	22	6166
VIF	IRPKVSEVH	47	8	34	53	6167
VIF	IRPKVSEVH	47	8	14	22	6168
VIF	IRPKVSEVH	47	8	34	53	6169
VIF	IRPKVSEVH	47	8	14	22	6170
VIF	IRPKVSEVH	47	8	34	53	6171
VIF	IRPKVSEVH	47	8	14	22	6172
VIF	IRPKVSEVH	47	8	34	53	6173
VIF	IRPKVSEVH	47	8	14	22	6174
VIF	IRPKVSEVH	47	8	34	53	6175
VIF	IRPKVSEVH	47	8	14	22	6176
VIF	IRPKVSEVH	47	8	34	53	6177
VIF	IRPKVSEVH	47	8	14	22	6178
VIF	IRPKVSEVH	47	8	34	53	6179
VIF	IRPKVSEVH	47	8	14	22	6180
VIF	IRPKVSEVH	47	8	34	53	6181
VIF	IRPKVSEVH	47	8	14	22	6182
VIF	IRPKVSEVH	47	8	34	53	6183
VIF	IRPKVSEVH	47	8	14	22	6184
VIF	IRPKVSEVH	47	8	34	53	6185
VIF	IRPKVSEVH	47	8	14	22	6186
VIF	IRPKVSEVH	47	8	34	53	6187
VIF	IRPKVSEVH	47	8	14	22	6188
VIF	IRPKVSEVH	47	8	34	53	6189
VIF	IRPKVSEVH	47	8	14	22	6190
VIF	IRPKVSEVH	47	8	34	53	6191
VIF	IRPKVSEVH	47	8	14	22	6192
VIF	IRPKVSEVH	47	8	34	53	6193
VIF	IRPKVSEVH	47	8	14	22	6194
VIF	IRPKVSEVH	47	8	34	53	6195
VIF	IRPKVSEVH	47	8	14	22	6196
VIF	IRPKVSEVH	47	8	34	53	6197
VIF	IRPKVSEVH	47	8	14	22	6198
VIF	IRPKVSEVH	47	8	34	53	6199
VIF	IRPKVSEVH	47	8	14	22	6200
VIF	IRPKVSEVH	47	8	34	53	6201
VIF	IRPKVSEVH	47	8	14	22	6202
VIF	IRPKVSEVH	47	8	34	53	6203
VIF	IRPKVSEVH	47	8	14	22	6204
VIF	IRPKVSEVH	47	8	34	53	6205
VIF	IRPKVSEVH	47	8	14	22	6206
VIF	IRPKVSEVH	47	8	34	53	6207
VIF	IRPKVSEVH	47	8	14	22	6208
VIF	IRPKVSEVH	47	8	34	53	6209
VIF	IRPKVSEVH	47	8	14	22	6210
VIF	IRPKVSEVH	47	8	34	53	6211
VIF	IRPKVSEVH	47	8	14	22	6212
VIF	IRPKVSEVH	47	8	34	53	6213
VIF	IRPKVSEVH	47	8	14	22	6214
VIF	IRPKVSEVH	47	8	34	53	6215
VIF	IRPKVSEVH	47	8	14	22	6216
VIF	IRPKVSEVH	47	8	34	53	6217
VIF	IRPKVSEVH	47	8	14	22	6218
VIF	IRPKVSEVH	47	8	34	53	6219
VIF	IRPKVSEVH	47	8	14	22	6220
VIF	IRPKVSEVH	47	8	34		

Table XII

HIV-E27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	LKQAVRIIE	26	9	11	17	6061
VPR	LKSEAVRIIE	26	9	15	23	6062
VPR	VRIIPRIWL	31	9	14	22	6063
VPR	VRIIPRIWL	31	9	34	53	6064
VPR	LHGLQHTY	39	9	20	31	6065
VPR	IRILQQLLE	61	10	30	69	6066
VPR	QRIKQQLLE	61	10	30	47	6067
VPR	IRILQQLLE	61	10	36	56	6068
VPR	FRIGCQISRI	73	10	44	69	6069
VPR	FRIGCQISRI	73	10	12	19	6070
VPR	RIFPRWLISL	32	11	10	16	6071
VPR	RIFPRWLISL	32	11	24	38	6072
VPR	PRFWLHGLQY	45	11	10	16	6073
VPR	PRFWLHGLQY	45	11	17	27	6074
VPR	QRIKQQLLE	44	11	13	20	6075
VPU	QRIKQQLLE	49	8	21	33	6076
VPU	AKVDYRVI	6	9	01	33	6077
VPU	RKLRQRKI	44	9	13	21	6078
VPU	LRQRKDRL	47	9	17	27	6079
VPU	YRKLRQRKI	42	10	13	21	6080
VPU	LRQRKDRL	47	10	01	50	6081
VPU	LRQRKDRL	47	10	15	24	6082
VPU	RKIDRLDRI	51	10	12	19	6083
VPU	QRKIDRLDRI	49	11	12	19	6084

Table XIII
ENV B53 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NTSPGRV	376	8	01	33	6085
ENV	NTSPGRV	376	10	01	33	6086
ENV	TAGNSRAAY	376	10	01	33	6087
ENV	TAGNSRAAY	376	10	01	33	6088
ENV	TGNSNSSTPI	375	11	01	33	6089
ENV	GTAGNSRAAY	375	11	01	33	6090
ENV	ITHEGNTL	478	8	01	50	6091
ENV	NAMTICRI	478	10	01	50	6092
ENV	STGDRKRAV	218	11	01	20	6093
ENV	STGDRKRAV	218	11	01	20	6094
ENV	SINGTEIF	537	8	01	17	6095
ENV	NTENKTEIF	537	10	01	17	6096
ENV	NTENKTEIF	537	10	01	17	6097
ENV	GRENGTEIF	538	9	02	16	6098
ENV	NTKRSIRI	351	8	02	16	6099
ENV	SLKGLKCLW	886	8	10	16	6100
ENV	SLKGLKCLW	886	10	10	16	6101
ENV	SCCTACGAI	264	8	10	16	6102
ENV	QSSGADPEI	423	9	10	16	6103
ENV	QSSGADPEI	423	10	10	16	6104
ENV	WSQLKNSAV	910	10	10	16	6105
ENV	FAIKCNDKKF	269	11	11	17	6106
ENV	RAVGGAAT	594	9	11	17	6107
ENV	RAVGGAAT	594	10	11	17	6108
ENV	AARTVELL	876	8	11	17	6109
ENV	GTRVIEV	932	8	11	17	6110
ENV	LALDKWASL	756	9	11	17	6111
ENV	IAARTVELL	874	9	11	17	6112
ENV	VSLNATAI	319	10	11	17	6113
ENV	TTANPNSSW	691	10	11	17	6114
ENV	LALDKWASLW	756	10	11	17	6115
ENV	ISNLWYIKI	770	10	11	17	6116
ENV	RSIRLWNGEL	841	10	11	17	6117
ENV	CTTNVWNSSW	690	11	11	17	6118
ENV	ISNLWYIKIF	770	11	11	17	6119
ENV	VSLNATAI	317	11	11	17	6120
ENV	VSLNATAI	317	11	11	17	6121
ENV	RAVGGAAT	594	8	12	19	6122
ENV	EAQHIHLKL	646	9	12	19	6123
ENV	EAQHIHLKL	646	11	12	19	6124
ENV	RAMYAPI	502	8	12	19	6125
ENV	GAFLGEL	874	8	12	19	6126
ENV	GAFLGEL	874	8	12	19	6127
ENV	PTHQIGQL	951	8	12	19	6128
ENV	ATGDIGDI	369	9	12	19	6129
ENV	RSIRLVNGF	841	9	12	19	6130
ENV	MTWMEWERI	721	10	12	19	6131
ENV	BALHPHRI	945	10	12	19	6132
ENV	PIDNPQEVVL	89	11	12	19	6133
ENV	TSVTQACPKV	242	11	12	19	6134

Table XIII
S6 HIV-158 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO
ENV	GTGRCKNVSTV	281	11	12	19	6135
ENV	TTISFNCGGF	432	11	12	19	6136
ENV	TSVLRKQV	654	11	12	19	6137
ENV	ITKWLWYKIF	770	11	12	19	6138
ENV	PSYIRLRDLL	863	11	12	19	6139
ENV	LAEEVVI	312	8	13	20	6140
ENV	GAMFGL	601	8	13	20	6141
ENV	RSRLVSGF	841	10	13	20	6142
ENV	PTNLRKQV	841	10	13	20	6143
ENV	SAITQCPV	243	10	13	20	6144
ENV	GSLAEEVVI	310	10	13	20	6145
ENV	SSGGDPEIV	424	10	13	20	6146
ENV	RSRLVSGF	841	10	13	20	6147
ENV	PSYIRLRDFT	863	10	13	20	6148
ENV	TSVLRKQV	654	11	13	20	6149
ENV	PSYIRLRDLL	863	11	13	20	6150
ENV	NAKTIIVOL	329	9	14	22	6151
ENV	QAMVAFPI	502	8	14	22	6152
ENV	ISNLWYVI	770	8	14	22	6153
ENV	GSLAEEVVI	310	9	14	22	6154
ENV	ITNWLWYKI	770	10	14	22	6155
ENV	ITNWLWYKI	863	10	14	22	6156
ENV	IAVAEGTRV	927	10	14	22	6157
ENV	ITNWLWYKIF	770	11	14	22	6158
ENV	IAVAEGTRVI	927	11	14	22	6159
ENV	ITKWLWYKI	770	10	15	23	6160
ENV	ITLPCRQKQI	932	11	15	23	6161
ENV	ITNWLWYKI	770	11	15	23	6162
ENV	GSLAEEVVI	310	8	16	25	6163
ENV	SSGDLEI	424	8	16	25	6164
ENV	ITKWLWYI	770	8	16	25	6165
ENV	VAEGTRV	929	8	16	25	6166
ENV	VSPKRGFF	434	9	16	25	6167
ENV	VAEGTRV	841	9	16	25	6168
ENV	VAEGTRVI	929	9	16	25	6169
ENV	HSFNCRGFF	434	10	16	25	6170
ENV	IAVAEGTRDI	927	10	16	25	6171
ENV	TTISFNCGGF	432	11	16	25	6172
ENV	HSFNCRGFF	434	11	16	25	6173
ENV	TSVLRKQV	654	11	17	27	6174
ENV	DAKAYDEV	70	8	17	27	6175
ENV	ASLWNWFI	762	9	17	27	6176
ENV	KAYDTLVINV	72	10	17	27	6177
ENV	VAPTKARRV	574	10	17	27	6178
ENV	VAPTKARRV	761	10	17	27	6179
ENV	WASLWNWFI	761	11	17	27	6180
ENV	ASLWNWFI	762	11	17	27	6181
ENV	WASLWNWFI	774	11	17	27	6182
ENV	VAPTKARRV	574	11	17	27	6183
ENV	CSGKICTTNV	684	11	17	27	6184
ENV	SSGGDPEIV	424	9	18	28	

Table XIII

HIV-159 Super-Natf Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	FSYIIRLDF	863	9	18	28	6185
ENV	VAEGTDRII	929	8	18	28	6186
ENV	QESITHW	75	8	19	30	6187
ENV	STGQV	15	8	19	30	6188
ENV	ITNWLYI	770	8	19	30	6189
ENV	VAEGTDRI	929	8	19	30	6190
ENV	CSSNITGLL	515	9	19	30	6191
ENV	CSSNITGLL	516	9	19	30	6192
ENV	CSSNITGLL	515	10	19	30	6193
ENV	CSKLCITIA	684	11	19	30	6194
ENV	CSKLCITIA	684	11	19	30	6195
ENV	LAWDDLSL	852	9	20	31	6196
ENV	LAWDDLSL	852	11	20	31	6197
ENV	CSSNITGL	515	8	21	33	6198
ENV	PTDNPQEV	89	9	21	33	6199
ENV	ETFRGGGDM	544	10	21	33	6200
ENV	PTKAKRV	576	8	22	34	6201
ENV	PTKAKRV	576	9	22	34	6202
ENV	PTKAKRV	576	9	22	34	6203
ENV	KAMYAPPI	502	8	23	36	6204
ENV	FSYIIRLRL	863	9	23	36	6205
ENV	SSGGDEI	424	8	24	38	6206
ENV	LALAWDDL	850	8	25	39	6207
ENV	PTDNPQEI	89	9	25	39	6208
ENV	PTDNPQEI	89	10	25	39	6209
ENV	ITNGQNNL	631	11	25	39	6210
ENV	CTHGRPV	294	8	26	41	6211
ENV	QSNLLRAI	638	8	26	41	6212
ENV	CTHGRPVV	294	9	26	41	6213
ENV	ITLTVOAROL	621	10	27	42	6214
ENV	ITLTVOARQL	621	11	27	42	6215
ENV	YSERFOTL	807	9	28	44	6216
ENV	YSERFOTL	807	10	28	44	6217
ENV	CAPAGFAI	264	9	29	45	6218
ENV	CAPAGFAI	264	9	29	45	6219
ENV	ITQACPKVSF	245	10	29	45	6220
ENV	VSEPHI	253	8	30	47	6221
ENV	WVSEPHI	253	8	30	47	6222
ENV	QACPKYSSEPI	761	11	30	47	6223
ENV	FVLSINVRV	794	10	31	48	6224
ENV	RSLCLFSYIRL	858	11	31	48	6225
ENV	CTHGRPVV	294	9	32	50	6226
ENV	LSGIVQQSNL	631	11	32	50	6227
ENV	CTHGRPV	294	8	33	52	6228
ENV	QSNLLAVRY	663	10	33	52	6229
ENV	QSNLLAVRY	663	11	33	52	6230
ENV	QSNLLAVRY	663	11	34	53	6231
ENV	EAQHLLQTV	646	11	34	53	6232
ENV	VTENFNMV	102	8	34	53	6233
ENV	AAGSTMGAASI	611	11	34	53	6234
ENV	LSYINRVQGY	797	11	34	53	6235

Table XIII
HIV B88 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	EAQQILLQL	646	9	35	56	6235
ENV	RSICLFSE	858	8	35	55	6236
ENV	ISFNCGGIEF	434	10	35	55	6237
ENV	ISFNCGGIEFF	434	11	35	55	6238
ENV	AASITLV	618	8	36	56	6239
ENV	ISFNCGGIEF	434	9	36	56	6240
ENV	ASASITLV	617	9	36	56	6241
ENV	LTQAQILL	627	9	36	56	6242
ENV	ITQACVY	245	9	37	58	6243
ENV	LTQAQQL	623	8	38	59	6244
ENV	QARQLLSGI	626	9	38	59	6245
ENV	QARQLLSGIV	626	10	38	59	6246
ENV	STMGAAIS	614	8	39	61	6247
ENV	GSTMGAAIS	613	9	39	61	6248
ENV	STMGAAISL	613	10	39	61	6249
ENV	GSTMGAAISL	613	11	39	61	6250
ENV	QACPKVSF	248	8	40	63	6251
ENV	CASDAKAY	67	8	42	66	6252
ENV	RAIEAQILL	643	10	44	69	6253
ENV	RAIEAQILL	643	9	45	70	6254
ENV	ISFNCGGIEF	434	9	45	70	6255
ENV	ISFNCGGIEF	434	9	48	75	6256
ENV	RSLEYKVKV	558	10	49	77	6257
ENV	RSLEYKVKV	558	9	50	78	6258
ENV	STVQCTHGI	289	9	51	80	6259
ENV	STVQCTHGI	288	10	51	80	6260
ENV	LTPLCVTL	135	8	54	84	6261
ENV	STVQCTHGI	288	9	55	86	6262
ENV	STVQCTHGI	288	10	55	86	6263
ENV	STVQCTHGI	288	10	57	89	6264
ENV	STVQCTHGI	288	10	57	89	6265
ENV	STVQCTHGI	288	11	57	92	6266
ENV	STVQCTHGI	288	11	57	92	6267
ENV	STVQCTHGI	288	11	57	92	6268
ENV	STVQCTHGI	288	11	57	92	6269
ENV	STVQCTHGI	288	11	57	92	6270
ENV	STVQCTHGI	288	11	57	92	6271
ENV	STVQCTHGI	288	11	57	92	6272
ENV	STVQCTHGI	288	11	57	92	6273
ENV	STVQCTHGI	288	11	57	92	6274
ENV	STVQCTHGI	288	11	57	92	6275
ENV	STVQCTHGI	288	11	57	92	6276
ENV	STVQCTHGI	288	11	57	92	6277
ENV	STVQCTHGI	288	11	57	92	6278
ENV	STVQCTHGI	288	11	57	92	6279
ENV	STVQCTHGI	288	11	57	92	6280
ENV	STVQCTHGI	288	11	57	92	6281
ENV	STVQCTHGI	288	11	57	92	6282
ENV	STVQCTHGI	288	11	57	92	6283
ENV	STVQCTHGI	288	11	57	92	6284

Table XIII
HIV-1 SIV Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	SEQ ID NO.
GAG	PAEPTAPAEI	492	11	01	50	6285
GAG	TAPAESEF	507	8	02	67	6286
GAG	PTAPAESEF	508	10	02	67	6287
GAG	PTAPAESEF	507	11	02	67	6288
GAG	GIRIGNYV	480	8	02	100	6289
GAG	ADKKYKSYN	129	11	02	18	6290
GAG	ADKKYKSYN	129	10	04	18	6291
GAG	ADKKYKSYN	129	10	04	18	6292
GAG	ADKKYKSYN	129	10	04	18	6293
GAG	ADKKYKSYN	129	10	04	18	6294
GAG	ADKKYKSYN	129	10	04	18	6295
GAG	ADKKYKSYN	129	10	04	18	6296
GAG	ADKKYKSYN	129	10	04	18	6297
GAG	ADKKYKSYN	129	10	04	18	6298
GAG	ADKKYKSYN	129	10	04	18	6299
GAG	ADKKYKSYN	129	10	04	18	6300
GAG	ADKKYKSYN	129	10	04	18	6301
GAG	ADKKYKSYN	129	10	04	18	6302
GAG	ADKKYKSYN	129	10	04	18	6303
GAG	ADKKYKSYN	129	10	04	18	6304
GAG	ADKKYKSYN	129	10	04	18	6305
GAG	ADKKYKSYN	129	10	04	18	6306
GAG	ADKKYKSYN	129	10	04	18	6307
GAG	ADKKYKSYN	129	10	04	18	6308
GAG	ADKKYKSYN	129	10	04	18	6309
GAG	ADKKYKSYN	129	10	04	18	6310
GAG	ADKKYKSYN	129	10	04	18	6311
GAG	ADKKYKSYN	129	10	04	18	6312
GAG	ADKKYKSYN	129	10	04	18	6313
GAG	ADKKYKSYN	129	10	04	18	6314
GAG	ADKKYKSYN	129	10	04	18	6315
GAG	ADKKYKSYN	129	10	04	18	6316
GAG	ADKKYKSYN	129	10	04	18	6317
GAG	ADKKYKSYN	129	10	04	18	6318
GAG	ADKKYKSYN	129	10	04	18	6319
GAG	ADKKYKSYN	129	10	04	18	6320
GAG	ADKKYKSYN	129	10	04	18	6321
GAG	ADKKYKSYN	129	10	04	18	6322
GAG	ADKKYKSYN	129	10	04	18	6323
GAG	ADKKYKSYN	129	10	04	18	6324
GAG	ADKKYKSYN	129	10	04	18	6325
GAG	ADKKYKSYN	129	10	04	18	6326
GAG	ADKKYKSYN	129	10	04	18	6327
GAG	ADKKYKSYN	129	10	04	18	6328
GAG	ADKKYKSYN	129	10	04	18	6329
GAG	ADKKYKSYN	129	10	04	18	6330
GAG	ADKKYKSYN	129	10	04	18	6331
GAG	ADKKYKSYN	129	10	04	18	6332
GAG	ADKKYKSYN	129	10	04	18	6333
GAG	ADKKYKSYN	129	10	04	18	6334

Table XIII
SHV-B5 Super Nucleo Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	YPTSLDI	301	9	13	20	6335
GAG	NSQTGSEEL	146	10	13	20	6336
GAG	NSQSQSNYPH	144	9	14	21	6337
GAG	NSQSQSNYPH	144	11	14	31	6338
GAG	TSSEGRQIL	55	9	14	22	6339
GAG	ETSEGRQIL	54	10	14	22	6340
GAG	AAEWDRVHPV	230	10	14	22	6341
GAG	TSNKGRTGNF	475	10	14	22	6342
GAG	TSNKGRTGNF	475	10	14	22	6343
GAG	EAENWDRVHPV	229	11	14	22	6344
GAG	PTAPPEESRF	495	11	14	22	6345
GAG	SSQSQSNYPH	145	8	15	31	6346
GAG	SSQSQSNYPH	145	10	15	31	6347
GAG	SSQSQSNYPH	145	11	15	31	6348
GAG	RSSTVVALY	78	10	15	24	6349
GAG	RSSTVVALY	78	11	15	24	6350
GAG	EAENWDRV	229	8	15	23	6351
GAG	ATQDVKNW	333	8	15	23	6352
GAG	TAPPEESF	496	8	15	23	6353
GAG	LASKSLF	549	8	15	23	6354
GAG	RAEDNTPQV	329	9	15	23	6355
GAG	ATQDVKNW	333	9	15	23	6356
GAG	ATQDVKNW	333	9	15	23	6357
GAG	PTAPPEESF	495	9	15	23	6358
GAG	ATLCVHIQRI	85	10	15	23	6359
GAG	QATQDVKNW	332	10	15	23	6360
GAG	VATLCVHIQRI	84	11	15	23	6361
GAG	TSNKGRTGNF	475	8	16	25	6362
GAG	TSSEGRQIL	55	8	16	25	6363
GAG	GSEELARL	73	8	16	25	6364
GAG	TSNHPHV	272	8	16	25	6365
GAG	PAATLEEM	363	8	16	25	6366
GAG	PAATLEEM	364	8	16	25	6367
GAG	PAATLEEM	364	8	16	25	6368
GAG	ETSEGRQIL	54	9	16	25	6369
GAG	MSNHPHV	271	9	16	25	6370
GAG	KALGPAATL	359	9	16	25	6371
GAG	PAATLEEM	363	9	16	25	6372
GAG	DAWEKIRL	14	8	17	27	6373
GAG	ASHELREAV	168	8	17	27	6374
GAG	ASHELREAV	168	10	17	27	6375
GAG	LSPTLNAWV	168	10	17	27	6376
GAG	HAGPIPTGOM	240	10	17	27	6377
GAG	WASKELEFV	37	11	17	27	6378
GAG	ATQEVKNW	333	8	18	28	6379
GAG	QATQDVKNW	332	9	18	28	6380
GAG	QATQDVKNW	332	9	18	28	6381
GAG	HAGPIPTGOM	240	10	18	28	6382
GAG	QATQEVKNW	332	10	18	28	6383
GAG	PSIKARVL	380	8	19	30	6384

Table XIII
HIV p58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO.
GAG	TKPAKSE	486	8	20	31	6385
GAG	MTNPPPV	479	9	20	31	6386
GAG	PIAPAFSE	495	9	20	31	6387
GAG	PALNPGLL	476	8	22	34	6388
GAG	ASRELERFAL	38	10	22	34	6389
GAG	ETNEEFAEW	224	10	22	34	6390
GAG	ETNEEFAEW	224	10	22	34	6391
GAG	PSHGRPGNEL	475	10	22	34	6392
GAG	PSHGRPGNEL	475	10	23	36	6393
GAG	AAQOMLKTH	217	10	26	41	6394
GAG	QAAMOMLKETH	216	11	26	41	6395
GAG	TTSILOQGW	260	11	27	43	6396
GAG	TTSILOQGW	260	11	27	43	6397
GAG	RAQADQEV	329	9	27	42	6398
GAG	TSLQFQGW	261	10	27	42	6399
GAG	TSLQFQGW	262	10	27	42	6400
GAG	TSLQFQGW	261	11	27	42	6401
GAG	VSNQYFVQNL	149	11	28	48	6402
GAG	RAQADQEV	329	9	28	44	6403
GAG	RASVSGEKL	4	10	28	44	6404
GAG	QAISPRTL	166	8	29	45	6405
GAG	GATLEEMM	364	8	29	45	6406
GAG	QAISPRTLNAW	166	11	29	45	6407
GAG	RTLNAWKVI	171	10	30	47	6408
GAG	ETNEEFAEW	224	11	31	48	6409
GAG	ETNEEFAEW	224	11	31	48	6410
GAG	DTKEALDKI	98	9	32	50	6411
GAG	AAQOMLKTH	217	10	33	52	6412
GAG	QAAMOMLKTH	216	11	33	52	6413
GAG	QAAMOMLKTH	216	11	34	53	6414
GAG	ETNEEFAEW	229	11	34	53	6415
GAG	EAIVIRLHV	387	8	36	57	6416
GAG	LAFAMSOV	168	9	36	56	6417
GAG	ISPRTLNAW	168	10	36	56	6418
GAG	ISPRTLNAW	168	10	36	56	6419
GAG	EAQEWDL	229	8	39	61	6420
GAG	EAQEWDL	229	8	40	63	6421
GAG	NTVALCY	82	9	41	66	6422
GAG	ATPDQNLTM	200	9	42	66	6423
GAG	GATPDQNLTM	199	10	42	66	6424
GAG	ATPDQNLTM	200	10	42	66	6425
GAG	GATPDQNLTM	199	11	42	66	6426
GAG	GATPDQNLTM	200	11	45	70	6427
GAG	NANPCKCI	349	9	45	70	6428
GAG	GTSTLQFQI	259	10	45	70	6429
GAG	NANPCKCKIL	349	10	45	70	6430
GAG	ASRELERF	38	8	46	72	6431
GAG	WAKRLERF	37	9	46	72	6432
GAG	WAKRLERF	37	8	47	73	6433
GAG	NTYGGIOAM	210	10	47	73	6434
GAG	GSDIAGTISTL	254	11	47	73	6435

Table XII
HIV-B58 Super Motif Patches

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	VSNQYIV	149	8	48	83	6435
GAG	IAGTISTL	257	8	48	75	6436
GAG	KAFSEVIM	181	8	50	78	6437
GAG	KAFSEVIM	183	10	50	78	6438
GAG	KAFSEVIM	183	11	50	78	6439
GAG	KAFSEVIM	183	11	53	83	6440
GAG	FSFEVIM	183	8	54	84	6441
GAG	FSFEVIM	183	9	54	84	6442
GAG	CTEQANF	459	8	55	87	6443
GAG	CTEQANF	459	9	55	87	6444
GAG	QANFLGKI	366	8	57	89	6445
GAG	QANFLGKI	366	9	57	89	6446
GAG	QANFLGKI	366	9	57	89	6447
GAG	QANFLGKI	366	10	58	91	6448
GAG	LSEGAHQDL	196	10	58	95	6449
GAG	RTLNAWYKV	171	9	61	95	6450
GAG	QAPFAAGV	34	9	01	33	6451
NEF	QAPFAAGV	34	9	01	17	6452
NEF	QAPFAAGV	32	9	01	17	6453
NEF	RIEPAAYGV	32	9	01	17	6454
NEF	RIEPAAYGV	33	9	01	17	6455
NEF	QAPFAAGV	33	9	01	17	6456
NEF	QAPFAAGV	32	11	01	17	6457
NEF	QAPFAAGV	32	11	01	16	6458
NEF	GADLSLEL	110	9	10	16	6459
NEF	MARELIPEY	321	10	10	16	6460
NEF	MARELIPEY	321	10	10	16	6461
NEF	AADGVGAV	42	8	11	18	6462
NEF	AADGVGAV	42	9	11	17	6463
NEF	VSRAADCAW	71	8	11	17	6464
NEF	VSRAADCAW	71	8	12	22	6465
NEF	ATNADCAW	70	9	12	22	6466
NEF	ATNADCAW	71	9	12	22	6467
NEF	ATNADCAW	71	10	12	22	6468
NEF	ATNADCAW	70	9	12	19	6469
NEF	ATNADCAW	108	9	12	19	6470
NEF	NIQGYFDW	194	10	12	19	6471
NEF	TAATNADCAW	69	10	12	19	6472
NEF	GTREPLFGW	213	10	12	19	6473
NEF	TAATNADCAW	68	11	12	19	6474
NEF	TAATNADCAW	68	11	12	20	6475
NEF	GTREPL	213	8	13	20	6476
NEF	YTFPGTRF	207	9	13	20	6477
NEF	YTFPGTRF	207	11	13	20	6478
NEF	ITQGFIPDW	194	9	14	22	6479
NEF	ITQGFIPDW	194	8	16	25	6480
NEF	EAQEEYVF	82	10	16	25	6481
NEF	YTFPGTRF	207	10	16	25	6482
NEF	AAEDGVAV	42	8	17	28	6483
NEF	YTFPGTRF	207	9	17	31	6484
NEF	WSKSGVGV	5	9	20	31	6485

Table XIII
 HIV-188 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIU ID NO.
NEF	YSKKROEL	176	8	22	34	6485
NEF	YSKKROEL	176	9	22	34	6486
NEF	YSKKROEL	176	11	22	34	6487
NEF	YSKKROEL	176	11	22	34	6488
NEF	ITGGYFDW	194	9	25	39	6489
NEF	LSIHLKKGGL	114	11	27	42	6490
NEF	LTFGWCFLV	221	10	35	55	6491
NEF	LITGWCFKL	221	9	39	61	6492
POL	NSPSREL	34	8	01	33	6493
POL	NSPSREL	34	8	01	33	6494
POL	PTNLQV	80	8	01	33	6495
POL	PTNLQV	80	8	01	33	6496
POL	PTNLQV	80	8	01	33	6497
POL	STNSPTREL	32	10	01	33	6498
POL	NSPTRELQV	34	10	01	33	6499
POL	NSPTRELQV	34	10	01	33	6500
POL	NSPTRELQV	34	10	01	33	6501
POL	PTNLQV	80	10	01	33	6502
POL	NSPTRELQV	34	11	01	33	6503
POL	NSPTRELQV	34	11	01	33	6504
POL	PTNLQV	80	11	01	33	6505
POL	NSPSREL	34	8	01	50	6506
POL	NSPSREL	34	8	01	50	6507
POL	NSPSREL	34	8	01	50	6508
POL	NSPSRELQV	39	10	01	50	6509
POL	NSPSRELQV	39	10	01	50	6510
POL	NSPTRELQV	39	10	01	50	6511
POL	NSPTRELQV	39	10	01	50	6512
POL	NSPTRELQV	39	10	01	50	6513
POL	NSPTRELQV	39	10	01	50	6514
POL	NSPTRELQV	39	10	01	50	6515
POL	NSPTRELQV	39	10	01	50	6516
POL	NSPTRELQV	39	10	01	50	6517
POL	NSPTRELQV	39	10	01	50	6518
POL	NSPTRELQV	39	10	01	50	6519
POL	NSPTRELQV	39	10	01	50	6520
POL	NSPTRELQV	39	10	01	50	6521
POL	NSPTRELQV	39	10	01	50	6522
POL	NSPTRELQV	39	10	01	50	6523
POL	NSPTRELQV	39	10	01	50	6524
POL	NSPTRELQV	39	10	01	50	6525
POL	NSPTRELQV	39	10	01	50	6526
POL	NSPTRELQV	39	10	01	50	6527
POL	NSPTRELQV	39	10	01	50	6528
POL	NSPTRELQV	39	10	01	50	6529
POL	NSPTRELQV	39	10	01	50	6530
POL	NSPTRELQV	39	10	01	50	6531
POL	NSPTRELQV	39	10	01	50	6532
POL	NSPTRELQV	39	10	01	50	6533
POL	NSPTRELQV	39	10	01	50	6534

Table XIII
 HIV-1 SS Super Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO.
POL	ETWETWWDYD	588	11	10	16	6535
POL	WAGIQDF	884	8	11	17	6536
POL	WAGIQDF	884	8	11	17	6537
POL	VTVKGGQL	98	9	11	17	6538
POL	STNNLTGI	323	9	11	17	6539
POL	GKALTEVI	474	9	11	17	6540
POL	GSNFTSTV	870	9	11	17	6541
POL	GVNFTSTV	114	10	11	17	6542
POL	GVNFTSTV	114	10	11	17	6543
POL	GVNFTSTV	114	10	11	17	6544
POL	GVNFTSTV	114	10	11	17	6545
POL	GVNFTSTV	114	10	11	17	6546
POL	GVNFTSTV	114	10	11	17	6547
POL	GVNFTSTV	114	10	11	17	6548
POL	GVNFTSTV	114	10	11	17	6549
POL	GVNFTSTV	114	10	11	17	6550
POL	GVNFTSTV	114	10	11	17	6551
POL	GVNFTSTV	114	10	11	17	6552
POL	GVNFTSTV	114	10	11	17	6553
POL	GVNFTSTV	114	10	11	17	6554
POL	GVNFTSTV	114	10	11	17	6555
POL	GVNFTSTV	114	10	11	17	6556
POL	GVNFTSTV	114	10	11	17	6557
POL	GVNFTSTV	114	10	11	17	6558
POL	GVNFTSTV	114	10	11	17	6559
POL	GVNFTSTV	114	10	11	17	6560
POL	GVNFTSTV	114	10	11	17	6561
POL	GVNFTSTV	114	10	11	17	6562
POL	GVNFTSTV	114	10	11	17	6563
POL	GVNFTSTV	114	10	11	17	6564
POL	GVNFTSTV	114	10	11	17	6565
POL	GVNFTSTV	114	10	11	17	6566
POL	GVNFTSTV	114	10	11	17	6567
POL	GVNFTSTV	114	10	11	17	6568
POL	GVNFTSTV	114	10	11	17	6569
POL	GVNFTSTV	114	10	11	17	6570
POL	GVNFTSTV	114	10	11	17	6571
POL	GVNFTSTV	114	10	11	17	6572
POL	GVNFTSTV	114	10	11	17	6573
POL	GVNFTSTV	114	10	11	17	6574
POL	GVNFTSTV	114	10	11	17	6575
POL	GVNFTSTV	114	10	11	17	6576
POL	GVNFTSTV	114	10	11	17	6577
POL	GVNFTSTV	114	10	11	17	6578
POL	GVNFTSTV	114	10	11	17	6579
POL	GVNFTSTV	114	10	11	17	6580
POL	GVNFTSTV	114	10	11	17	6581
POL	GVNFTSTV	114	10	11	17	6582
POL	GVNFTSTV	114	10	11	17	6583
POL	GVNFTSTV	114	10	11	17	6584

Table XIII
 HIV-158 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consequence (%)	SFQ ID NO.
POL	BSAHTNDV	550	8	15	23	6585
POL	VSAGIRKV	744	8	15	23	6586
POL	SAGIRKVL	745	8	15	23	6587
POL	TVKAACW	876	8	15	23	6588
POL	KTELQAIL	668	9	15	23	6589
POL	VSAGIRKVL	744	8	15	23	6590
POL	SAGIRKVL	745	8	15	23	6591
POL	STTVKACW	875	9	15	23	6592
POL	TVKAACW	876	8	15	23	6593
POL	GADDTVLEH	114	10	15	23	6594
POL	LYQLGCTLF	177	10	15	23	6595
POL	LFERKALV	213	10	15	23	6596
POL	VSAGIRKVL	744	8	15	23	6597
POL	SAGIRKVL	745	8	15	23	6598
POL	STTVKACW	875	10	15	23	6599
POL	KTELQAIL	668	11	15	23	6600
POL	VSAGIRKVL	744	11	15	23	6601
POL	KACDHRY	739	9	16	25	6602
POL	VSAGIRKVL	744	8	16	25	6603
POL	KALTVPL	476	9	16	25	6604
POL	RANSPTRREL	26	10	16	25	6605
POL	SAITNDVKQL	551	10	16	25	6606
POL	NSPTRREL	28	8	17	27	6607
POL	VTIKIGQQL	98	9	17	27	6608
POL	KALTVPL	474	9	17	27	6609
POL	GAKALTVPL	474	11	17	27	6610
POL	FSVPLDKDF	305	9	18	28	6611
POL	YAGIKVKQL	460	9	18	28	6612
POL	GADDTVLEH	114	10	18	28	6613
POL	ITLWQRLTV	90	11	18	28	6614
POL	VSAGIRKVL	744	8	19	30	6615
POL	STTVKACW	875	8	19	30	6616
POL	GKALIEV	474	8	19	30	6617
POL	ATISVIV	568	8	19	30	6618
POL	GAITNDVKQL	551	10	19	30	6619
POL	KSESELVQI	704	10	19	30	6620
POL	KSESELVQI	704	10	19	30	6621
POL	VSAGIRKVL	744	11	19	30	6622
POL	LTDTTNDKFEI	661	11	19	30	6623
POL	KSESELVQI	704	11	19	30	6624
POL	VSQIEQL	710	8	20	31	6625
POL	VSQIEQL	710	9	20	31	6626
POL	MAESELVQI	706	8	21	33	6627
POL	WAGKQFF	884	8	21	33	6628
POL	KALTDVPL	476	9	21	33	6629
POL	ESELVQI	706	9	21	33	6630
POL	ASDNLPHV	775	10	21	33	6631
POL	VSAGIRKVL	744	10	21	33	6632
POL	LAWVIRKGI	725	10	22	34	6633
POL	LAWVIRKGI	725	10	22	34	6634

Table XIII
 SCRY-B58 Super-Nob1 Peptides, 60

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	MASDFNLPPI	774	10	22	34	6635
POL	LAGRWYKVI	775	10	22	34	6636
POL	CTHLEGGVIL	817	10	23	36	6637
POL	CTHLEGGVIL	817	10	23	36	6638
POL	GAKALDIV	474	9	24	38	6639
POL	WLEYQATW	594	9	24	38	6640
POL	WLEYQATW	594	10	24	38	6641
POL	WLEYQATW	594	10	24	38	6642
POL	WLEYQATW	594	10	24	38	6643
POL	GAKALDIV	474	8	25	39	6644
POL	DSGEVNI	680	8	25	39	6645
POL	DSGEVNI	680	9	25	39	6646
POL	ASDFNLPPI	775	9	25	39	6647
POL	ALQDSGEV	676	10	25	39	6648
POL	ASDFNLPPI	775	10	25	39	6649
POL	ASDFNLPPI	775	10	25	39	6650
POL	ASDFNLPPI	775	10	25	39	6651
POL	LTETTNQK TEL	661	11	25	39	6652
POL	VSSGIRKVLFL	744	11	25	39	6653
POL	MASDFNLPPI	774	11	25	39	6654
POL	WLEYQATW	594	10	26	41	6655
POL	VSSGIRKVL	744	8	26	41	6656
POL	VSSGIRKVL	745	8	26	41	6657
POL	CTHLEGGVIL	817	8	26	41	6658
POL	CTHLEGGVIL	817	8	26	41	6659
POL	DTNCKTEL	513	9	26	41	6660
POL	CTHLEGGVIL	817	9	26	41	6661
POL	VSSGIRKVL	745	9	26	41	6662
POL	CTHLEGGVIL	817	9	26	41	6663
POL	GSNFTSAV	870	9	26	41	6664
POL	VSSGIRKVL	744	10	26	41	6665
POL	ETQQTATYLL	844	10	26	41	6666
POL	ETQQTATYLL	845	11	26	41	6667
POL	WASQVAGIKV	455	11	26	41	6668
POL	ETQQTATYLL	844	11	26	41	6669
POL	ASQVAGI	456	8	27	43	6670
POL	KAEPEHKY	759	9	27	43	6671
POL	ASQVAGIKV	456	10	27	43	6672
POL	ESLNVQI	706	8	27	42	6673
POL	ESLNVQI	706	8	27	42	6674
POL	FAVFLKL	849	8	27	42	6675
POL	WASQVAGI	455	9	27	42	6676
POL	ESLNVQI	706	9	27	42	6677
POL	FAVFLKL	848	9	27	42	6678
POL	CTHLEGGVIL	817	10	27	42	6679
POL	LAIDSGEVL	676	10	27	42	6680
POL	TSAAVKAACW	874	10	27	42	6681
POL	WASQVAGIKV	455	11	27	42	6682
POL	FAVFLKL	873	11	27	42	6683
POL	TSAAVKAACW	874	11	27	42	6684

Table XIII
CHY-BSR Super-Nat Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consistency (%)	SHQ ID NO.
POL	NIVQPIQL	428	8	28	44	6685
POL	DSGLVNV	429	8	28	44	6686
POL	AAVKAACW	876	8	28	44	6687
POL	DSGLEVNIV	680	9	28	44	6688
POL	SAAVKAACW	875	9	28	44	6689
POL	AAVKAACWW	876	9	28	44	6690
POL	VYDRGRQVY	650	10	28	44	6691
POL	SAVKAACWW	875	10	28	44	6692
POL	ASDVTEG	456	8	29	45	6693
POL	WASDIYGI	455	9	29	45	6694
POL	KTKRFLPI	577	9	29	45	6695
POL	ETNQKTEL	663	9	29	45	6696
POL	AAARETEL	637	8	30	47	6697
POL	GAARETEL	636	9	30	47	6698
POL	LAGRWPKY	856	9	30	47	6699
POL	KAACWWAGI	879	9	31	49	6700
POL	ETAYFILKL	848	9	31	48	6701
POL	PSINNETGI	322	10	31	48	6702
POL	CTLLEGRKIL	817	10	31	48	6703
POL	ETAYFILKL	848	10	31	48	6704
POL	CTLLEGRKILY	817	11	31	48	6705
POL	ETQQTATFIL	844	11	31	48	6706
POL	TAYFILKL	849	8	32	50	6707
POL	AACWWAGI	880	8	32	50	6708
POL	HSNWRAMASDF	768	11	32	50	6709
POL	ETAYFILKL	848	10	32	50	6710
POL	SSNATKLEFF	330	11	33	52	6711
POL	LEAVOKI	560	11	34	53	6712
POL	CTLLEGI	817	8	35	55	6713
POL	ETKLGKAGY	641	9	35	55	6714
POL	CTLLEGI	817	9	35	55	6715
POL	ETKLGKAGY	641	10	35	55	6716
POL	ETKLGKAGY	641	10	35	55	6717
POL	IATDQIKEL	956	10	35	55	6718
POL	ITKIQNFV	969	9	36	57	6719
POL	ITKIQNFVY	969	10	36	57	6720
POL	ITKIQNFVY	969	11	36	57	6721
POL	YAHGSSSTRI	446	11	36	56	6722
POL	QAAATKLEFF	469	11	36	56	6723
POL	YATFTPSI	317	8	37	58	6724
POL	YTAFTPSI	316	9	37	58	6725
POL	LTEGALEL	484	9	37	58	6726
POL	LSWPAIRKGI	725	10	37	58	6727
POL	GAAYIQNSDI	799	11	37	58	6728
POL	GAAYIQNSDI	799	11	38	59	6729
POL	KAKIRDY	1017	8	41	64	6730
POL	RAMASDINI	772	9	41	64	6731
POL	SAGERIDI	947	10	41	64	6732
POL	LTQIGCTLNF	177	10	41	64	6733

Table XIII
 HIV-1 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO.
POL	YSAGERIDI	946	10	41	64	6735
POL	SAGERIDIH	947	10	41	64	6736
POL	YAGERIDIH	948	11	41	64	6737
POL	YAGERIDIH	177	8	42	66	6738
POL	PAFQSSM	346	8	42	66	6739
POL	YSAGERII	946	8	42	66	6740
POL	ISKIGPENP	236	10	42	66	6741
POL	GSFAHQSSM	344	10	42	66	6742
POL	YAGERIDH	947	11	42	66	6743
POL	ITMQRLEQAI	664	11	43	67	6744
POL	DSWTNDI	739	8	43	67	6745
POL	ASCDKCOL	430	8	43	67	6746
POL	VASCDKCOL	789	9	43	67	6747
POL	DSWTNDIQKL	439	11	43	67	6748
POL	MTLHPLP	553	8	44	69	6749
POL	QLELEQI	96	8	46	72	6750
POL	ITLWQPLV	90	8	47	72	6751
POL	ITLWQPLV	90	9	47	73	6752
POL	KAIGTVLV	157	8	48	75	6753
POL	ITINDVKOL	553	8	49	77	6754
POL	PAQLKKKSSV	586	10	50	78	6755
POL	QSWTNDI	592	11	51	80	6756
POL	KSVTVLDV	293	8	51	80	6757
POL	ITDNGSNF	866	8	51	80	6758
POL	ATWPEWEFV	600	10	51	80	6759
POL	ETVPVKLKQGM	192	11	51	80	6760
POL	ETPGRYQYQV	327	10	51	80	6761
POL	ETPGRYQYQV	327	11	51	80	6762
POL	ETPGRYQYQV	327	9	52	81	6763
POL	ETPGRYQYQV	327	9	52	81	6764
POL	ATWPEWEF	600	600	52	81	6765
POL	VASGYEAEV	831	10	52	81	6766
POL	VASGYEAEVI	831	11	52	81	6767
POL	ASGYEAEV	832	9	53	83	6768
POL	QSWTNDI	866	9	53	83	6769
POL	GTVLVGPV	160	10	53	83	6770
POL	RTQDFWEVOL	272	10	53	83	6771
POL	VAVIVASGYI	827	10	53	83	6772
POL	ASGYEAEVI	832	10	53	83	6773
POL	ISPRVTKKLI	964	11	53	83	6774
POL	ESMKEKAKKI	964	11	53	83	6775
POL	QATWPEW	599	8	54	86	6776
POL	RTQDFWEV	272	8	55	86	6777
POL	DAVESVPL	302	8	55	86	6778
POL	ISPRVTKKLI	964	8	55	86	6779
POL	ISPRVTKKLI	964	8	56	88	6780
POL	LTEKIKAL	213	9	56	88	6781
POL	VTVLVDGDAY	295	10	56	88	6782
POL	KIADVMAVI	925	10	56	88	6783
POL	VTVLVDGDAYF	295	11	56	88	6784

Table XIII
SHY J58 Super Mutant Sequences

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PAETGQETAYVF	842	11	56	88	6785
POL	LAENREIL	492	8	57	89	6786
POL	NITPLVKL	610	8	57	89	6787
POL	STKWKRLVDF	842	8	57	89	6788
POL	KIAYOMAV	925	8	57	89	6789
POL	NITPLVKLW	610	9	57	89	6790
POL	ETGQETAYVF	844	9	57	89	6791
POL	KIAYOMAVF	925	9	57	89	6792
POL	NITPLVKLWV	610	10	57	89	6793
POL	STKWKRLVDF	842	11	57	89	6794
POL	QAEILKTAGVM	920	11	58	89	6795
POL	STKWKRLVDF	257	10	58	91	6796
POL	VTDQYALGI	688	10	58	91	6797
POL	PAETGQETAY	842	10	58	91	6798
POL	ISTKWKRLVDF	256	11	58	91	6799
POL	STKWKRLVDF	842	11	58	91	6800
POL	ISTKWKRLV	256	8	59	92	6801
POL	STKWKRLV	257	8	59	92	6802
POL	VTDQYAL	688	8	59	92	6803
POL	DSQYALGI	690	8	59	92	6804
POL	ETGQETAYVF	844	8	59	92	6805
POL	DSQYALGI	256	9	59	92	6806
POL	DSQYALGI	690	9	59	92	6807
POL	VAVIVASGY	827	9	59	92	6808
POL	QAEHLKTAGV	920	9	59	92	6809
POL	TAYOMAVFI	926	9	59	92	6810
POL	MAVPHIHF	930	8	60	94	6811
POL	QAEHLKTAGV	926	10	60	94	6812
POL	TAYOMAVF	926	8	61	95	6813
POL	DTGADDTVL	112	9	61	95	6814
POL	WTVNDIQKL	441	10	61	95	6815
POL	WTVNDIQKL	441	9	62	97	6816
REV	DTGADDTVL	112	8	63	98	6817
REV	WTGQVGSQII	52	10	63	98	6818
REV	GTQVGSQII	97	10	11	18	6819
REV	KSAPFVPL	70	8	12	19	6820
REV	KSAPFVPLQ	71	9	12	19	6821
REV	KSAPFVPLQ	70	10	12	19	6822
REV	KSAPFVPLQ	4	10	16	25	6823
REV	QAEHLKTAGV	4	10	16	25	6824
REV	KSQDSQII	4	9	17	27	6825
REV	GTSGTQGV	94	8	21	33	6826
REV	PAEPVPLQ	71	9	21	33	6827
REV	QAEHLKTAGV	40	10	38	59	6828
VIF	FTVNDIQKL	28	11	12	19	6829
VIF	FTVNDIQKL	28	11	12	19	6830
VIF	FSASAKAI	120	10	10	16	6831
VIF	YSTQIDTDL	99	9	11	17	6832
VIF	YSTQIDTDL	99	9	11	17	6833
VIF	STQVDPGL	100	8	11	17	6834

Table XIII
 HIV-1 Gag Super Nucleocapsid Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	KSLVKIIMYVI	22	10	11	17	6835
VIF	ESAIRKAI	46	10	11	17	6836
VIF	ESAIRKAI	170	11	11	17	6837
VIF	GSQYLALAL	148	11	11	17	6838
VIF	STQIPDL	100	8	12	19	6839
VIF	ESAIRNAI	122	8	12	19	6840
VIF	SAIRNAI	123	8	12	19	6841
VIF	QAIIRNAI	73	9	12	19	6842
VIF	ESAIRNAI	172	9	12	19	6843
VIF	KTKPIIPSV	164	9	12	19	6844
VIF	ESAIRKAI	120	10	12	19	6845
VIF	ESAIRNAI	120	10	12	19	6846
VIF	ESAIRNAI	120	11	12	19	6847
VIF	GSQYLALAL	148	11	12	19	6848
VIF	LADQLIIMYV	107	10	13	20	6849
VIF	ESIRPKVSSIV	45	11	13	20	6850
VIF	LADQLIIMYV	107	11	13	20	6851
VIF	PSYKLTEDRW	173	11	13	20	6852
VIF	NSLVKIIIMYV	22	10	14	22	6853
VIF	NSLVKIIIMYV	107	10	14	22	6854
VIF	NSLVKIIIMYV	107	10	14	22	6855
VIF	RTWNSLVKIIIM	107	11	14	22	6856
VIF	LADQLIILYF	107	9	15	23	6857
VIF	LADQLIILYF	107	9	15	23	6858
VIF	KTKGIIRGSIIM	188	11	15	23	6859
VIF	ESAIRKAI	122	9	16	25	6860
VIF	LADQLIIM	107	8	17	27	6861
VIF	ESAIRKAI	172	8	17	27	6862
VIF	ESAIRKAI	172	8	18	28	6863
VIF	KSLVKIIMYV	22	9	18	28	6864
VIF	DSAIRKAI	122	9	19	30	6865
VIF	DSAIRKAI	122	8	20	31	6866
VIF	RTWNSLVKIIIM	15	9	21	33	6867
VIF	NSLVKIIIMYV	22	9	21	33	6868
VIF	RTWNSLVKIIIM	19	9	24	38	6869
VIF	LADQLIIL	107	8	25	39	6870
VIF	NSLVKIIIM	22	8	27	42	6871
VIF	ESSEVIHPL	51	9	27	42	6872
VIF	NSLVKIIIM	148	9	27	42	6873
VIF	GSQYLALAL	148	11	31	55	6874
VIF	SAIRKAI	123	8	35	59	6875
VIF	QAGINKVGSL	141	10	38	86	6876
VIF	SSEVIHPL	52	8	55	91	6877
VIF	GSQYLAL	148	8	58	91	6878
VIF	SAIRKAI	148	8	60	91	6879
VPR	ETADITMGV	48	10	14	22	6880
VPR	EAVRIIPRIW	29	9	14	22	6881
VPR	EAVRIIPRIW	29	10	14	22	6882
VPR	EAVRIIPRIW	29	11	14	22	6883
VPR	KSEAVRIIF	27	8	15	23	6884
VPR	WAGVAVIRI	54	10	15	23	6885

Table XIII
CHYB58 Super Motif Peptides


Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	WAGVFAIRIL	54	11	15	23	6885
VPR	WAGVFAIRIL	54	8	16	25	6886
VPR	DTWAGVEAI	52	9	16	25	6887
VPR	DTWAGVEAI	52	10	16	25	6888
VPR	ETYGDTWAGV	48	10	16	25	6889
VPR	NIYGDITWEGV	48	10	16	25	6890
VPR	DTWAGVEAI	52	10	19	30	6891
VPR	DTWAGVEAI	52	9	20	31	6892
VPR	DTWAGVEAI	52	10	33	52	6893
VPR	DTWAGVEAI	52	11	33	52	6894
VPR	FAIRILQQL	58	10	34	53	6895
VPR	FAIRILQQL	58	11	34	53	6896
VPR	EAVRIEPRFW	29	10	42	69	6897
VPR	EAVRIEPRFW	29	11	42	69	6898
VPR	WTLLEEL	18	8	01	25	6899
VPR	LAKVDYRI	5	8	01	25	6900
VPR	LAKVDYRI	5	9	01	25	6901
VPR	LAKVDYRI	5	10	01	25	6902
VPR	LAKVDYRI	5	10	01	25	6903
VPR	LAKVDYRI	5	11	01	25	6904
VPR	LAKVDYRI	5	11	01	50	6905
VPR	VTLSSSKL	94	8	12	20	6906
VPR	LAIVLVV	34	8	12	19	6907
VPR	LAIVLVV	34	9	13	20	6908
VPR	LAIVLVV	34	9	13	20	6909
VPR	ESGDTIEL	75	9	13	20	6910
VPR	LAIVVWTV	28	9	20	36	6911
VPR	LAIVVWTV	28	9	20	36	6912
VPR	LAIVVWTV	28	9	20	36	6913
VPR	LAIVVWTV	28	9	20	36	6914
VPR	LAIVVWTV	28	9	20	36	6915
VPR	LAIVVWTV	28	9	20	36	6916
VPR	LAIVVWTV	28	9	20	36	6917
VPR	LAIVVWTV	28	9	20	36	6918
VPR	LAIVVWTV	28	9	20	36	6919
VPR	LAIVVWTV	28	9	20	36	6920

Table XIV
HIV-B62 Super Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	GIGPQTF	340	8	01	33	6911
ENV	SIGSGOAF	360	8	01	33	6912
ENV	KLREIROF	405	8	01	25	6913
ENV	EDRPERI	823	8	01	33	6914
ENV	PDRPTEG	823	8	01	33	6915
ENV	GIGPQTFY	360	9	01	33	6916
ENV	SIGSGOAFY	360	9	01	33	6917
ENV	SIGSGOAFY	360	9	01	33	6918
ENV	KQIYATVY	34	8	01	50	6919
ENV	QIYATVYAGV	34	10	01	50	6920
ENV	KQIYATVYSGV	34	11	01	50	6921
ENV	TIGAMHLGF	599	9	03	27	6922
ENV	SLRGLRQGW	889	9	04	36	6923
ENV	SLRGLRQGW	889	9	04	36	6924
ENV	RLGWEGKLVW	894	11	07	23	6925
ENV	RLGWEGKLVW	894	9	09	29	6926
ENV	GLRUGWEGKLVW	892	11	09	29	6927
ENV	LILQLVII	21	8	09	15	6928
ENV	HLRGLRQGW	889	9	10	16	6929
ENV	HLRGLRQGW	889	9	10	16	6930
ENV	HLRGLRQGW	889	9	10	16	6931
ENV	HLRGLRQGW	889	9	10	16	6932
ENV	HLRGLRQGW	889	9	10	16	6933
ENV	HLRGLRQGW	889	9	10	16	6934
ENV	HLRGLRQGW	889	9	10	16	6935
ENV	HLRGLRQGW	889	9	10	16	6936
ENV	HLRGLRQGW	889	9	10	16	6937
ENV	HLRGLRQGW	889	9	10	16	6938
ENV	HLRGLRQGW	889	9	10	16	6939
ENV	HLRGLRQGW	889	9	10	16	6940
ENV	HLRGLRQGW	889	9	10	16	6941
ENV	HLRGLRQGW	889	9	10	16	6942
ENV	HLRGLRQGW	889	9	10	16	6943
ENV	HLRGLRQGW	889	9	10	16	6944
ENV	HLRGLRQGW	889	9	10	16	6945
ENV	HLRGLRQGW	889	9	10	16	6946
ENV	HLRGLRQGW	889	9	10	16	6947
ENV	HLRGLRQGW	889	9	10	16	6948
ENV	HLRGLRQGW	889	9	10	16	6949
ENV	HLRGLRQGW	889	9	10	16	6950
ENV	HLRGLRQGW	889	9	10	16	6951
ENV	HLRGLRQGW	889	9	10	16	6952
ENV	HLRGLRQGW	889	9	10	16	6953
ENV	HLRGLRQGW	889	9	10	16	6954
ENV	HLRGLRQGW	889	9	10	16	6955
ENV	HLRGLRQGW	889	9	10	16	6956
ENV	HLRGLRQGW	889	9	10	16	6957
ENV	HLRGLRQGW	889	9	10	16	6958
ENV	HLRGLRQGW	889	9	10	16	6959
ENV	HLRGLRQGW	889	9	10	16	6960

Table XIV
 HIV B62 Super-Nat Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO
ENV	NILPCKRIQI	482	11	11	17	6961
ENV	NIKPKKQI	482	11	11	17	6962
ENV	NIKPKKQI	732	11	11	17	6963
ENV	LLALDSKWSIW	107	8	12	19	6964
ENV	NMWKNDIV	202	8	12	19	6965
ENV	ALFYRLDV	488	8	12	19	6966
ENV	RIKQVNM	488	8	12	19	6967
ENV	KLICITTV	687	8	12	19	6968
ENV	NWQVNM	723	8	12	19	6969
ENV	ILKQNMKE	272	9	12	19	6970
ENV	RIKQVNM	488	9	12	19	6971
ENV	LICTITTV	688	9	12	19	6972
ENV	GOELNSAI	911	9	12	19	6973
ENV	ALIHPRRI	946	9	12	19	6974
ENV	ALICHNDKRF	270	10	12	19	6975
ENV	KLITVW	687	10	12	19	6976
ENV	NKIWMWIRI	720	11	12	19	6977
ENV	IVGGLGLRI	783	11	12	19	6978
ENV	ELYKYVVEI	560	10	13	21	6979
ENV	DPNPQEVV	91	8	13	20	6980
ENV	HLIKITVW	650	8	13	20	6981
ENV	NWQVNM	673	8	13	20	6982
ENV	EWNDNIW	716	8	13	20	6983
ENV	SIRLVNGF	842	8	13	20	6984
ENV	SIRLVSGF	842	8	13	20	6985
ENV	RLRDLLI	867	8	13	20	6986
ENV	ILIHPRRI	947	8	13	20	6987
ENV	ELKNGCVI	101	9	13	20	6988
ENV	AIQACPKV	244	9	13	20	6989
ENV	SLAEIEVVI	311	9	13	20	6990
ENV	QOIILKLTIV	648	9	13	20	6991
ENV	LLKITVWGH	651	9	13	20	6992
ENV	QOIILKLTIV	647	10	13	20	6993
ENV	QOIILKLTIV	647	10	13	20	6994
ENV	HLIKITVWGH	650	10	13	20	6995
ENV	EQELLELDKW	752	10	13	20	6996
ENV	VPTDPNPQEVV	38	11	13	20	6997
ENV	VMIISPKCGGEI	432	11	13	20	6998
ENV	NIKPKKQI	482	11	13	20	6999
ENV	ALIHPRRI	946	11	13	20	7000
ENV	SLAEIEVVI	311	8	14	22	7001
ENV	TITLPCRI	482	8	14	22	7002
ENV	SLINATAI	920	8	14	22	7003
ENV	DPEIVMISF	428	9	14	22	7004
ENV	QOMYAPHI	501	9	14	22	7005
ENV	QOMYAPHI	501	9	14	22	7006
ENV	AVAEGTDRV	928	9	14	22	7007
ENV	EQQLALDKW	752	10	14	22	7008
ENV	RHFVLSIV	791	10	14	22	7009
ENV	SLINATAIV	920	10	14	22	7010
ENV	AVAEGTDRVI	928	10	14	22	7010

Table XIV


Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO
ENV	VITQACPKVSF	244	11	14	22	7011
ENV	ALVAEGTTRV	926	11	14	22	7012
ENV	RLNQCNTSRI	236	10	15	24	7014
ENV	GLIGLRRI	786	8	15	23	7015
ENV	IHAVLSI	792	8	15	23	7016
ENV	GPDRPEGI	822	8	15	23	7017
ENV	QVQCKNKAIV	234	9	15	23	7018
ENV	VQVCKNKAIV	234	9	15	23	7019
ENV	GPCNKNSTV	283	9	15	23	7020
ENV	DIRQAHCNI	380	9	15	23	7021
ENV	GLIGLRIF	786	9	15	23	7022
ENV	IIFAVLSV	792	9	15	23	7023
ENV	ILNIAIAV	921	9	15	23	7024
ENV	GLIGLRIF	786	10	15	23	7025
ENV	TLIKRCKRI	484	10	15	23	7026
ENV	NKQVGVGKAM	494	10	15	23	7027
ENV	AVAEGTDRII	928	10	15	23	7028
ENV	NKQVGVGKAM	494	11	15	23	7029
ENV	GLIGLRIF	786	11	15	23	7030
ENV	GLIGLRIF	786	11	15	23	7031
ENV	VQVCKNKAIV	234	9	16	25	7032
ENV	VQVCKNKAIV	234	9	16	25	7033
ENV	AVAEGTDRI	928	10	16	25	7034
ENV	RVVQREKRAV	587	10	16	25	7035
ENV	GLIGLRIF	787	10	16	25	7036
ENV	LVSGFLALAW	845	10	16	25	7037
ENV	LVSGFLALAW	845	10	16	25	7038
ENV	LVSGFLALAW	845	11	16	25	7039
ENV	ELDKWASLWNN	757	11	16	25	7040
ENV	LVSGFLALAW	844	11	16	25	7041
ENV	ALVAEGTDRI	926	11	16	25	7042
ENV	VQVCKNKAIV	234	8	17	27	7043
ENV	IKCTIV	682	8	17	27	7044
ENV	IKCTIV	682	8	17	27	7045
ENV	SLNWNFDI	763	8	17	27	7046
ENV	DLNLCLE	856	8	17	27	7047
ENV	QINMWQEV	491	9	17	27	7048
ENV	LICTINVPW	688	9	17	27	7049
ENV	KNNNTRKAL	347	10	17	27	7050
ENV	KNNNTRKAL	347	10	17	27	7051
ENV	EFRRGGDM	544	10	17	27	7052
ENV	KLICTINVPW	687	10	17	27	7053
ENV	RIVFAVLSI	791	10	17	27	7054
ENV	GVAPFKAKRRV	573	11	17	27	7055
ENV	WQVGVKAM	496	8	18	28	7056
ENV	WQVGVKAM	496	8	18	28	7057
ENV	WQVGVKAM	496	9	18	28	7058
ENV	ELDKWASLW	757	9	18	28	7059
ENV	IVFAVLSI	792	9	18	28	7060
ENV	YLRDQQLGI	672	10	18	28	7061

Table XIV
S-HIV-B2 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	SEQ ID NO.
ENV	LPRLQQLNM	485	11	18	28	7061
ENV	YVGMAMAPPI	498	11	18	28	7062
ENV	YLRDQQLGIW	672	11	18	28	7063
ENV	LLELDKWSLW	755	11	18	28	7064
ENV	CLFSYIRLRF	861	11	18	28	7065
ENV	KLCTTAV	687	9	19	30	7066
ENV	YVGMAMAPPI	498	9	19	30	7067
ENV	RUFVLSI	791	9	19	30	7068
ENV	KLCTTAVPW	687	10	19	30	7069
ENV	GLRIVFVLSI	789	11	19	30	7070
ENV	ELLELDKW	754	8	20	31	7071
ENV	TFVAVLSI	792	8	20	31	7072
ENV	YVGMAMAPPI	498	9	20	31	7073
ENV	YVGMAMAPPI	498	10	20	31	7074
ENV	NAVQEMIEDI	112	10	20	31	7075
ENV	DLALADKW	754	8	21	33	7076
ENV	DLLETTISF	428	9	21	33	7077
ENV	VPIDPNQEV	88	10	21	33	7078
ENV	YVGMAMAPPI	498	10	21	33	7079
ENV	CVPTDNPQEV	9	11	21	33	7080
ENV	GLIGRIVPAV	786	11	21	33	7081
ENV	APFKAKRRV	575	9	22	34	7082
ENV	APIKAKRRV	575	10	22	34	7083
ENV	IVELLGRGW	879	10	22	34	7084
ENV	YVGMAMAPPI	498	11	22	34	7085
ENV	LVNHEISLW	115	11	22	34	7086
ENV	TVQCTHGIRTV	290	11	22	34	7087
ENV	RIVELLGRGW	878	11	22	34	7088
ENV	ELLGRGW	881	8	23	37	7089
ENV	NAVQEMIEDI	113	9	23	36	7090
ENV	YVGMAMAPPI	498	9	23	36	7091
ENV	NAVQEMIEDI	113	10	23	36	7092
ENV	KVVKIETLGV	565	10	23	36	7093
ENV	EQMIEDI	115	8	24	38	7094
ENV	VVEREKRAV	588	9	25	39	7095
ENV	VPIDPNQEV	88	10	25	39	7096
ENV	YVGMAMAPPI	498	10	25	39	7097
ENV	RVVEREKRAV	587	10	25	39	7098
ENV	QOQSNLLRAI	636	10	25	39	7099
ENV	CVPTDNPQEV	87	11	25	39	7100
ENV	VQCTHGIRTV	292	11	25	39	7101
ENV	VQOQSNLLRAI	635	11	25	39	7102
ENV	YVGMAMAPPI	498	9	26	41	7103
ENV	QOQSNLLRAI	637	9	26	41	7104
ENV	QOQSNLLRAI	637	9	26	41	7105
ENV	QOQSNLLRAI	636	10	26	41	7106
ENV	IPHYCAPAGF	259	11	26	41	7107
ENV	VQOQSNLLRAI	635	11	26	41	7108
ENV	IPHYCAPAGF	260	10	27	42	7109
ENV	YLRDQQLGIW	672	10	27	42	7110

Table XIV
 HY-B62 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	YLDQQLGHW	672	11	27	42	7111
ENV	KVSEPIPIHY	252	11	28	44	7112
ENV	TQCTTGKPV	290	11	28	44	7113
ENV	ELGKLVKGL	586	10	29	46	7114
ENV	GLGKLV	787	8	29	45	7115
ENV	GLRYFAV	789	8	29	45	7116
ENV	GLGLRVF	786	9	29	45	7117
ENV	QMEEDISLW	116	10	29	45	7118
ENV	RIKQINM	488	8	30	47	7119
ENV	QKQKLV	527	8	30	47	7120
ENV	CPKVSFEPI	250	11	30	47	7121
ENV	KVSEPIPI	252	9	30	47	7122
ENV	RIKQINM	488	9	30	47	7123
ENV	NMWKNMVEQM	107	11	30	47	7124
ENV	CPKVSFEPI	250	11	30	47	7125
ENV	IVGLGLRV	783	11	30	47	7126
ENV	AVLSINRV	485	8	31	48	7127
ENV	AVLSINRV	795	11	31	48	7128
ENV	VQCTTGKPV	292	11	31	48	7129
ENV	KIPMIVGGLI	778	11	31	48	7130
ENV	GLGLRV	786	8	32	50	7131
ENV	VQCTTGKPV	292	10	32	50	7132
ENV	QKQKLV	527	8	33	52	7133
ENV	RLVAVRY	665	8	33	52	7134
ENV	QLQARVLAV	661	9	33	52	7135
ENV	QLQARVLAV	660	10	33	52	7136
ENV	IQARVLAVRY	662	11	33	52	7137
ENV	NLWTVTV	44	10	34	54	7138
ENV	NVTENNFGV	101	8	34	53	7139
ENV	NMWKNM	107	8	34	53	7140
ENV	HLQLTVW	650	8	34	53	7141
ENV	NVTENNFGV	101	9	34	53	7142
ENV	QKQLQTV	648	9	34	53	7143
ENV	QKQLQTV	647	10	34	53	7144
ENV	QKQLQTV	647	10	34	53	7145
ENV	QKQLQTV	648	10	34	53	7146
ENV	ILLQLTVWGH	650	10	34	53	7147
ENV	ILLQLTVWGH	647	11	34	53	7148
ENV	NLWTVTV	44	8	35	56	7149
ENV	FMVGGELI	780	9	35	55	7150
ENV	FMVGGELI	780	10	35	55	7151
ENV	DLRSICLFSY	856	10	35	56	7152
ENV	VQARQLSGH	625	10	36	56	7153
ENV	SIVNRPROGY	798	10	36	56	7154
ENV	TMGAASTILTV	615	11	36	56	7155
ENV	VQARQLSGH	625	11	36	56	7156
ENV	VQARQLSGH	625	11	36	56	7157
ENV	FMVGGELI	782	11	36	56	7158
ENV	DMRIDNWRSELY	552	11	37	58	7159
ENV	VLSINRV	796	8	38	59	7160

Table XIV
 HIV-1 Gag Super-Nucleotide Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SUQ ID NO.
ENV	DLRLCLF	856	8	38	59	7161
ENV	LYNRVQGY	799	9	38	59	7162
ENV	RYQVQGYLW	847	11	39	59	7163
ENV	YKIKIMIV	776	9	39	59	7164
ENV	GKOLDARV	658	9	40	63	7165
ENV	TLFCASDAKAY	64	11	40	63	7166
ENV	IVGGLGLRI	783	10	42	66	7167
ENV	YKIKIMIA	776	8	43	67	7168
ENV	WYKIMIMIA	773	10	43	67	7169
ENV	WLYYKIMIA	773	11	43	67	7170
ENV	WLYYKIMIA	773	11	43	67	7171
ENV	LOLTWVGI	652	8	44	69	7172
ENV	SLWDQSLKPCV	123	11	47	75	7173
ENV	RVQGYSPLSF	802	11	47	75	7174
ENV	ROGYSPLSF	804	9	48	73	7175
ENV	GWGCTSGLI	680	10	48	75	7176
ENV	GWGCTSGLI	680	10	48	75	7177
ENV	GWGCTSGLI	680	10	48	75	7178
ENV	NWATATACV	80	9	49	77	7179
ENV	WLYYKIFI	773	9	49	77	7180
ENV	DQSLKPCV	126	8	50	78	7181
ENV	WLYYKIF	773	8	50	78	7182
ENV	WLYYKIF	773	8	50	78	7183
ENV	VQCITIGI	290	8	51	80	7184
ENV	WLYYKIF	773	8	51	80	7185
ENV	NVSTVQCTIIB	287	11	51	80	7186
ENV	KPCVRLTLCV	130	11	54	84	7187
ENV	TVYGVFV	48	8	55	86	7188
ENV	TVYGVFV	48	8	55	86	7189
ENV	TVYGVFV	48	8	55	86	7190
ENV	CVKLTPLCV	132	9	55	86	7191
ENV	CVKLTPLCV	132	9	55	86	7192
ENV	CVKLTPLCV	132	9	55	86	7193
ENV	WLYYGVFV	46	10	55	86	7194
ENV	WLYYGVFV	46	10	55	86	7195
ENV	WLYYGVFV	46	10	55	86	7196
ENV	ELYKYKV	560	8	56	89	7197
ENV	WLYYGVFV	46	8	58	91	7198
ENV	PPUSFRF	510	8	58	91	7199
ENV	PPUSFRF	510	8	58	91	7200
ENV	PPUSFRF	510	8	58	91	7201
ENV	APPESFRF	509	9	59	91	7202
ENV	KOEPIKELY	535	10	61	95	7203
ENV	KQETDKDLY	535	10	61	95	7204
ENV	EPLTALRSF	547	10	61	95	7205
ENV	EPLTALRSF	547	10	61	95	7206
ENV	EPLTALRSF	547	10	61	95	7207
ENV	EPLTALRSF	547	10	61	95	7208
ENV	EFTAPPESE	506	10	61	95	7209
ENV	PPAESFRF	510	8	62	67	7210
ENV	PPAESFRF	509	9	62	67	7211
ENV	PPAESFRF	509	9	62	67	7212
ENV	PPAESFRF	509	9	62	67	7213
ENV	PPAESFRF	509	9	62	67	7214
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ENV	PPAESFRF	509	9	62	67	7234
ENV	PPAESFRF	509	9	62	67	7235
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ENV	PPAESFRF	509	9	62	67	7262
ENV	PPAESFRF	509	9	62	67	7263
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ENV	PPAESFRF	509	9	62	67	7281
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ENV	PPAESFRF	509	9	62	67	7289
ENV	PPAESFRF	509	9	62	67	7290
ENV	PPAESFRF	509	9	62	67	7291
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ENV	PPAESFRF	509	9	62	67	7293
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ENV	PPAESFRF	509	9	62	67	7362
ENV	PPAESFRF	509	9	62	67	7363
ENV	PPAESFRF	509	9	62	67	7364
ENV	PPAESFRF	509	9	62	67	7365
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ENV	PPAESFRF	509	9	62	67	7367
ENV	PPAESFRF	509	9	62	67	7368
ENV	PPAESFRF	509	9	62	67	7369
ENV	PPAESFRF	509	9	62	67	7370
ENV	PPAESFRF	509	9	62	67	7371
ENV	PPAESFRF	509	9	62	67	7372
ENV	PPAESFRF	509	9	62	67	7373</

Table XIV
 HIV-1 Gag Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	SH ID NO.
GAG	NPTPVGDHY	277	10	10	16	7211
GAG	QIGWMTSNPII	267	11	10	16	7212
GAG	KLDKWEKI	12	8	10	16	7213
GAG	QVAGVGGI	278	8	10	16	7214
GAG	PIPVGDHY	278	8	10	16	7215
GAG	PIAESIGF	498	8	10	16	7216
GAG	PIPVGDHY	278	9	10	16	7217
GAG	APAESIEGF	497	9	10	16	7218
GAG	ALSPRTLNAY	167	10	10	16	7219
GAG	QVAGVGGI	278	11	10	16	7220
GAG	IPGVGDKAW	282	11	10	16	7221
GAG	VONANPDCKSI	347	11	10	16	7222
GAG	PIPVGDHY	279	8	11	17	7223
GAG	SPVKNWM	334	8	11	17	7224
GAG	IMMOKSNE	408	8	11	17	7225
GAG	QVAGVGGI	278	10	11	17	7226
GAG	IPGVGDKAW	282	10	11	17	7227
GAG	IQASQEVKNW	331	10	11	17	7228
GAG	TPQDLNMLNI	201	11	11	17	7229
GAG	PDNLNMLNIV	202	11	11	17	7230
GAG	IVGHIQAAOM	211	11	11	17	7231
GAG	TPQDLNMLNI	201	11	11	17	7232
GAG	IQASQEVKNW	331	11	11	17	7233
GAG	WSSSKRGNGF	474	11	11	17	7234
GAG	EPDKELY	533	8	12	19	7235
GAG	KQEPDKELY	531	8	12	19	7236
GAG	TPQDLNMLNI	201	8	12	19	7237
GAG	IQASQEVKNW	331	8	12	19	7238
GAG	TLQEQIAY	263	8	12	19	7239
GAG	TLQCVHOKI	86	9	12	19	7240
GAG	DLNMLNIV	204	9	12	19	7241
GAG	IVGHIQAAOM	211	9	12	19	7242
GAG	TPQDLNMLNI	201	9	12	19	7243
GAG	PLTSLSLF	568	9	12	19	7244
GAG	PLTSLSLF	568	9	12	19	7245
GAG	NIVGGIQAAM	210	10	12	19	7246
GAG	TLRAEQASQEV	327	11	12	19	7247
GAG	TIMMQRGNF	407	9	13	22	7248
GAG	QVAGVGGI	278	11	13	20	7249
GAG	RMYSPTSLDI	299	11	13	22	7250
GAG	LOEQIAYM	264	8	14	22	7251
GAG	RMYSPTSLDI	299	8	14	22	7252
GAG	VQNAQQQMV	156	9	14	22	7253
GAG	IVQNAQQQMV	155	10	14	22	7254
GAG	QVAGVGGI	278	10	14	22	7255
GAG	IVRMYSPTSLDI	297	10	14	22	7256
GAG	PVQNAQQQMV	154	11	14	22	7257
GAG	KIVRMYSPTSLDI	296	11	14	22	7258
GAG	WSSSKRGNGF	474	11	14	22	7259
GAG	KVSQNYPI	148	8	15	27	7260

Table XIV
 HIV-1 B62 Super Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	KVQNYIV	148	9	15	27	7261
GAG	TDYKNM	334	8	15	23	7262
GAG	ELRSNTV	498	8	15	23	7263
GAG	TYCVIQR	78	9	15	23	7264
GAG	APRESFR	86	9	15	23	7265
GAG	PLASLSF	497	9	15	23	7266
GAG	VLSGRLLDAW	548	9	15	23	7267
GAG	YVQVQVQVQ	7	10	15	23	7268
GAG	LOGGVQVQVQ	7	10	15	23	7269
GAG	EQATDQVKNW	159	10	15	23	7270
GAG	EPTAPPESE	331	10	15	23	7271
GAG	SVLSGRLLDAW	494	10	15	23	7272
GAG	NLQGVQVQVQ	6	11	15	23	7273
GAG	WMTSNPIV	138	11	15	23	7274
GAG	GPAATLEEM	331	11	15	23	7275
GAG	WMTSNPIV	270	11	16	25	7276
GAG	GPAATLEEM	362	10	16	25	7277
GAG	LLETSGCRQI	52	11	16	25	7278
GAG	ALLETSGCRQI	240	11	16	25	7279
GAG	EPYPCQW	242	8	17	27	7280
GAG	DIYKRWI	284	8	17	27	7281
GAG	PVGDYKRWI	281	10	17	27	7282
GAG	PVGHYKRWI	281	11	17	27	7283
GAG	ALGRGATLEEM	360	11	17	27	7284
GAG	QVLDANW	367	11	18	29	7285
GAG	QVLDANW	1	8	18	28	7286
GAG	IOEVKNM	334	8	18	28	7287
GAG	PVGDYKRW	281	9	18	28	7288
GAG	GPATLEEM	362	9	18	28	7289
GAG	EQATQVKNW	331	10	18	28	7290
GAG	EQATQVKNW	331	10	18	28	7291
GAG	EQATQVKNW	331	10	18	28	7292
GAG	EQATQVKNW	331	10	18	28	7293
GAG	EQATQVKNW	331	10	18	28	7294
GAG	GPATQVKNW	242	8	19	30	7295
GAG	GPATQVKNW	379	8	19	30	7296
GAG	DIKQKPEPF	308	10	19	30	7297
GAG	DIKQKPEPF	35	11	19	30	7298
GAG	DIKQKPEPF	35	11	19	30	7299
GAG	DIKQKPEPF	35	11	19	30	7300
GAG	WMTNNPIV	270	8	20	31	7301
GAG	WMTNNPIV	270	10	20	31	7302
GAG	EPTAPPESE	494	10	20	31	7303
GAG	YPIVQVQVQ	153	11	20	31	7304
GAG	VIEKQVQVQ	179	11	20	31	7305
GAG	VIEKQVQVQ	316	8	21	33	7306
GAG	KQKPEPF	155	9	21	33	7307
GAG	IVQVQVQ	154	10	21	33	7308
GAG	PIVQVQVQ	310	10	21	33	7309
GAG	KQKPEPF	154	11	21	33	7310
GAG	SVQVQVQ	146	9	22	44	7311

Table XIV
HIV B67 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO
GAG	SOVSQNYHV	146	10	22	44	7311
GAG	WMTDTLLV	340	8	22	34	7312
GAG	SLYNVATILY	79	10	22	34	7313
GAG	WVSHKGRGNE	474	11	24	36	7314
GAG	KVIEKAF	178	8	24	38	7316
GAG	WKVVEKAF	176	10	24	38	7317
GAG	TLMAKQATQEV	327	11	24	38	7318
GAG	LVAWSRELRE	35	11	25	39	7319
GAG	ANQMLKTI	218	9	26	41	7320
GAG	ONSONYH	148	8	27	42	7322
GAG	QVSQNYHV	148	9	27	48	7323
GAG	TLQEQIGW	263	8	27	42	7324
GAG	IMMQRGNE	408	8	27	42	7325
GAG	GVNVIQAI	161	8	28	44	7326
GAG	KVVEKAF	178	8	28	44	7328
GAG	WKVVEKAF	176	10	28	44	7329
GAG	VVEKATSPKV	179	11	28	44	7330
GAG	EPFRDYVDREY	315	11	28	44	7331
GAG	QVQVQVQV	155	9	29	45	7332
GAG	LVQEQIGW	263	8	29	45	7333
GAG	QVQVQVQV	155	9	29	45	7334
GAG	QVQVQVQV	155	9	29	45	7335
GAG	QVQVQVQV	155	9	29	45	7336
GAG	QVQVQVQV	155	10	29	45	7337
GAG	QVQVQVQV	155	10	29	45	7338
GAG	QVQVQVQV	155	11	29	45	7339
GAG	QVQVQVQV	155	11	29	45	7340
GAG	QVQVQVQV	155	11	29	45	7341
GAG	QVQVQVQV	155	11	29	45	7342
GAG	QVQVQVQV	155	9	30	47	7343
GAG	QVQVQVQV	155	9	31	48	7344
GAG	QVQVQVQV	155	9	32	48	7345
GAG	QVQVQVQV	155	9	33	52	7346
GAG	QVQVQVQV	155	9	33	52	7347
GAG	QVQVQVQV	155	10	33	52	7348
GAG	QVQVQVQV	155	10	34	54	7349
GAG	QVQVQVQV	155	10	34	54	7350
GAG	QVQVQVQV	155	10	34	53	7351
GAG	QVQVQVQV	155	10	34	53	7352
GAG	QVQVQVQV	155	11	34	53	7353
GAG	QVQVQVQV	155	11	35	55	7354
GAG	QVQVQVQV	155	8	35	55	7355
GAG	QVQVQVQV	155	8	35	55	7356
GAG	QVQVQVQV	155	9	35	55	7357
GAG	QVQVQVQV	155	11	35	55	7358
GAG	QVQVQVQV	155	11	35	55	7359
GAG	QVQVQVQV	155	11	36	56	7360

Table XIV
 HIV-1 p62 Super Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Convergency (%)	SEQ ID NO.
GAG	WTEITLV	340	8	37	58	7361
GAG	HPVHAGPI	227	8	38	59	7362
GAG	RMYSFVSILDI	299	11	38	59	7363
GAG	RMYSFVSILDI	284	8	39	61	7364
GAG	PVGEVYKRW	281	11	39	61	7365
GAG	KIVRMYSFVS	296	11	39	61	7366
GAG	RMYSFVS	299	8	40	63	7367
GAG	SPVSILDI	302	8	40	63	7368
GAG	PVGEVYKRW	281	9	40	63	7369
GAG	RMYSFVS	296	10	40	63	7370
GAG	KIVRMYSFVS	299	10	41	64	7371
GAG	TVATVYCV	83	8	41	64	7372
GAG	KIVRMYSFVS	296	9	41	64	7373
GAG	DIRQGPKEPF	308	10	41	64	7374
GAG	PODINTMLNTV	202	11	41	64	7375
GAG	PQDLNTIM	201	8	42	66	7376
GAG	TVATVYCV	83	8	42	66	7377
GAG	ROGPKEPF	310	8	42	66	7378
GAG	DLNTMLNTV	204	9	42	66	7379
GAG	ROGPKEPF	310	11	42	66	7380
GAG	QNRKPEPGSDI	248	10	44	69	7381
GAG	QNRKPEPGSDI	247	11	44	69	7382
GAG	TVATVYCV	83	11	45	73	7383
GAG	TVATVYCV	83	9	47	73	7384
GAG	TVATVYCV	83	11	47	73	7385
GAG	TVATVYCV	83	11	53	83	7386
GAG	TVATVYCV	83	8	55	86	7387
GAG	SPKPKCCV	440	8	55	86	7388
GAG	SPKPKCCV	440	11	55	86	7389
GAG	SPKPKCCV	440	11	56	88	7390
GAG	ROANFLGKI	465	10	56	88	7391
GAG	ROANFLGKI	465	11	56	88	7392
GAG	ILGLNKNIVRM	290	11	56	88	7393
GAG	SPRTLNW	169	8	57	89	7394
GAG	ILGLNKNIV	290	8	57	89	7395
GAG	SPRTLNW	169	11	57	89	7396
GAG	WILLGNKI	289	9	57	89	7397
GAG	ILGLNKNIV	290	9	57	89	7398
GAG	WILLGNKNIV	289	10	57	89	7399
GAG	ILGLNKNIVRM	291	11	57	89	7400
GAG	ILGLNKNIVRM	291	11	57	89	7401
GAG	EMMTACQGV	369	9	59	92	7402
GAG	GLNKNIVRM	293	8	60	94	7403
GAG	MMTACQGV	370	8	60	94	7404
GAG	GLNKNIVRM	293	9	60	94	7405
GAG	TLNNAWKV	172	8	61	95	7406
GAG	TLNNAWKV	172	11	61	95	7407
GAG	GPKEPF	312	10	63	98	7408
GAG	GPKEPF	312	10	63	98	7409
GAG	EPREDYVDRF	315	10	63	98	7410
NEF	APTAAKGV	34	8	01	33	7411

Table XIV
 HIV B62 Super-Mutif-Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO
NEF	APTAACGAGV	34	11	01	33	7411
NEF	KQAPFAAGV	32	10	01	32	7412
NEF	KQAPFAAGV	32	10	01	17	7413
NEF	QAEPAAAGV	33	10	01	17	7414
NEF	EPAAADGAGV	40	10	04	15	7415
NEF	VILRPMTE	101	8	10	16	7416
NEF	QVPLRMTE	99	9	10	16	7417
NEF	QVPLRMTE	101	9	10	16	7418
NEF	QVPLRMTE	99	10	10	16	7419
NEF	LLIIPICQIGM	257	10	10	16	7420
NEF	IMARELLIPEY	320	10	10	16	7421
NEF	EPQVLRPMIT	98	11	10	16	7422
NEF	LLIIPASQIGM	256	11	10	16	7423
NEF	WQNYTGGV	230	10	11	16	7424
NEF	WQNYTGGV	204	10	11	17	7425
NEF	WQNYTGGV	230	8	11	17	7426
NEF	VPAVDPREV	229	9	11	17	7427
NEF	LVVVDPREV	228	10	11	17	7428
NEF	KLVPVDPREV	228	10	11	17	7429
NEF	PMYKGA	105	8	12	19	7430
NEF	PMYKGA	105	8	12	19	7431
NEF	RMVYAGAF	257	9	12	19	7432
NEF	LLIIPNSQIGM	257	10	12	19	7433
NEF	PLRPMYKGA	102	11	12	19	7434
NEF	SQRQDLDLW	177	11	12	19	7435
NEF	WVYHTQGF	191	8	13	20	7436
NEF	WVYHTQGF	208	8	13	20	7437
NEF	GRVYLT	213	9	13	20	7438
NEF	WVYHTQGF	191	9	13	20	7439
NEF	DLWVYHTQGF	188	10	13	20	7440
NEF	GGIRYPLT	210	10	13	20	7441
NEF	GGIRYPLT	210	10	13	20	7442
NEF	DLWVYHTQGF	188	10	13	20	7443
NEF	DLWVYHTQGF	188	11	14	22	7444
NEF	ILEKIGAI	57	8	14	24	7445
NEF	WLEAQEEV	79	10	15	27	7446
NEF	AQEEVEGV	83	9	17	24	7447
NEF	AQEEVEGV	83	11	17	27	7448
NEF	EPVQRY	208	8	17	27	7449
NEF	EPVQRY	208	8	17	27	7450
NEF	TQGEFFDQWNY	195	11	18	29	7451
NEF	WQNYTGGV	204	10	18	28	7452
NEF	GLYSKKRQEI	174	11	18	28	7453
NEF	GLYSKKRQEI	173	11	18	31	7454
NEF	DLDLWV	185	8	20	31	7455
NEF	DLDLWV	185	8	20	31	7456
NEF	RQDLDLWV	182	10	20	31	7457
NEF	WVYHTQGF	191	8	21	33	7458
NEF	WVYHTQGF	191	9	21	33	7459
NEF	DLWVYHTQGF	188	10	21	33	7460
NEF	DLWVYHTQGF	188	11	21	33	7460

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	TQGFDDW	195	8	22	34	7461
NEF	YLTGWCFC	217	9	24	38	7462
NEF	RQDILDW	182	8	25	39	7463
NEF	YLTGWCFC	183	8	32	40	7464
NEF	FILIDAWV	185	8	33	41	7465
NEF	ROHLDLWV	182	9	35	55	7466
NEF	PLTGWCFKLW	219	11	35	55	7467
NEF	RQVILRPMTY	98	11	36	56	7468
NEF	TQGYFDWQNY	195	11	36	56	7469
NEF	YLTGWCFC	182	8	37	58	7470
NEF	TQGFDDW	195	8	37	58	7471
NEF	EVGFVPRQV	91	10	40	63	7472
NEF	PLTGWCF	219	8	43	67	7473
NEF	PQVILRPMTY	99	10	45	70	7474
NEF	VILRPMTY	101	8	46	73	7475
NEF	YLTGWCFC	182	8	46	72	7476
NEF	RQVILRPMTY	98	9	47	73	7477
NEF	RQVILRPMTY	98	9	47	71	7478
NEF	PVHQVILRIM	95	11	47	71	7479
NEF	PQVILRPM	99	8	56	88	7479
POL	SPISRELQV	35	9	01	33	7480
POL	ASLSLPOI	80	9	01	33	7481
POL	ASLSLPOI	80	8	01	50	7482
POL	ASLSLPOI	78	8	01	48	7483
POL	GREALS	79	8	01	48	7484
POL	VPIENPOI	69	8	01	17	7485
POL	EGEDRELSV	69	10	01	17	7486
POL	GORQGTVLSF	69	11	01	17	7487
POL	PQGEAREF	9	8	10	16	7488
POL	YLTGWCFC	182	8	10	16	7489
POL	YLTGWCFC	182	8	10	16	7490
POL	LIBGUKAI	150	10	10	16	7491
POL	AVOKIATESI	563	10	10	16	7492
POL	MLTQLGCLNF	176	11	10	16	7493
POL	AVOKIATESIV	563	11	10	16	7494
POL	AVKAAACWAGI	877	11	10	16	7495
POL	YLTGWCFC	182	11	10	17	7496
POL	YLTGWCFC	235	8	11	17	7497
POL	YOLETEH	619	8	11	17	7498
POL	AQEDIEKY	760	8	11	17	7499
POL	QIQQFEG	886	8	11	17	7500
POL	KVYPRKVV	1011	8	11	17	7501
POL	KVYPRKVV	1011	8	11	17	7502
POL	VYPRKVKI	1012	9	11	17	7503
POL	VYPRKVKI	1013	9	11	17	7504
POL	IKDYQKQM	1020	9	11	17	7505
POL	GIQGEFIPY	886	10	11	17	7506
POL	KVYPRKVKI	1011	10	11	17	7507
POL	KVYPRKVKI	1012	10	11	17	7508
POL	KIKLYGKQM	1012	10	11	17	7509
POL	KIKLYGKQM	235	11	11	17	7510
POL	IPSTNNEITGI	321	11	11	17	7511
POL	KLWYQLETEH	616	11	11	17	7512

Table XIV
 HIV-1 Super-Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KVPRRKVKII	1011	11	11	17	7311
POL	KQIKQNF	967	9	12	19	7312
POL	IKQIKQNF	967	9	12	19	7313
POL	IKQIKQNF	967	9	12	19	7314
POL	IKQIKQNF	967	11	12	19	7315
POL	IKQIKQNF	969	11	12	19	7316
POL	RPLVTVKI	95	8	12	19	7317
POL	ENLPCKW	122	8	12	19	7318
POL	ENLPCKW	108	8	12	19	7319
POL	VIQDNSEI	1003	9	12	19	7320
POL	VIQDNSEI	395	9	12	19	7321
POL	ROKLLAWGF	666	9	12	19	7322
POL	NQKTELIAT	952	9	12	19	7323
POL	IDIHASDI	952	9	12	19	7324
POL	VDIATDI	1002	9	12	19	7325
POL	VIQDNSEI	1002	9	12	19	7326
POL	VDIATDI	1002	9	12	19	7327
POL	WORPLTVKI	91	10	12	19	7328
POL	ROYDQIPI	144	10	12	19	7329
POL	GODQWYQIV	525	10	12	19	7330
POL	RMKGAIINDV	548	10	12	19	7331
POL	NQKTELIAT	666	10	12	19	7332
POL	NQKTELIAT	951	10	12	19	7333
POL	RVDIATDI	951	10	12	19	7334
POL	QIKQIKQNF	968	10	12	19	7335
POL	AVIQDNSEI	1000	10	12	19	7336
POL	VIQDNSEI	1003	10	12	19	7337
POL	VIQDNSEI	1004	10	12	19	7338
POL	VIQDNSEI	1004	10	12	19	7339
POL	VIQDNSEI	1004	10	12	19	7340
POL	ELKQIKQNF	393	11	12	19	7341
POL	ELKQIKQNF	424	11	12	19	7342
POL	IPQKWTQVPI	521	11	12	19	7343
POL	IKQIKQNF	965	11	12	19	7344
POL	IKQIKQNF	1008	11	12	19	7345
POL	VIQDNSEI	1002	11	12	19	7346
POL	VIQDNSEI	1003	11	12	19	7347
POL	ELKQIKQNF	964	9	13	21	7348
POL	NLKTGKYAKM	540	10	13	21	7349
POL	ENLPCKW	122	8	13	20	7350
POL	ENLPCKW	144	8	13	20	7351
POL	QIKQIKQNF	414	8	13	20	7352
POL	VIQDNSEI	414	8	13	20	7353
POL	LOKQIKQNF	965	8	13	20	7354
POL	LOKQIKQNF	433	9	13	20	7355
POL	LOKQIKQNF	433	9	13	20	7356
POL	LOKQIKQNF	433	9	13	20	7357
POL	LOKQIKQNF	433	9	13	20	7358
POL	LOKQIKQNF	433	9	13	20	7359
POL	LOKQIKQNF	433	9	13	20	7360
POL	LOKQIKQNF	433	9	13	20	7361
POL	LOKQIKQNF	433	9	13	20	7362
POL	LOKQIKQNF	433	9	13	20	7363
POL	LOKQIKQNF	433	9	13	20	7364
POL	LOKQIKQNF	433	9	13	20	7365
POL	LOKQIKQNF	433	9	13	20	7366
POL	LOKQIKQNF	433	9	13	20	7367
POL	LOKQIKQNF	433	9	13	20	7368
POL	LOKQIKQNF	433	9	13	20	7369
POL	LOKQIKQNF	433	9	13	20	7370
POL	LOKQIKQNF	433	9	13	20	7371
POL	LOKQIKQNF	433	9	13	20	7372
POL	LOKQIKQNF	433	9	13	20	7373
POL	LOKQIKQNF	433	9	13	20	7374
POL	LOKQIKQNF	433	9	13	20	7375
POL	LOKQIKQNF	433	9	13	20	7376
POL	LOKQIKQNF	433	9	13	20	7377
POL	LOKQIKQNF	433	9	13	20	7378
POL	LOKQIKQNF	433	9	13	20	7379
POL	LOKQIKQNF	433	9	13	20	7380
POL	LOKQIKQNF	433	9	13	20	7381
POL	LOKQIKQNF	433	9	13	20	7382
POL	LOKQIKQNF	433	9	13	20	7383
POL	LOKQIKQNF	433	9	13	20	7384
POL	LOKQIKQNF	433	9	13	20	7385
POL	LOKQIKQNF	433	9	13	20	7386
POL	LOKQIKQNF	433	9	13	20	7387
POL	LOKQIKQNF	433	9	13	20	7388
POL	LOKQIKQNF	433	9	13	20	7389
POL	LOKQIKQNF	433	9	13	20	7390
POL	LOKQIKQNF	433	9	13	20	7391
POL	LOKQIKQNF	433	9	13	20	7392
POL	LOKQIKQNF	433	9	13	20	7393
POL	LOKQIKQNF	433	9	13	20	7394
POL	LOKQIKQNF	433	9	13	20	7395
POL	LOKQIKQNF	433	9	13	20	7396
POL	LOKQIKQNF	433	9	13	20	7397
POL	LOKQIKQNF	433	9	13	20	7398
POL	LOKQIKQNF	433	9	13	20	7399
POL	LOKQIKQNF	433	9	13	20	7400
POL	LOKQIKQNF	433	9	13	20	7401
POL	LOKQIKQNF	433	9	13	20	7402
POL	LOKQIKQNF	433	9	13	20	7403
POL	LOKQIKQNF	433	9	13	20	7404
POL	LOKQIKQNF	433	9	13	20	7405
POL	LOKQIKQNF	433	9	13	20	7406
POL	LOKQIKQNF	433	9	13	20	7407
POL	LOKQIKQNF	433	9	13	20	7408
POL	LOKQIKQNF	433	9	13	20	7409
POL	LOKQIKQNF	433	9	13	20	7410
POL	LOKQIKQNF	433	9	13	20	7411
POL	LOKQIKQNF	433	9	13	20	7412
POL	LOKQIKQNF	433	9	13	20	7413
POL	LOKQIKQNF	433	9	13	20	7414
POL	LOKQIKQNF	433	9	13	20	7415
POL	LOKQIKQNF	433	9	13	20	7416
POL	LOKQIKQNF	433	9	13	20	7417
POL	LOKQIKQNF	433	9	13	20	7418
POL	LOKQIKQNF	433	9	13	20	7419
POL	LOKQIKQNF	433	9	13	20	7420
POL	LOKQIKQNF	433	9	13	20	7421
POL	LOKQIKQNF	433	9	13	20	7422
POL	LOKQIKQNF	433	9	13	20	7423
POL	LOKQIKQNF	433	9	13	20	7424
POL	LOKQIKQNF	433	9	13	20	7425
POL	LOKQIKQNF	433	9	13	20	7426
POL	LOKQIKQNF	433	9	13	20	7427
POL	LOKQIKQNF	433	9	13	20	7428
POL	LOKQIKQNF	433	9	13	20	7429
POL	LOKQIKQNF	433	9	13	20	7430
POL	LOKQIKQNF	433	9	13	20	7431
POL	LOKQIKQNF	433	9	13	20	7432
POL	LOKQIKQNF	433	9	13	20	7433
POL	LOKQIKQNF	433	9	13	20	7434
POL	LOKQIKQNF	433	9	13	20	7435
POL	LOKQIKQNF	433	9	13	20	7436
POL	LOKQIKQNF	433	9	13	20	7437
POL	LOKQIKQNF	433	9	13	20	7438
POL	LOKQIKQNF	433	9	13	20	7439
POL	LOKQIKQNF	433	9	13	20	7440
POL	LOKQIKQNF	433	9	13	20	7441
POL	LOKQIKQNF	433	9	13	20	7442
POL	LOKQIKQNF	433	9	13	20	7443
POL	LOKQIKQNF	433	9	13	20	7444
POL	LOKQIKQNF	433	9	13	20	7445
POL	LOKQIKQNF	433	9	13	20	7446
POL	LOKQIKQNF	433	9	13	20	7447
POL	LOKQIKQNF	433	9	13	20	7448
POL	LOKQIKQNF	433	9	13	20	7449
POL	LOKQIKQNF	433	9	13	20	7450
POL	LOKQIKQNF	433	9	13	20	7451
POL	LOKQIKQNF	433	9	13	20	7452
POL	LOKQIKQNF	433	9	13	20	7453
POL	LOKQIKQNF	433	9	13	20	7454
POL	LOKQIKQNF	433	9	13	20	7455
POL	LOKQIKQNF	433	9	13	20	7456
POL	LOKQIKQNF	433	9	13	20	7457
POL	LOKQIKQNF	433	9	13	20	7458
POL	LOKQIKQNF	433	9	13	20	7459
POL	LOKQIKQNF	433	9	13	20	7460
POL	LOKQIKQNF	433	9	13	20	7461
POL	LOKQIKQNF	433	9	13	20	7462
POL	LOKQIKQNF	433	9	13	20	7463
POL	LOKQIKQNF	433	9	13	20	7464
POL	LOKQIKQNF	433	9	13	20	7465
POL	LOKQIKQNF	433	9	13	20	7466
POL	LOKQIKQNF	433	9	13	20	7467
POL	LOKQIKQNF	433	9	13	20	7468
POL	LOKQIKQNF	433	9	13	20	7469
POL	LOKQIKQNF	433	9	13	20	7470
POL	LOKQIKQNF	433	9	13	20	7471
POL	LOKQIKQNF	433	9	13	20	7472
POL	LOKQIKQNF	433	9	13	20	7473
POL	LOKQIKQNF	433	9	13	20	7474
POL	LOKQIKQNF	433	9	13	20	7475
POL	LOKQIKQNF	433	9	13	20	7476
POL	LOKQIKQNF	433	9	13	20	7477
POL	LOKQIKQNF	433	9	13	20	7478
POL	LOKQIKQNF	433	9	13	20	7479
POL	LOKQIKQNF	433	9	13	20	7480
POL	LOKQIKQNF	433	9	13	20	7481
POL	LOKQIKQNF	433	9	13	20	7482
POL	LOKQIKQNF	433	9	13	20	7483
POL	LOKQIKQNF	433	9	13	20	7484
POL	LOKQIKQNF	433	9	13	20	7485
POL	LOKQIKQNF	433	9	13	20	7486
POL	LOKQIKQNF	433	9	13	20	7487
POL	LOKQIKQNF	433	9	13	20	7488
POL	LOKQIKQNF	433	9	13	20	7489
POL	LOKQIKQNF	433	9	13	20	7490
POL	LOKQIKQNF	433	9	13	20	7491
POL	LOKQIKQNF	433	9	13	20	7492
POL	LOKQIKQNF	433	9	13	20	7493
POL	LOKQIKQNF	433	9	13	20	7494
POL	LOKQIKQNF	433	9	13	20	7495
POL	LOKQIKQNF	433	9	13	20	7496
POL	LOKQIKQNF	433	9	13	20	7497
POL	LOKQIKQNF	433	9	13	20	7498
POL	LOKQIKQNF	433	9	13	20	7499
POL	LOKQIKQNF	433	9	13	20	7500
POL	LOKQIKQNF	433	9	13	20	7501
POL	LOKQIKQNF	433	9	13	20	7502
POL	LOKQIKQNF	433	9	13	20	7503
POL	LOKQIKQNF	433	9	13	20	7504
POL	LOKQIKQNF	433	9	13	20	7505
POL	LOKQIKQNF	433	9	13	20	7506
POL	LOKQIKQNF	433	9	13	20	7507
POL	LOKQIKQNF	433	9	13	20	7508
POL	LOKQIKQNF	433	9	13	20	7509
POL	LOKQIKQNF	433	9	13	20	7510
POL	LOKQIKQNF	433	9	13	20	7511
POL	LOKQIKQNF	433	9	13	20	7512
POL	LOKQIKQNF	433	9	13	20	7513
POL	LOKQIKQNF	433	9	13	20	7514
POL	LOKQIKQNF	433	9	13	20	7515
POL	LOKQIKQNF	433	9	13	20	7516
POL	LOKQIKQNF	433	9	13	20	7517

Table XIV
 CATHY B62 Super Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SIQ ID NO.
POL	PVLPEKDSW	432	10	13	20	7561
POL	PLPEKDSW	434	10	13	20	7562
POL	VLPPEKDSW	434	10	13	20	7563
POL	EPKQGGQDW	520	10	13	20	7564
POL	EQAHILKTAV	919	10	13	20	7565
POL	VLEDINLPGRW	119	11	13	20	7566
POL	ILIEICCKKAI	149	11	13	20	7567
POL	QVLPPEKDSW	431	11	13	20	7568
POL	QVLPPEKDSW	431	11	13	20	7569
POL	QVLPPEKDSW	433	11	13	20	7570
POL	QVLPPEKDSW	433	11	13	20	7571
POL	KQGGQDWTYQI	523	11	13	20	7572
POL	LKKEKXYLWS	717	11	13	20	7573
POL	KLAKGRWPKTI	855	11	13	20	7574
POL	KQGGQDWTYQI	523	11	13	22	7575
POL	KQGGQDWTYQI	523	11	14	22	7576
POL	KQGGQDWTYQI	523	11	14	22	7577
POL	KQGGQDWTYQI	523	11	14	22	7578
POL	KQGGQDWTYQI	523	11	14	22	7579
POL	KQGGQDWTYQI	523	11	14	22	7580
POL	KQGGQDWTYQI	523	11	14	22	7581
POL	KQGGQDWTYQI	523	11	14	22	7582
POL	KQGGQDWTYQI	523	11	14	22	7583
POL	KQGGQDWTYQI	523	11	14	22	7584
POL	KQGGQDWTYQI	523	11	14	22	7585
POL	KQGGQDWTYQI	523	11	14	22	7586
POL	KQGGQDWTYQI	523	11	14	22	7587
POL	KQGGQDWTYQI	523	11	14	22	7588
POL	KQGGQDWTYQI	523	11	14	22	7589
POL	KQGGQDWTYQI	523	11	14	22	7590
POL	KQGGQDWTYQI	523	11	14	22	7591
POL	KQGGQDWTYQI	523	11	14	24	7592
POL	KQGGQDWTYQI	523	11	15	24	7593
POL	KQGGQDWTYQI	523	11	15	24	7594
POL	KQGGQDWTYQI	523	11	15	23	7595
POL	KQGGQDWTYQI	523	11	15	23	7596
POL	KQGGQDWTYQI	523	11	15	23	7597
POL	KQGGQDWTYQI	523	11	15	23	7598
POL	KQGGQDWTYQI	523	11	15	23	7599
POL	KQGGQDWTYQI	523	11	15	23	7600
POL	KQGGQDWTYQI	523	11	15	23	7601
POL	KQGGQDWTYQI	523	11	15	23	7602
POL	KQGGQDWTYQI	523	11	15	23	7603
POL	KQGGQDWTYQI	523	11	15	23	7604
POL	KQGGQDWTYQI	523	11	15	23	7605
POL	KQGGQDWTYQI	523	11	15	23	7606
POL	KQGGQDWTYQI	523	11	15	23	7607
POL	KQGGQDWTYQI	523	11	15	23	7608
POL	KQGGQDWTYQI	523	11	15	23	7609
POL	KQGGQDWTYQI	523	11	15	23	7610

Table XIV
 HIV P62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	SEQ ID NO.
POL	PKQETKAGAWV	584	11	15	23	7611
POL	IKALDSQSLV	625	11	15	23	7612
POL	EDVDKLYSAGV	738	11	15	23	7613
POL	LVSAGRKVLV	743	11	15	23	7614
POL	QLGCTLNF	179	8	16	25	7615
POL	QLEKEPV	620	8	16	25	7616
POL	QLEKEPV	620	8	16	25	7617
POL	QLEKEPV	620	8	16	25	7618
POL	QLEKEPV	620	8	16	25	7619
POL	YOLEKEPV	619	9	16	25	7620
POL	IOOEHGIPY	887	9	16	25	7621
POL	QLGCTLNF	179	10	16	25	7622
POL	EPFRKQNDI	358	10	16	25	7623
POL	TKRKLTV	378	8	17	27	7624
POL	NIHIVQYM	393	9	17	27	7625
POL	ELREHLKW	364	10	17	27	7626
POL	NDIVIVQYM	176	11	17	27	7627
POL	MLIQGCTLNF	176	11	17	27	7628
POL	NLKITGYAKM	540	10	18	29	7629
POL	SVYLDKDF	366	8	18	28	7630
POL	SVYLDKDF	366	8	18	28	7631
POL	TLWQRFLVTV	91	10	18	28	7632
POL	IGRNALTV	171	10	18	28	7633
POL	VPLDKDFRKY	307	10	18	28	7634
POL	NIGRNALTV	170	11	18	28	7635
POL	SVYLDKDF	366	11	18	28	7636
POL	ELREHLKW	471	11	18	28	7637
POL	ELVNOIEOLI	708	11	18	28	7638
POL	AMASDFNLPI	773	11	18	28	7639
POL	PLWKGPAKLW	985	11	18	28	7640
POL	PLDKDFRKY	308	9	19	30	7641
POL	ELVNOIEOLI	152	8	19	30	7642
POL	ELVNOIEOLI	152	8	19	30	7643
POL	LYNOIEOLI	709	10	19	30	7644
POL	LYSQUEOLI	709	10	19	30	7645
POL	ELGHIKAGTV	152	11	19	30	7646
POL	ELVNOIEOLI	708	11	19	30	7647
POL	SVYLDKDF	366	8	20	32	7648
POL	ROYDOLIEI	144	8	20	31	7649
POL	SOIEOLI	711	8	20	31	7650
POL	KLPIQKETW	582	9	20	31	7651
POL	KVRYDOLIEI	142	10	20	31	7652
POL	ROYDOLIEI	144	10	20	31	7653
POL	KLPIQKETW	582	11	20	31	7654
POL	LIKKEKVLW	711	11	20	31	7655
POL	TVKAAACWVAGI	877	11	20	31	7656
POL	KVHTDNGSNF	863	11	21	33	7657
POL	WQPLVTV	93	8	21	33	7658
POL	ELGHIKTV	383	9	21	33	7659
POL	ELVNOIEOLI	624	11	21	33	7660
POL	TLWQRFLVTV	91	10	21	33	7661

Table XIV
 HIV B67 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	IGRNLLTQI	171	10	21	33	7661
POL	EPVGAETFY	624	10	21	33	7662
POL	NIQRNLLTQI	170	11	21	33	7663
POL	EPVGAETFY	624	11	21	33	7664
POL	EPVGAETFY	624	11	21	33	7665
POL	EPVGAETFY	624	11	21	33	7666
POL	EPVGAETFY	624	11	21	33	7667
POL	EPVGAETFY	624	11	21	33	7668
POL	EPVGAETFY	624	11	21	33	7669
POL	EPVGAETFY	624	11	21	33	7670
POL	EPVGAETFY	624	11	21	33	7671
POL	EPVGAETFY	624	11	21	33	7672
POL	EPVGAETFY	624	11	21	33	7673
POL	EPVGAETFY	624	11	21	33	7674
POL	EPVGAETFY	624	11	21	33	7675
POL	EPVGAETFY	624	11	21	33	7676
POL	EPVGAETFY	624	11	21	33	7677
POL	EPVGAETFY	624	11	21	33	7678
POL	EPVGAETFY	624	11	21	33	7679
POL	EPVGAETFY	624	11	21	33	7680
POL	EPVGAETFY	624	11	21	33	7681
POL	EPVGAETFY	624	11	21	33	7682
POL	EPVGAETFY	624	11	21	33	7683
POL	EPVGAETFY	624	11	21	33	7684
POL	EPVGAETFY	624	11	21	33	7685
POL	EPVGAETFY	624	11	21	33	7686
POL	EPVGAETFY	624	11	21	33	7687
POL	EPVGAETFY	624	11	21	33	7688
POL	EPVGAETFY	624	11	21	33	7689
POL	EPVGAETFY	624	11	21	33	7690
POL	EPVGAETFY	624	11	21	33	7691
POL	EPVGAETFY	624	11	21	33	7692
POL	EPVGAETFY	624	11	21	33	7693
POL	EPVGAETFY	624	11	21	33	7694
POL	EPVGAETFY	624	11	21	33	7695
POL	EPVGAETFY	624	11	21	33	7696
POL	EPVGAETFY	624	11	21	33	7697
POL	EPVGAETFY	624	11	21	33	7698
POL	EPVGAETFY	624	11	21	33	7699
POL	EPVGAETFY	624	11	21	33	7700
POL	EPVGAETFY	624	11	21	33	7701
POL	EPVGAETFY	624	11	21	33	7702
POL	EPVGAETFY	624	11	21	33	7703
POL	EPVGAETFY	624	11	21	33	7704
POL	EPVGAETFY	624	11	21	33	7705
POL	EPVGAETFY	624	11	21	33	7706
POL	EPVGAETFY	624	11	21	33	7707
POL	EPVGAETFY	624	11	21	33	7708
POL	EPVGAETFY	624	11	21	33	7709
POL	EPVGAETFY	624	11	21	33	7710

Table XIV
 HIV-1 p62 Super Motif Peptides


Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KLVSQIRKV	742	10	26	41	7711
POL	NLPVVAKEI	779	10	26	41	7712
POL	RLQVQIRKAI	780	10	26	41	7713
POL	RLQVQIRKAI	781	10	26	41	7714
POL	LYSSGIRKYL	743	11	26	41	7715
POL	NLPVVAKEIV	779	11	26	41	7716
POL	QIVAGIRK	458	8	27	43	7717
POL	QIVPGIRK	458	8	27	43	7718
POL	QIVPGIRK	458	8	27	42	7719
POL	QIVPGIRK	458	8	27	42	7720
POL	QIVPGIRK	458	8	27	42	7721
POL	QIVPGIRK	458	8	27	42	7722
POL	PIVVAKEI	781	8	27	42	7723
POL	SIQVAGIRK	457	9	27	42	7724
POL	SIQVPGIRK	457	9	27	42	7725
POL	IQKETWETW	585	9	27	42	7726
POL	IQKETWETW	585	9	27	42	7727
POL	ALQDSGLEV	677	9	27	42	7728
POL	ALQDSGLEV	677	9	27	42	7729
POL	POKEIWEIWW	584	10	27	42	7730
POL	POKEIWEIWW	585	10	27	42	7731
POL	LODSGLEVNI	678	10	27	42	7732
POL	NLPVVAKEI	779	10	27	42	7733
POL	NLPVVAKEI	779	10	27	42	7734
POL	NLPVVAKEI	779	10	27	42	7735
POL	POKETWETW	584	11	27	42	7736
POL	YVTDGRQKVV	649	11	27	42	7737
POL	ALQDSGLEVNI	677	11	27	42	7738
POL	ALQDSGLEVNI	678	11	27	42	7739
POL	NLPVVAKEIV	779	11	27	42	7740
POL	NLPVVAKEIV	779	11	27	42	7741
POL	KIKALTEI	217	8	28	44	7742
POL	PIVGAETFF	625	8	28	44	7743
POL	IVGAETFF	626	8	28	44	7744
POL	OLIKKERK	716	8	28	44	7745
POL	OLIKKERK	782	8	28	44	7746
POL	PIVGAETFF	625	8	28	44	7747
POL	IVGAETFF	626	9	28	44	7748
POL	OLIKKERK	715	9	28	44	7749
POL	OLIKKERK	716	9	28	44	7750
POL	LPVVAKEI	780	9	28	44	7751
POL	LPVVAKEI	781	9	28	44	7752
POL	PIVGAETFF	625	10	28	44	7753
POL	PIVGAETFF	626	10	28	44	7754
POL	HEQIKKERK	713	11	28	44	7755
POL	PIVVAKEI	781	8	29	45	7756
POL	IDIHATDI	952	9	29	45	7757
POL	YVTDGRQKVV	649	10	29	45	7758
POL	YVTDGRQKVV	649	10	29	45	7759
POL	RIDHATDI	951	10	29	45	7760
POL	EQVDKLVSSGI	738	11	30	47	7761
POL	TPKRLPI	578	8	30	47	7762
POL	ILVAVIIV	824	8	30	47	7763

Table XIV
 HIV B62 Super-N motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHQ ID NO
POL	KILVAVIH	823	9	30	47	7761
POL	KLGVAVIV	823	10	55	47	7762
POL	KLGVAVIV	823	8	31	48	7763
POL	YOLEKEPI	846	8	31	48	7764
POL	GOETAYFI	846	8	31	48	7765
POL	ILEGRULV	819	9	31	48	7766
POL	IPSINNETGI	321	11	31	48	7767
POL	QVDFYSKLI	508	11	31	48	7768
POL	ILVAVIV	819	11	31	48	7769
POL	ILEGRULV	819	11	31	48	7770
POL	KOLTEAVOKI	558	10	32	51	7771
POL	AVKAAACWW	877	8	32	50	7772
POL	SINNETGI	323	9	32	50	7773
POL	ILVAVIV	823	9	32	50	7774
POL	ILVAVIV	823	9	32	50	7775
POL	SINNETGI	323	11	32	50	7776
POL	SINNETGI	323	11	32	50	7777
POL	FLKLAGRWIV	852	11	32	50	7778
POL	QLDCTILLEGKI	814	11	33	52	7779
POL	DVKQLTLAV	556	9	33	52	7780
POL	ELCOTI	964	9	34	54	7781
POL	KILVAVIV	823	9	34	54	7782
POL	KOTIKONERV	967	11	34	54	7783
POL	ILKLAGRW	853	8	34	53	7784
POL	QLTEAVOKI	559	9	34	53	7785
POL	ILKLAGRWIV	853	10	34	53	7786
POL	LQKQITIK	965	11	34	53	7787
POL	ILKLAGRW	853	11	34	53	7788
POL	LIKLEKVV	717	8	35	55	7789
POL	QTIKIQNF	968	8	35	55	7790
POL	NLPGKWKPKM	124	10	35	55	7791
POL	QITIKONERV	968	10	35	55	7792
POL	ILKLAGRW	853	11	35	55	7793
POL	QITIKONERV	968	11	35	55	7794
POL	PNWKGPAKLLW	985	11	35	55	7795
POL	KLKGKAGTV	643	8	36	56	7796
POL	LQKQITIK	965	8	36	56	7797
POL	ALFQSSMTKI	347	10	36	56	7798
POL	QVDFYSKLI	508	11	36	56	7799
POL	VIQDSDIH	1003	8	37	58	7800
POL	VVIQDSDIH	1002	9	37	58	7801
POL	NPYNTPFAL	243	10	37	58	7802
POL	QPDKSESELV	701	10	37	58	7803
POL	AVVIQDSDIH	1000	10	37	58	7804
POL	VLKSNVAKIKGI	724	10	37	58	7805
POL	VVIQDSDIH	1002	11	37	58	7806
POL	VVIQDSDIH	1002	11	37	58	7807
POL	NPYNTPFV	1003	11	37	58	7808
POL	NPYNTPFV	243	8	38	59	7809
POL	FOSSMTKI	349	8	38	59	7810
POL	IQDSDIH	1004	9	38	59	7811

Table XIV
 HIV-1 B6 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO
POL	GPENPNTPV	240	10	38	59	7811
POL	IDNSDKVY	1004	10	38	59	7812
POL	QENYNTVY	240	11	38	59	7813
POL	QENYNTVY	240	11	38	59	7814
POL	LFKQWPKM	125	9	39	61	7815
POL	LFKQWPKM	125	10	39	61	7816
POL	LFKQSWTV	435	9	40	63	7817
POL	ILKEPVHGV	498	10	40	63	7818
POL	ILKEPVHGV	497	11	40	63	7819
POL	ILKEPVHGV	497	11	40	63	7820
POL	QIGCTLNF	179	8	41	64	7821
POL	EPVIGVY	504	8	41	64	7822
POL	TQIGCTLNF	178	9	41	64	7823
POL	ILKEPVHGV	498	9	41	64	7824
POL	FKRYVDQI	140	10	41	64	7825
POL	FKRYVDQI	140	11	41	64	7826
POL	ELKEPVHGV	497	10	41	64	7827
POL	TQIGCTLNF	178	11	41	64	7828
POL	KISKIGPENY	235	11	41	64	7829
POL	SVYWGKTRF	571	11	41	64	7830
POL	SMKEGKGI	229	8	42	66	7831
POL	SMKEGKGI	229	8	42	66	7832
POL	NKTELOI	666	9	42	66	7833
POL	IVYGYMDLY	367	11	42	66	7834
POL	YQIQEPI	531	8	43	67	7835
POL	SMKLEIF	352	9	43	67	7836
POL	QMGDDCV	1027	8	44	69	7837
POL	QMGDDCV	1027	8	44	69	7838
POL	IQKELOKH	960	10	44	69	7839
POL	DIQKELOKH	959	11	44	69	7840
POL	EPKRLKTKY	536	11	45	70	7841
POL	DQAEHLKTV	919	10	46	72	7842
POL	LOCKETV	583	9	47	73	7843
POL	YQIQEPI	531	9	47	73	7844
POL	QTLWQPLV	89	10	47	73	7845
POL	IVWGKTRF	572	10	47	73	7846
POL	QTLWQPLV	88	11	47	73	7847
POL	KLFGMDGPKV	197	11	47	73	7848
POL	KLFGMDGPKV	197	11	47	73	7849
POL	IVWGKTRF	572	8	49	77	7850
POL	GLKKKSYV	288	10	49	77	7851
POL	GIRKVLFDGI	747	11	49	77	7852
POL	KVLFELDI	750	8	50	78	7853
POL	VPRKAKII	1013	9	50	78	7854
POL	YPRKAKII	1013	10	50	78	7855
POL	VPRKAKII	1012	10	50	78	7856
POL	KIRYDGKM	1019	10	50	78	7857
POL	HPAGLKKKSV	285	11	50	78	7858
POL	KVPRKAKII	1011	11	50	78	7859
POL	KIGPENY	238	8	51	80	7860

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	VPRKAKI	1013	8	51	80	7861
POL	KQMDGPKV	199	9	51	80	7862
POL	QKQKQKQKQ	1012	9	51	80	7863
POL	GADGPKKQW	201	10	51	80	7864
POL	TPGIRYQYN	328	10	51	80	7865
POL	VIVQYADLL	368	10	51	80	7866
POL	KVPRKAKI	1011	10	51	80	7867
POL	VLGPTPVNI	162	11	51	80	7868
POL	VWQKQKQKQ	1010	11	51	80	7869
POL	VWQKQKQKQ	602	11	51	80	7870
POL	WPRKQKQ	972	8	52	81	7871
POL	IONFRVY	288	8	52	81	7872
POL	GLKKKSV	328	8	52	81	7873
POL	TPGIRYQY	330	8	52	81	7874
POL	QIRYQYN	330	8	52	81	7875
POL	KQKQKQKQ	971	9	52	81	7876
POL	KQKQKQKQ	971	9	52	81	7877
POL	LVGPTPVNI	163	10	52	81	7878
POL	WQATWIPWEF	598	11	52	81	7879
POL	IVASGYEAEV	830	11	52	81	7880
POL	VLGPTPV	162	8	53	83	7881
POL	QKQKQKQ	1010	8	53	83	7882
POL	SPKQKQKQ	895	8	53	83	7883
POL	TVLVGPTV	161	9	53	83	7884
POL	AVIVASGY	828	9	53	83	7885
POL	SNKELKKI	905	9	53	83	7886
POL	VLGPTPVNI	162	10	53	83	7887
POL	ELKQKQKQ	424	10	53	83	7888
POL	ELKQKQKQ	424	10	53	83	7889
POL	LVAVIVASGY	826	10	53	83	7890
POL	POSGQVWESM	897	10	53	83	7891
POL	SNKELKKI	905	10	53	83	7892
POL	GQGHKQKQY	136	11	53	83	7893
POL	VLGPTPVNI	162	11	53	83	7894
POL	VLGPTPVNI	291	11	53	83	7895
POL	QKQKQKQKQ	796	11	53	83	7896
POL	ILVAVIVASGY	825	11	53	83	7897
POL	NPOSGQVWESM	896	11	53	83	7898
POL	FVNTPPLV	608	8	54	86	7899
POL	PNVQKQKQKQ	608	11	54	86	7900
POL	VLGPTPVNI	163	8	54	86	7901
POL	DVGDAVFSV	299	9	54	84	7902
POL	WQATWIPW	598	9	54	84	7903
POL	TPVPLKQKQ	193	10	54	84	7904
POL	PHSIEETVY	186	11	55	86	7905
POL	TPVPLKQKQ	187	11	55	86	7906
POL	SPETQVY	189	8	56	88	7907
POL	PVKKQKQ	195	8	56	88	7908
POL	WPLTEKI	211	8	56	88	7909
POL	PHSIEETV	186	9	56	88	7910

Table XIV
 HIV-160 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SHO ID NO.
POL	VFVKLPGM	194	9	56	88	7911
POL	FISPIETVPV	187	10	56	88	7912
POL	QWVTERK	209	10	56	88	7913
POL	SYDQVETV	209	11	56	88	7914
POL	FISPIETV	187	8	57	89	7915
POL	ELAEKREI	491	8	57	89	7916
POL	TPLVLKLV	611	8	57	89	7917
POL	PLPLVKLV	612	8	57	89	7918
POL	QYDCSPGI	805	8	57	89	7919
POL	ILNKRRTQDF	825	8	57	89	7920
POL	ELNKRRTQDF	268	9	57	89	7921
POL	TVLDVGDAY	296	9	57	89	7922
POL	TPLVLKLV	611	9	57	89	7923
POL	GOVDCSPGI	804	9	57	89	7924
POL	QYDCSPGI	805	9	57	89	7925
POL	ILNKRRTQDF	825	9	57	89	7926
POL	AIKKQSTKW	251	10	57	89	7927
POL	ELNKRRTQDF	268	10	57	89	7928
POL	TVLDVGDAY	296	10	57	89	7929
POL	GOVDCSPGI	804	10	57	89	7930
POL	ILNKRRTQDF	825	10	57	89	7931
POL	ILNKRRTQDF	825	11	57	89	7932
POL	GHGYSAGERI	942	11	57	89	7933
POL	LPGWKGSIM	338	11	58	92	7934
POL	YVGSDEL	377	8	58	91	7935
POL	DLYVGSDEL	375	10	58	91	7936
POL	INTDSOYALGI	687	11	58	91	7937
POL	ELNKRRTQDF	825	11	58	91	7938
POL	ELNKRRTQDF	933	11	58	91	7939
POL	SOYALGI	691	8	59	92	7940
POL	GIGGNEQV	733	8	59	92	7941
POL	AVIVASGY	828	8	59	92	7942
POL	KLGRWTV	855	8	59	92	7943
POL	NKQVGSIM	844	8	59	92	7944
POL	POGWKGSIM	339	10	59	92	7945
POL	ENVITDSQV	684	10	59	92	7946
POL	POGWKGSIM	339	11	59	92	7947
POL	IPYNQSGQVV	893	11	59	92	7948
POL	KLWKGEQAVV	962	11	59	92	7949
POL	KLWKGEQAVV	962	11	59	92	7950
POL	KLWKGEQAVV	130	8	60	94	7951
POL	KLWKGEQAVV	962	8	60	94	7952
POL	VLVDGDAY	297	8	60	94	7953
POL	AVQMAVH	927	8	60	94	7954
POL	VLVDGDAY	297	9	60	94	7955
POL	ELIDKWTV	422	9	60	94	7956
POL	QMAVTHNE	929	9	60	94	7957
POL	QMAVTHNE	928	10	60	94	7958
POL	KLWKGEQAVV	992	10	60	94	7959
POL	KPKMIGIGGF	130	11	60	94	7960

Table XIV
66 HIVB2 Super Motif Peptides 50

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WNGVELIPPKW	418	11	60	94	7961
POL	WNGVELIPPKW	418	11	60	94	7962
POL	AVOKNAVELINE	927	11	61	94	7963
POL	TLNFPISH	183	9	61	95	7964
POL	YQYMDLLY	370	8	61	95	7965
POL	KLINWASQI	452	8	61	95	7966
POL	YQYMDLLY	370	9	61	95	7967
POL	YQYMDLLY	370	9	61	95	7968
POL	LLWKSGGAVV	993	10	61	95	7969
POL	ALLDTGADDTV	109	11	61	95	7970
POL	MIGGIGGF	133	8	62	97	7971
POL	KLVLKLNW	448	8	62	97	7972
POL	NVITDSQY	686	8	62	97	7973
POL	MIGGIGGF	133	9	62	97	7974
POL	MIGGIGGF	133	9	62	97	7975
POL	HOKEPPELW	410	9	62	97	7976
POL	LLWKHEGAV	993	9	62	97	7977
POL	KMIGGIGGF	132	10	62	97	7978
POL	HOKEPPELW	410	10	62	97	7979
POL	LLWKHEGAV	993	10	62	97	7980
POL	MIGGIGGF	133	11	62	97	7981
POL	MIGGIGGF	133	11	62	97	7982
POL	DIGLKGKLNW	445	11	62	98	7983
POL	WVFAIKGI	727	8	63	98	7984
POL	EPPELWNGY	413	9	63	98	7985
POL	LLDTGADDTV	110	10	63	98	7986
POL	LLWKHEGAV	993	10	63	98	7987
POL	HYNPGSQGV	892	11	63	98	7988
POL	GIGGFHKV	136	8	64	100	7989
POL	PPLWNGY	414	8	64	100	7990
REV	POQTEIGV	101	8	05	18	7991
REV	POQTEIGV	101	8	05	18	7992
REV	QOQTEIGV	100	9	05	18	7993
REV	CLGRPAEIV	67	9	10	16	7994
REV	TQGVGSPIQ	98	9	11	18	7995
REV	LLKTVRLI	12	8	11	17	7996
REV	RQKQHSI	52	8	11	17	7997
REV	WVFAIKGI	727	8	11	17	7998
REV	PVPLQLPI	74	9	11	17	7999
REV	EPVFLQPLI	17	10	13	20	8000
REV	AVRIUKILY	39	11	16	25	8002
REV	ROARKNNRRRW	39	11	18	28	8003
REV	IKLQYSNFY	20	11	18	28	8004
REV	IKLQYSNFY	22	11	26	41	8005
REV	ILYQSNFY	23	8	27	50	8006
REV	ROARKNNRRRW	39	11	38	59	8007
TAT	GPESKKKV	90	13	13	20	8008
TAT	EPVDRLEFW	2	10	13	22	8009
TAT	FLNKGGLI	41	8	14	22	8010
TAT	PVDPLEFW	3	9	14	22	8010

Table XIV
 1-11-16 Super Motif Peptides

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
TAT	EPVPLPFW	2	10	14	22	8011
TAT	FUNGGLGIST	41	10	14	22	8012
VIF	PDPLPFW	3	9	20	31	8013
VIF	PLGGLPFW	157	9	10	16	8014
VIF	PLGGLRLVI	58	9	10	16	8015
VIF	QYDMRINTW	12	10	10	16	8016
VIF	IIPLGDLRLV	56	10	10	16	8017
VIF	IIPLGDLRLV	57	10	10	16	8018
VIF	WQYDRMLV	11	11	10	16	8019
VIF	WQYDRMLV	56	11	10	16	8020
VIF	GVSEWRLRY	87	11	10	16	8021
VIF	QIPLDLAQLI	102	11	10	16	8022
VIF	PLGDLRLV	58	8	11	17	8023
VIF	IIPLGDLRLV	57	9	11	17	8024
VIF	HEWRRLRY	89	9	11	17	8025
VIF	GLVYITW	65	11	10	17	8026
VIF	RLVYITW	65	8	12	19	8027
VIF	LOTGERDW	74	8	12	19	8028
VIF	KIRTWNSLV	17	9	12	19	8029
VIF	GLQTERDW	73	9	12	19	8030
VIF	WQYDRMKI	9	10	12	19	8031
VIF	WQYDRMKI	12	10	12	19	8032
VIF	WQYDRMKI	11	11	12	19	8033
VIF	RMKRTWNSLV	15	11	12	19	8034
VIF	WQYDRMKI	11	8	13	20	8035
VIF	IIPLKISSEV	48	8	13	20	8036
VIF	IIPLKISSEV	48	8	13	20	8037
VIF	IIPLKISSEV	48	8	13	20	8038
VIF	IIPLKISSEV	109	9	13	20	8039
VIF	IIPLKISSEV	109	9	13	20	8040
VIF	IIPLKISSEV	48	10	13	20	8041
VIF	IIPLKISSEV	48	10	13	20	8042
VIF	SVKSLTEDRW	174	10	13	20	8043
VIF	IIPLKISSEV	109	11	13	20	8044
VIF	IIPLKISSEV	109	8	14	22	8045
VIF	IIPLKISSEV	110	8	14	22	8046
VIF	IIPLKISSEV	110	8	14	22	8047
VIF	IIPLKISSEV	133	8	14	22	8048
VIF	IIPLKISSEV	109	9	14	22	8049
VIF	IIPLKISSEV	102	11	14	22	8050
VIF	IIPLKISSEV	102	11	14	22	8051
VIF	IIPLKISSEV	50	8	15	23	8052
VIF	IIPLKISSEV	50	8	15	23	8053
VIF	IIPLKISSEV	113	8	15	23	8054
VIF	IIPLKISSEV	17	9	15	23	8055
VIF	IIPLKISSEV	106	9	15	23	8056
VIF	IIPLKISSEV	106	9	15	23	8057
VIF	IIPLKISSEV	111	10	15	23	8058
VIF	IIPLKISSEV	15	11	15	23	8059
VIF	IIPLKISSEV	15	11	15	23	8060
VIF	IIPLKISSEV	113	8	16	25	8061

Table XIV
Sequence of Super-Nutrient Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	LHLVYDFCF	11	10	16	25	8061
VIF	LVKHIIMVY	14	8	19	30	8062
VIF	LVKHIIMVY	48	8	19	30	8063
VIF	PLGEARLV	58	8	19	30	8064
VIF	SLVKHIIMVY	23	9	19	30	8065
VIF	IPLGEARLV	57	9	19	30	8066
VIF	DPDLADQLI	104	9	19	30	8067
VIF	IPCLADQLI	104	9	19	30	8068
VIF	IPKLSSEVY	104	9	19	30	8069
VIF	IPKLSSEVY	48	10	19	30	8070
VIF	IPPLGEARLV	56	10	19	30	8071
VIF	KVSSSEVY	50	8	20	31	8072
VIF	LVKHIIMVY	24	8	21	33	8073
VIF	SLVKHIIMVY	23	9	21	33	8074
VIF	GLVGERVY	73	9	22	34	8075
VIF	GLVGERVY	83	8	22	34	8076
VIF	HLGIGVSEW	83	10	25	39	8077
VIF	HLGIGVSI	83	8	26	41	8078
VIF	GGGVSEW	85	8	26	41	8079
VIF	HLGGGVSEW	83	10	26	41	8080
VIF	SLQYLAIALI	149	11	27	42	8081
VIF	SLQYLAIALI	152	11	27	42	8082
VIF	LOYLALALI	150	10	28	44	8083
VIF	QYDRMRIRIY	12	10	31	48	8084
VIF	WQVDRMRIRIY	11	11	31	48	8085
VIF	YOAGINKY	140	8	38	59	8086
VIF	QYMWQVQY	6	8	43	67	8087
VIF	QYMWQVQY	5	8	43	67	8088
VIF	QYMWQVQY	6	11	43	67	8089
VIF	QYMWQVQY	8	11	43	67	8090
VIF	SLVKHIIMVY	23	8	44	69	8091
VIF	VAMVQVQY	7	10	44	69	8092
VIF	QYMWQVQY	8	9	46	72	8093
VIF	QYMWQVQY	9	10	46	72	8094
VIF	WQVDRM	11	8	48	75	8095
VIF	VWQVDRM	9	8	59	92	8096
VPR	RPWLHLGQY	36	10	10	16	8097
VPR	QQLFVIF	65	8	10	16	8098
VPR	EQQLLVIF	64	9	10	16	8099
VPR	QQLLVIF	65	10	10	16	8100
VPR	QQLLVIF	65	10	10	16	8101
VPR	QQLLVIF	64	11	10	16	8102
VPR	KQEAIRIF	27	8	11	17	8103
VPR	WLHLGQY	38	8	11	17	8104
VPR	RIGCRHSRIGI	74	11	11	17	8105
VPR	RPWLHLGQY	36	11	12	19	8106
VPR	QQLLVIF	65	8	12	19	8107
VPR	RIGCRHSRI	74	8	12	19	8108
VPR	QYHYNVY	43	8	13	20	8109
VPR	AVRHEPR	30	8	14	22	8110

Table XIV
 HIV-1 B2 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	GQYIVETV	43	8	14	22	8111
VPR	AVRIIFRW	30	9	14	22	8112
VPR	VNYTGDW	45	10	14	22	8113
VPR	WVLSAARH	45	10	14	22	8114
VPR	ELKSEAARH	25	10	15	21	8115
VPR	QQRSGH	77	9	16	25	8116
VPR	LLEELKEAV	22	10	16	25	8117
VPR	ELLEELKNEAV	21	11	16	25	8118
VPR	ELLEELKNEAV	11	11	16	25	8119
VPR	ELLEELKNEAV	1	11	16	25	8120
VPR	ELLEELKNEAV	22	10	17	27	8121
VPR	LLEELKNEAV	25	10	17	27	8122
VPR	ELKNEAVRIH	25	10	17	27	8123
VPR	HIYETGDTW	45	10	17	27	8124
VPR	WLHGLQHI	38	9	20	31	8125
VPR	WLHGLQHI	38	10	20	31	8126
VPR	WLHGLQHI	38	11	20	31	8127
VPR	WVLSAARH	45	10	34	53	8128
VPR	GVEARL	56	8	34	53	8129
VPR	AVRIIFRW	30	9	34	53	8130
VPR	RIQQLLFIH	62	11	34	53	8131
VPR	RIQQLLFIH	63	10	35	55	8132
VPR	RIQQLLFIH	62	9	36	56	8133
VPR	RIQQLLFIH	62	8	37	58	8134
VPR	POPEYNEW	10	9	37	58	8135
VPR	QQRSTYNEW	9	10	37	58	8136
VPR	AIIRLQQLF	59	11	38	59	8137
VPR	AIIRLQQLF	7	9	41	64	8138
VPR	AIIRLQQLF	60	10	41	64	8139
VPR	AIIRLQQLF	60	10	41	64	8140
VPR	LIHIFRI	67	8	44	69	8141
VPR	LIHIFRI	67	8	44	69	8142
VPR	LIHIFRI	66	9	44	69	8143
VPR	LIHIFRI	66	9	44	69	8144
VPR	LIHIFRI	65	10	44	69	8145
VPR	LIHIFRI	64	11	44	69	8146
VPR	LIHIFRI	62	11	45	70	8147
VPR	COISGHI	77	8	45	70	8148
VPR	RIGCOISGHI	74	11	45	70	8149
VPR	RIGCOISGHI	74	9	47	73	8150
VPR	KVDYRIV	7	8	01	33	8151
VPR	KVDYRIV	7	8	01	33	8152
VPR	KVDYRIV	7	8	01	33	8153
VPR	KVDYRIV	7	8	01	33	8154
VPR	KVDYRIV	7	8	01	33	8155
VPR	KVDYRIV	7	8	01	33	8156
VPR	KVDYRIV	7	8	01	33	8157
VPR	KVDYRIV	7	8	01	33	8158
VPR	KVDYRIV	7	8	01	33	8159
VPR	KVDYRIV	7	8	01	33	8160
VPR	KVDYRIV	7	8	01	33	8161
VPR	KVDYRIV	7	8	01	33	8162
VPR	KVDYRIV	7	8	01	33	8163
VPR	KVDYRIV	7	8	01	33	8164
VPR	KVDYRIV	7	8	01	33	8165
VPR	KVDYRIV	7	8	01	33	8166
VPR	KVDYRIV	7	8	01	33	8167
VPR	KVDYRIV	7	8	01	33	8168
VPR	KVDYRIV	7	8	01	33	8169
VPR	KVDYRIV	7	8	01	33	8170
VPR	KVDYRIV	7	8	01	33	8171
VPR	KVDYRIV	7	8	01	33	8172
VPR	KVDYRIV	7	8	01	33	8173
VPR	KVDYRIV	7	8	01	33	8174
VPR	KVDYRIV	7	8	01	33	8175
VPR	KVDYRIV	7	8	01	33	8176
VPR	KVDYRIV	7	8	01	33	8177
VPR	KVDYRIV	7	8	01	33	8178
VPR	KVDYRIV	7	8	01	33	8179
VPR	KVDYRIV	7	8	01	33	8180
VPR	KVDYRIV	7	8	01	33	8181
VPR	KVDYRIV	7	8	01	33	8182
VPR	KVDYRIV	7	8	01	33	8183
VPR	KVDYRIV	7	8	01	33	8184
VPR	KVDYRIV	7	8	01	33	8185
VPR	KVDYRIV	7	8	01	33	8186
VPR	KVDYRIV	7	8	01	33	8187
VPR	KVDYRIV	7	8	01	33	8188
VPR	KVDYRIV	7	8	01	33	8189
VPR	KVDYRIV	7	8	01	33	8190
VPR	KVDYRIV	7	8	01	33	8191
VPR	KVDYRIV	7	8	01	33	8192
VPR	KVDYRIV	7	8	01	33	8193
VPR	KVDYRIV	7	8	01	33	8194
VPR	KVDYRIV	7	8	01	33	8195
VPR	KVDYRIV	7	8	01	33	8196
VPR	KVDYRIV	7	8	01	33	8197
VPR	KVDYRIV	7	8	01	33	8198
VPR	KVDYRIV	7	8	01	33	8199
VPR	KVDYRIV	7	8	01	33	8200
VPR	KVDYRIV	7	8	01	33	8201
VPR	KVDYRIV	7	8	01	33	8202
VPR	KVDYRIV	7	8	01	33	8203
VPR	KVDYRIV	7	8	01	33	8204
VPR	KVDYRIV	7	8	01	33	8205
VPR	KVDYRIV	7	8	01	33	8206
VPR	KVDYRIV	7	8	01	33	8207
VPR	KVDYRIV	7	8	01	33	8208
VPR	KVDYRIV	7	8	01	33	8209
VPR	KVDYRIV	7	8	01	33	8210
VPR	KVDYRIV	7	8	01	33	8211
VPR	KVDYRIV	7	8	01	33	8212
VPR	KVDYRIV	7	8	01	33	8213
VPR	KVDYRIV	7	8	01	33	8214
VPR	KVDYRIV	7	8	01	33	8215
VPR	KVDYRIV	7	8	01	33	8216
VPR	KVDYRIV	7	8	01	33	8217
VPR	KVDYRIV	7	8	01	33	8218
VPR	KVDYRIV	7	8	01	33	8219
VPR	KVDYRIV	7	8	01	33	8220
VPR	KVDYRIV	7	8	01	33	8221
VPR	KVDYRIV	7	8	01	33	8222
VPR	KVDYRIV	7	8	01	33	8223
VPR	KVDYRIV	7	8	01	33	8224
VPR	KVDYRIV	7	8	01	33	8225
VPR	KVDYRIV	7	8	01	33	8226
VPR	KVDYRIV	7	8	01	33	8227
VPR	KVDYRIV	7	8	01	33	8228
VPR	KVDYRIV	7	8	01	33	8229
VPR	KVDYRIV	7	8	01	33	8230
VPR	KVDYRIV	7	8	01	33	8231
VPR	KVDYRIV	7	8	01	33	8232
VPR	KVDYRIV	7	8	01	33	8233
VPR	KVDYRIV	7	8	01	33	8234
VPR	KVDYRIV	7	8	01	33	8235
VPR	KVDYRIV	7	8	01	33	8236
VPR	KVDYRIV	7	8	01	33	8237
VPR	KVDYRIV	7	8	01	33	8238
VPR	KVDYRIV	7	8	01	33	8239
VPR	KVDYRIV	7	8	01	33	8240
VPR	KVDYRIV	7	8	01	33	8241
VPR	KVDYRIV	7	8	01	33	8242
VPR	KVDYRIV	7	8	01	33	8243
VPR	KVDYRIV	7	8	01	33	8244
VPR	KVDYRIV	7	8	01	33	8245
VPR	KVDYRIV	7	8	01	33	8246
VPR	KVDYRIV	7	8	01	33	8247
VPR	KVDYRIV	7	8	01	33	8248
VPR	KVDYRIV	7	8	01	33	8249
VPR	KVDYRIV	7	8	01	33	8250
VPR	KVDYRIV	7	8	01	33	8251
VPR	KVDYRIV	7	8	01	33	8252
VPR	KVDYRIV	7	8	01	33	8253
VPR	KVDYRIV	7	8	01	33	8254
VPR	KVDYRIV	7	8	01	33	8255
VPR	KVDYRIV	7	8	01	33	8256
VPR	KVDYRIV	7	8	01	33	8257
VPR	KVDYRIV	7	8	01	33	8258
VPR	KVDYRIV	7	8	01	33	8259
VPR	KVDYRIV	7	8	01	33	8260
VPR	KVDYRIV	7	8	01	33	8261
VPR	KVDYRIV	7	8	01	33	8262
VPR	KVDYRIV	7	8	01	33	8263
VPR	KVDYRIV	7	8	01	33	8264
VPR	KVDYRIV	7	8	01	33	8265
VPR	KVDYRIV	7	8	01	33	8266
VPR	KVDYRIV	7	8	01	33	8267
VPR	KVDYRIV	7	8	01	33	8268
VPR	KVDYRIV	7	8	01	33	8269
VPR	KVDYRIV	7	8	01	33	8270
VPR	KVDYRIV	7	8	01	33	8271
VPR	KVDYRIV	7	8	01	33	8272
VPR	KVDYRIV	7	8	01	33	8273
VPR	KVDYRIV	7	8	01	33	8274
VPR	KVDYRIV	7	8	01	33	8275
VPR	KVDYRIV	7	8	01	33	8276
VPR	KVDYRIV	7	8	01	33	8277
VPR	KVDYRIV	7	8	01	33	8278
VPR	KVDYRIV	7	8	01	33	8279
VPR	KVDYRIV	7	8	01	33	8280
VPR	KVDYRIV	7	8	01	33	8281
VPR	KVDYRIV	7	8	01	33	8282
VPR	KVDYRIV	7	8	01	33	8283
VPR	KVDYRIV	7	8	01	33	8284
VPR	KVDYRIV	7	8	01	33	8285
VPR	KVDYRIV	7	8	01	33	8286
VPR	KVDYRIV	7	8	01	33	8287
VPR	KVDYRIV	7	8	01	33	8288
VPR	KVDYRIV	7	8	01	33	8289
VPR	KVDYRIV	7	8	01	33	8290
VPR	KVDYRIV	7	8	01	33	8291
VPR	KVDYRIV	7	8	01	33	8292
VPR	KVDYRIV	7	8	01	33	8293
VPR	KVDYRIV	7	8	01	33	8294
VPR	KVDYRIV	7	8	01	33	8295
VPR	KVDYRIV	7	8	01	33	8296
VPR	KVDYRIV	7	8	01	33	8297
VPR	KVDYRIV	7	8	01	33	8298
VPR	KVDYRIV	7	8	01	33	8299
VPR	KVDYRIV	7	8	01	33	8300
VPR	KVDYRIV	7	8	01	33	8301
VPR	KVDYRIV	7	8	01	33	8302
VPR	KVDYRIV	7	8	01	33	8303
VPR	KVDYRIV	7	8	01	33	8304
VPR	KVDYRIV	7	8	01	33	8305
VPR	KVDYRIV	7	8	01	33	8306
VPR	KVDYRIV	7	8	01	33	8307
VPR	KVDYRIV	7	8	01	33	8308
VPR	KVDYRIV	7	8	01	33	8309
VPR	KVDYRIV	7	8	01	33	8310
VPR	KVDYRIV	7	8	01	33	8311
VPR	KVDYRIV	7	8	01	33	8312
VPR	KVDYRIV	7	8	01	33	8313
VPR	KVDYRIV	7	8	01	33	8314
VPR	KVDYRIV	7	8	01	33	8315
VPR	KVDYRIV	7	8	01	33	8316
VPR	KVDYRIV	7	8	01	33	8317
VPR	KVDYRIV	7	8	01	33	8318
VPR	KVDYRIV	7	8	01	33	8319
VPR	KVDYRIV	7	8	01	33	8320
VPR	KVDYRIV	7	8	01	33	8321
VPR	KVDYRIV	7	8	01	33	8322
VPR	KVDYRIV	7	8	01	33	8323
VPR	KVDYRIV	7	8	01	33	8324
VPR	KVDYRIV	7	8	01	33	8325
VPR	KVDYRIV	7	8	01	33	8326
VPR	KVDYRIV	7	8	01	33	8327
VPR	KVDYRIV	7	8	01	33	8328
VPR	KVDYRIV	7	8	01	33	8329
VPR	KVDYRIV	7	8	01	33	8330
VPR	K					

Table XIV
 GHV-B62 Super-Model Peptides 60

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VP1	IVRIEYKLI	36	9	12	19	8161
VP1	VVITIVIEY	31	10	12	19	8162
VP1	IVVITIVIEY	30	11	12	19	8163
VP1	ILRQRKIDRLI	46	11	13	20	8164
VP1	AIIVVITIVF	29	9	14	22	8165
VP1	KIDRLIDRI	52	10	14	22	8166
VP1	IVVITIVIEY	36	10	14	22	8167
VP1	AIIVVITIVF	30	8	15	23	8168
VP1	VVITIVIEY	31	8	15	23	8169
VP1	KILRQKI	45	8	15	23	8170
VP1	IVVITIVIEY	30	9	15	23	8171
VP1	RQRKIDRLI	48	9	17	31	8172
VP1	IIAIVVITIV	27	9	20	31	8173
VP1	IIAIVVITIV	28	9	23	36	8174
VP1	AIIVVITIV	29	8	29	45	8175

Table XV
 HIV-1 *gag* Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
ENV	IGSQAPFY	361	8	01	25		8176
ENV	GKDWYVY	42	9	01	33		8177
ENV	GDWVWYV	42	10	01	33		8178
ENV	MTSPSRVAY	376	10	01	33		8179
ENV	GTAGNSRRAA	375	11	01	33		8180
ENV	DSNSSTGNY	218	9	01	20		8181
ENV	TNSSTYNDTY	458	10	01	17		8182
ENV	WDTHTWLW	767	10	01	16		8183
ENV	WDTHTWLV	767	11	01	16		8184
ENV	WDTHTWLVN	723	12	01	17		8185
ENV	EWRETDNY	723	9	11	23		8186
ENV	NMWQEVGKA	494	11	15	23		8187
ENV	ISHNCRGIEFF	434	11	16	28		8188
ENV	WQEVGRKAMY	496	9	18	28		8189
ENV	VSELPPIHY	253	10	28	44		8190
ENV	ISVSEPHIHY	252	11	28	44		8191
ENV	SPVSRVAV	252	9	33	52		8192
ENV	LDARVAVR	662	11	33	52		8193
ENV	LSVNVVRQGY	797	11	34	53		8194
ENV	RSCLUSY	858	8	35	55		8195
ENV	LRSLCLUSY	857	9	35	55		8196
ENV	SRPCCGGRHY	454	11	35	55		8197
ENV	DRPCCGGRHY	454	11	35	55		8198
ENV	MRDNRWSELY	553	10	40	63	0.0010	8199
ENV	CASDAKAY	67	8	42	66		8200
ENV	TCASDAKAY	66	9	42	66		8201
ENV	WRSELYKY	557	8	54	84		8202
ENV	ETDKDLY	537	8	01	25		8203
ENV	ETDKDLY	538	8	01	25		8204
GAG	KQETDKELY	535	10	01	25		8205
GAG	KQETDKELY	535	10	01	25		8206
GAG	AADKGVSNQY	130	10	01	50		8207
GAG	ASAGQDLKGG	392	11	01	50		8208
GAG	ATAQDLKGG	392	11	01	50		8209
GAG	ADKGVSNQY	129	10	04	18		8210
GAG	EADEKGVSNQY	129	10	04	18		8211
GAG	GNSGVSNQY	140	10	12	23		8212
GAG	KQETDKELY	531	10	12	19		8213
GAG	SEELRSLY	74	8	12	19		8214
GAG	GSEELRSLY	73	9	12	19		8215
GAG	SEELRSLY	74	10	14	31		8216
GAG	NSGVSNQY	144	9	14	31		8217
GAG	SSGVSNQY	145	8	15	24		8218
GAG	RSLYNTVATL	78	11	15	31		8219
GAG	FRDYVDREY	317	9	29	45	0.0900	8220
GAG	PKREFRDY	313	8	63	98		8221
NEF	IMAKELHREY	320	10	10	16		8222
NEF	IMAKELHREY	320	11	10	16		8223
NEF	ARELLIREY	322	11	17	17		8224
NEF	YTPGVGIRY	207	9	17	27		8225
NEF	RQDILLVWV	182	10	20	31		8226

Table XV
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (P)	A*101	SEG ID NO
NEF	ARELIQRYV	322	9	21	33		8226
NEF	ARELIQRYV	322	8	24	36		8227
NEF	ROELDLVVV	182	10	32	50		8228
POL	TWETWATDY	589	9	10	16		8229
POL	TWETWATDY	589	9	10	16		8230
POL	ETWETWATDY	588	10	10	16		8231
POL	ETWETWATDY	588	10	10	16		8232
POL	ARELIQRYV	726	8	11	17		8233
POL	ISRIQSPENY	236	11	11	17		8234
POL	KSRIGPENY	235	11	11	17		8235
POL	SINNETGIRY	323	11	11	17		8236
POL	KTELQAIY	668	8	12	19		8237
POL	GDQNTYQIV	525	10	12	19		8238
POL	ADQELQRYV	728	8	12	23		8239
POL	ADQELQRYV	728	8	12	23		8240
POL	ADQELQRYV	728	8	12	23		8241
POL	NDIVIVQY	364	9	17	27	0.0011	8242
POL	PLDKDKRYV	308	9	19	30		8243
POL	QZELGPY	888	8	20	32		8244
POL	NPEIVQY	364	9	23	36		8245
POL	ADQELQRYV	728	8	25	39		8246
POL	ADQELQRYV	728	8	25	39		8247
POL	KQELGPY	888	8	28	44		8248
POL	NREIKLGKAG	639	11	35	55		8249
POL	ETKLGKAGY	641	9	35	55	0.0010	8250
POL	ITKQNFYV	969	10	36	57	0.0010	8251
POL	ITKQNFYV	969	10	36	57	0.0010	8252
POL	ITKQNFYV	969	10	36	57	0.0010	8253
POL	LKEPMQYV	502	9	41	64	0.0007	8254
POL	KKAKIRDY	1016	9	41	64		8255
POL	KSRIGPENY	235	11	41	64		8256
POL	ISKIGPENY	236	10	42	66	0.0130	8257
POL	NNEITGIRY	323	9	51	80	0.0007	8258
POL	ETPQRQYV	327	11	52	81	0.0052	8259
POL	LVAIVIVASGY	826	10	53	83	0.0380	8260
POL	VTVDVGDAY	295	10	56	88	0.2800	8261
POL	NTPLVKLWY	610	10	57	89	0.0041	8262
POL	PAETUGQETV	842	10	58	91		8263
POL	PAETUGQETV	842	10	58	91		8264
POL	ETGQETVAY	844	8	59	92	0.0130	8265
POL	VLDVGDAY	297	8	60	94		8266
POL	QKEPELWMG	411	11	63	98	0.0004	8267
VIF	GYSIEWRLRR	87	11	10	16		8268
VIF	SIWRLRRY	89	9	11	17		8269
VIF	SIWRLRRY	89	9	11	17		8270
VIF	GLADLIIMH	106	10	11	17		8271
VIF	GLADLIIMH	107	10	13	20		8272
VIF	IVSPREY	133	8	14	22		8273
VIF	LADQLIILY	107	10	14	22		8274
VIF	LADQLIILY	107	9	15	23		8275

Table XV
HIV A01 Motif Epitopes with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
VIF	KSLVKHIMV	22	9	18	28		8276
VIF	NSLKKHIM	21	10	18	28		8277
VIF	NSLKKHIM	22	9	24	38		8278
VIF	NSLKKHIM	21	10	24	38		8279
VIF	WNSLKKHIM	21	10	37	38		8280
VPR	PELDGQREPY	5	11	12	19		8281
VPV	WTIVFIEY	34	8				

HIV-1 Gag Motif Peptides with Binding Information
Table XVI

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	GIGGQTF	360	8	01	33		8282
ENV	SIGSGQAF	360	8	01	33		8283
ENV	IGGQTFY	361	8	01	25		8284
ENV	IGGQTFY	361	8	01	25		8285
ENV	IGGQTFY	375	8	01	33		8286
ENV	TAGNSRA	376	8	01	33		8287
ENV	KLREIQF	405	8	01	25		8288
ENV	ADNLWTVY	42	9	01	33		8289
ENV	GIGGQTFY	360	9	01	33		8290
ENV	SIGSGQAF	360	9	01	33		8291
ENV	IGGQTFY	361	9	01	25		8292
ENV	GTAGNSRA	375	9	01	33		8293
ENV	NTPSRIVA	376	9	01	33		8294
ENV	TAGNSRAA	376	9	01	33		8295
ENV	ADNLWTVY	42	10	01	33		8296
ENV	EGKRGDTY	217	10	01	33		8297
ENV	EGKRGDTY	217	10	01	33		8298
ENV	GTAGNSRA	375	10	01	33		8299
ENV	NTPSRIVA	376	10	01	33		8300
ENV	TAGNSRAA	376	10	01	33		8301
ENV	FGLGALFLG	597	10	01	33		8302
ENV	VLGGALFLG	577	10	01	33		8303
ENV	GTAGNSRA	375	11	01	25		8304
ENV	KLREIQENK	405	11	01	25		8305
ENV	QLYATVYA	34	8	01	50		8306
ENV	INIHITH	584	8	01	50		8307
ENV	VISTRITIR	584	8	01	50		8308
ENV	STRTHREK	586	8	01	50		8309
ENV	STRTHREK	586	8	01	50		8310
ENV	INIHITH	584	9	01	50		8311
ENV	ISTRTHREK	585	9	01	50		8312
ENV	NHTPHREK	586	9	01	50		8313
ENV	STRTHREK	586	9	01	50		8314
ENV	STRTHREK	586	10	01	50		8315
ENV	ISTRTHREK	585	10	01	50		8316
ENV	NHTPHREK	586	10	01	50		8317
ENV	STRTHREK	586	10	01	50		8318
ENV	ITTEGNTLQCR	478	11	01	50		8319
ENV	NAMTHPCRK	478	11	01	50		8320
ENV	NHTPHREK	586	11	01	50		8321
ENV	VISTRTHREK	585	11	01	50		8322
ENV	ISTRTHREK	585	11	01	50		8323
ENV	NHTPHREK	586	11	01	50		8324
ENV	VISTGNSA	161	8	01	20		8325
ENV	DSNSTGNY	218	9	01	20		8326
ENV	SINGLETIF	537	8	01	17		8327
ENV	STRTHREK	586	9	01	17		8328
ENV	NHTPHREK	537	10	01	17		8329
ENV	NTEKNTIEF	537	10	01	17		8330
ENV	NTEKNTIEF	537	10	01	17		8331

Table XVI
HIV-AIDS Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	NDIENKTEIF	537	11	01	17		8332
ENV	NTEINKTEIF	537	11	01	17		8333
ENV	NTGNTETIF	537	10	02	17		8334
ENV	NGSENGTEIF	537	10	02	33		8335
ENV	NGSENGTEIF	537	9	02	33		8336
ENV	NGSENGTEIF	538	10	02	18		8337
ENV	CSSENGTEIF	538	10	02	18		8338
ENV	TIGAMFELG	599	9	03	27		8339
ENV	NDITLPCR	477	9	03	20		8340
ENV	NDITLPCR	477	11	03	20		8341
ENV	MLGAMTLOF	399	9	04	36		8342
ENV	MLGAMTLOF	399	8	04	36		8343
ENV	KGLRLGWEGI	891	11	08	27		8344
ENV	LQWEGLY	895	8	09	29		8345
ENV	RLQWEGLY	894	9	09	29		8346
ENV	GLRLQWEGLY	892	11	09	29		8347
ENV	GLRLQWEGLY	883	10	09	15		8348
ENV	LQRRGWEGLY	882	11	09	15		8349
ENV	ELGIDRQA	372	9	09	15		8350
ENV	LGLGVICS-A	21	11	09	15		8351
ENV	TGELGIDRQA	370	11	09	15		8352
ENV	RLQWEGLY	894	8	10	32		8353
ENV	GLQWEGLY	892	10	10	32		8354
ENV	GLQWEGLY	892	9	10	32		8355
ENV	LLGRGWEEA	882	9	10	16		8356
ENV	DHGDQRQAI	372	10	10	16		8357
ENV	ELLGRGWEEA	881	10	10	16		8358
ENV	TGHDGDRQA	370	11	10	16		8359
ENV	GLGVICS-A	28	8	10	16		8360
ENV	GLGVICS-A	28	8	10	16		8361
ENV	PLGVAPTR	571	8	10	16		8362
ENV	LGVAPTR	572	8	10	16		8363
ENV	DTNWLRY	769	8	10	16		8364
ENV	RDPLIAA	869	8	10	16		8365
ENV	RDPLIAA	870	8	10	16		8366
ENV	DTNWLRY	921	8	10	16		8367
ENV	LGLGVICS-A	27	9	10	16		8368
ENV	STTQACPK	243	9	10	16		8369
ENV	IGRCQTFFA	358	9	10	16		8370
ENV	FDITNWLRY	768	9	10	16		8371
ENV	RDPLIAA	869	9	10	16		8372
ENV	RDPLIAA	870	9	10	16		8373
ENV	ILGLGVICS-A	26	10	10	16		8374
ENV	LLGLMLICS-A	26	10	10	16		8375
ENV	PHYCTPAGF	260	10	10	16		8376
ENV	FAIKCNDKK	269	10	10	16		8377
ENV	RGPQQTFFA	357	10	10	16		8378
ENV	RDPLIAA	870	10	10	16		8379
ENV	RVLAVERYLR	665	10	10	16		8380
ENV	WFDITNWLRY	767	10	10	16		8381

Table XVI
HIV-1 Modif. Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0.01	SEQ ID NO
ENV	EGIEEGGER	828	10	10	16		8382
ENV	GHYCTPAGRA	260	11	10	16		8383
ENV	GHYCTPAGRA	260	11	10	16		8384
ENV	PAIKGNDSKE	269	11	10	16		8385
ENV	GDIGDIRQAH	371	11	10	16		8386
ENV	NVTPNSWSN	693	11	10	16		8387
ENV	WMEWEREDN	723	11	10	16		8388
ENV	NSVSLDNAT	916	11	10	16		8389
ENV	NSVSLDNAT	916	11	10	16		8390
ENV	RGWEALYK	888	8	11	18		8391
ENV	GIGAVELGF	598	9	11	18		8392
ENV	KLWTVVYV	44	8	11	17		8393
ENV	AYGIGAVF	595	8	11	17		8394
ENV	RAVGIGAVF	594	9	11	17		8395
ENV	AYGIGAVF	595	11	11	17		8396
ENV	YIGIGAVF	244	8	11	17		8397
ENV	YCTPAGRA	263	8	11	17		8398
ENV	RIGGGQTF	357	8	11	17		8399
ENV	IGPGQTFY	358	8	11	17		8400
ENV	LFLGELGA	603	8	11	17		8401
ENV	AVRYEYLR	667	8	11	17		8402
ENV	NSVSLDNAT	916	8	11	17		8403
ENV	SAVSLNA	917	8	11	17		8404
ENV	VSLNATA	919	8	11	17		8405
ENV	LGMMLCSA	27	9	11	17		8406
ENV	RIGPGQTFY	357	9	11	17		8407
ENV	YCTPAGRA	263	9	11	17		8408
ENV	YCTPAGRA	263	9	11	17		8409
ENV	ALFLGELGA	603	9	11	17		8410
ENV	LFLGELGA	603	9	11	17		8411
ENV	VLAVERYLR	666	9	11	17		8412
ENV	ISNWLWYIK	770	9	11	17		8413
ENV	NLCFSYHK	839	9	11	17		8414
ENV	NSVSLDNAT	916	9	11	17		8415
ENV	GDIGDIRQAH	371	10	11	17		8416
ENV	ETITISINCR	430	10	11	17		8417
ENV	VGIGAVELGF	596	10	11	17		8418
ENV	GALFLGELGA	601	10	11	17		8419
ENV	ALFLGELGA	602	10	11	17		8420
ENV	NSVSLDNAT	916	10	11	17		8421
ENV	VSLNATA	919	10	11	17		8422
ENV	YATGIDGIR	268	11	11	17		8423
ENV	GALFLGELGA	601	11	11	17		8424
ENV	ISNWLWYIKF	770	11	11	17		8425
ENV	DLNLCLFSYH	836	11	11	17		8426
ENV	NLCFSYHKL	839	11	11	17		8427
ENV	NSVSLDNAT	916	11	11	17		8428
ENV	PTIRIGELRA	951	11	11	17		8429
ENV	TGIDIGDIR	370	11	12	19		8430
ENV	DIIGDIRQA	372	9	12	19		8431

Table XVI
HIV-1 M13 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A *0.001	SEQ ID NO.
ENV	EAQDILK	646	8	12	19		8432
ENV	GLMUSCA	78	8	12	19		8433
ENV	ILKNDKK	271	8	12	19		8434
ENV	THSNCR	432	8	12	19		8435
ENV	IGAVFLGF	600	8	12	19		8436
ENV	MTWMEWER	721	8	12	19		8437
ENV	GLMUSCA	74	8	12	19		8438
ENV	ILKNDKK	271	9	12	19		8439
ENV	ILKNDKKE	271	9	12	19		8440
ENV	LAEEVVR	312	9	12	19		8441
ENV	AMFLGLGA	602	9	12	19	0.0002	8442
ENV	NMTWMEWER	720	9	12	19		8443
ENV	HEEGGGR	829	9	12	19		8444
ENV	GLMUSCA	78	9	12	19		8445
ENV	RSILVNGF	841	9	12	19		8446
ENV	WGDLKNSA	910	9	12	19		8447
ENV	WSQLKNSA	910	9	12	19		8448
ENV	KTLFLCASA	60	10	12	19		8449
ENV	ALKNDKKE	270	10	12	19		8450
ENV	GLMUSCA	78	10	12	19		8451
ENV	ATGDHGR	360	10	12	19		8452
ENV	INNAWQVGR	492	10	12	19		8453
ENV	GAMFLGLGA	601	10	12	19		8454
ENV	AMFLGLGA	602	10	12	19		8455
ENV	ALQAQDILK	644	10	12	19		8456
ENV	GLMUSCA	78	10	12	19		8457
ENV	SRLVSGFLA	842	10	12	19		8458
ENV	SRLVSGFLA	842	10	12	19		8459
ENV	LLOYWSQELK	906	10	12	19		8460
ENV	ALIHPRKR	946	10	12	19		8461
ENV	PTIRQGLR	951	10	12	19		8462
ENV	KTLFLCASA	60	11	12	19		8463
ENV	SLLEWQVGR	491	11	12	19		8464
ENV	TSFSCGGE	432	11	12	19		8465
ENV	QINNAWQVGR	491	11	12	19		8466
ENV	INNAWQVGR	492	11	12	19		8467
ENV	GAMFLGLGA	601	11	12	19		8468
ENV	ITKWLWYKIF	770	11	12	19		8469
ENV	HEEGGGR	829	11	12	19		8470
ENV	GLMUSCA	78	11	12	19		8471
ENV	NLLOYWSQEL	905	11	12	19		8472
ENV	RAILHIPRER	945	11	12	19		8473
ENV	NTSVITQA	241	8	13	20		8474
ENV	SVENCTR	340	8	13	20		8475
ENV	ODIGDIR	371	8	13	20		8476
ENV	GLMUSCA	78	8	13	20		8477
ENV	KLVYGRK	653	8	13	20		8478
ENV	SRLVNGF	842	8	13	20		8479
ENV	SRLVSGF	842	8	13	20		8480
ENV	RLVNGFLA	844	8	13	20		8481
ENV	RAILHIPR	945	8	13	20		8482

Table XVI
 HIV-1 X3 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	ALIHRR	946	8	13	20		8482
ENV	KARRVQVR	579	9	13	20	0.0002	8483
ENV	SLGAGVA	843	9	13	20		8484
ENV	PSILSGF	844	9	13	20		8485
ENV	RALIUPRR	945	9	13	20		8486
ENV	ILIHRR	947	9	13	20		8487
ENV	SGGDEPMH	425	10	13	20		8488
ENV	LEKLYWGR	651	10	13	20		8489
ENV	SLGAGVA	843	9	13	20		8490
ENV	CTNSVQCT	385	11	13	20		8491
ENV	SGGDELETH	424	11	13	20		8492
ENV	SGGDEPMH	424	11	13	20		8493
ENV	VMSFNCGE	432	11	13	20		8494
ENV	PTKARRVQ	576	11	13	20		8495
ENV	KARRVQVR	579	11	13	20		8496
ENV	ILKLYWGR	649	11	13	20		8497
ENV	VGGELGRIF	784	11	13	20		8498
ENV	SLLNATAIYA	920	11	13	20		8499
ENV	TGEIGDIR	370	9	14	23		8500
ENV	NTSAITQA	241	8	14	22		8501
ENV	ATQACPK	244	8	14	22		8502
ENV	GVHPEPMH	426	8	14	22		8503
ENV	QILLALDK	753	8	14	22		8504
ENV	NATAIYA	923	8	14	22		8505
ENV	SATQACPK	243	9	14	22		8506
ENV	FAIKCNDR	269	9	14	22	0.0002	8507
ENV	GVHPEPMH	426	9	14	22		8508
ENV	TLNATAIYA	920	9	14	22		8509
ENV	SLLNATAIYA	920	9	14	22		8510
ENV	NCNTSAITQA	239	10	14	22		8511
ENV	TSATQACPK	242	10	14	22		8512
ENV	TSVITQACPK	242	10	14	22		8513
ENV	GVHPEPMH	426	10	14	22		8514
ENV	GVHPEPMH	426	10	14	22		8515
ENV	IFAVLSVNR	793	10	14	22		8516
ENV	LLNATAIYA	921	10	14	22		8517
ENV	NTSAITQACPK	241	11	14	22		8518
ENV	VITQACPKVF	244	11	14	22		8519
ENV	FAIKCNDR	269	11	14	22		8520
ENV	GVHPEPMH	426	11	14	22		8521
ENV	ITNLWLWYKIF	770	11	14	22		8522
ENV	IFAVLSVNR	792	11	14	22		8523
ENV	KIEPLGVAPTK	568	11	15	24		8524
ENV	FDPIPHY	255	8	15	23		8525
ENV	PAGYALLK	266	8	15	23		8526
ENV	GVHPEPMH	426	8	15	23		8527
ENV	LLNATAIYA	921	8	15	23		8528
ENV	NMWQEVGKA	494	9	15	23		8529
ENV	DLALDKWA	754	9	15	23		8530
ENV	ITNLWLWYK	770	9	15	23		8531

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.301$	SEQ ID NO.
ENV	GLGLRIF	786	9	15	23		8532
ENV	DDLRLNCLF	855	9	15	23		8533
ENV	SGDLEITLIL	425	10	15	23		8534
ENV	LVSGFLALA	844	10	15	23		8535
ENV	GLGLRIFA	785	10	15	23		8536
ENV	WDLRLNCLF	786	10	15	23		8537
ENV	NHWQEVGKA	854	10	15	23		8538
ENV	EFRRGGDMR	494	11	15	23		8539
ENV	LVSGFLALA	544	11	15	23		8540
ENV	DDLRLNCLF	855	11	15	23		8541
ENV	DDLRLNCLF	855	11	15	23		8542
ENV	SPNCRGEF	437	8	16	25		8543
ENV	LGLRMIF	787	8	16	25		8544
ENV	VSGLFALA	846	8	16	25		8545
ENV	IISNCRGEF	434	9	16	25		8546
ENV	SPNCRGEF	437	9	16	25		8547
ENV	SPNCRGEF	787	9	16	25		8548
ENV	LGLRIFA	787	9	16	25		8549
ENV	LVSGFLALA	845	9	16	25		8550
ENV	IISNCRGEF	434	10	16	25		8551
ENV	SPNCRGEF	437	10	16	25		8552
ENV	LVSGFLALA	844	10	16	25		8553
ENV	LVSGFLALA	844	10	16	25		8554
ENV	TVISNGGGE	432	11	16	25		8555
ENV	IISNCRGEF	434	11	16	25		8556
ENV	RLNCRNTSA	236	9	17	27		8557
ENV	KAYDTEVII	72	8	17	27		8558
ENV	RVQREKRA	587	8	17	27		8559
ENV	RVQREKRA	587	8	17	27		8560
ENV	RVQREKRA	587	8	17	27	0.0003	8561
ENV	IGLRIFA	788	8	17	27		8562
ENV	DDLRLNCLF	856	8	17	27		8563
ENV	DDLRLNCLF	856	8	17	27		8564
ENV	DDLRLNCLF	856	8	17	27		8565
ENV	DDLRLNCLF	856	8	17	27		8566
ENV	YVQREKRA	587	9	17	27	0.0002	8567
ENV	RVQREKRA	587	9	17	27		8568
ENV	DAKAYDTEVII	70	10	17	27		8569
ENV	YDTEVINWVA	74	10	17	27		8570
ENV	GVAPTKAKRR	573	10	17	27		8571
ENV	GVAPTKAKRR	573	10	17	27		8572
ENV	SDAKAYDTEVII	69	11	17	27		8573
ENV	DTEVINWVAT	75	11	17	27		8574
ENV	NCRPNNTIR	344	11	17	27		8575
ENV	LGVAPTKAKR	572	11	17	27		8576
ENV	IVAVLSVNR	792	11	17	27		8577
ENV	PLHCTTA	260	8	18	28		8578
ENV	PLHCTTA	260	8	18	28		8579
ENV	DTEVINWVA	75	9	18	28		8580
ENV	VLAVERYLK	666	9	18	28		8581
ENV	ELLELDKWA	754	9	18	28		8582

Table XVI
HIV-A03-Motif-Peptides-with-Binding-Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SFQ ID NO.
ENV	FSYIRLRDF	863	9	18	28		8582
ENV	PIHIVCTPA	258	10	18	28		8583
ENV	RVLAVERLYLK	665	10	18	28		8584
ENV	LFYSIRLRDF	862	10	18	28		8585
ENV	GVAPTKAK	574	8	19	30		8586
ENV	NGRGEFF	439	8	19	30		8587
ENV	GVAPTKAK	573	8	19	30		8588
ENV	VAPTKAKR	574	8	19	30		8589
ENV	VELFLGA	603	8	19	30		8590
ENV	LLALDKWA	755	8	19	30		8591
ENV	GVAPTKAK	572	9	19	30		8592
ENV	GVAPTKAKR	571	9	19	30		8593
ENV	AVFLFLGA	602	9	19	30		8594
ENV	VHFLFLGA	603	9	19	30		8595
ENV	SGKLICTA	685	9	19	30		8596
ENV	PLGVAPTKAK	571	10	19	30		8597
ENV	LVGVAPTKAKR	572	10	19	30		8598
ENV	AVFLFLGA	602	10	19	30		8599
ENV	AVFLFLGA	602	10	19	30		8600
ENV	CSGKLICTA	684	10	19	30		8601
ENV	SSNTIGLLTR	516	11	19	30		8602
ENV	PLGVAPTKAK	571	11	19	30		8603
ENV	GVAPTKAKR	571	11	19	30		8604
ENV	GVAPTKAKR	571	11	19	30		8605
ENV	SGKLICTA	683	11	19	30		8606
ENV	ALKGNOK	270	8	20	31		8607
ENV	RLVSGILA	844	8	20	31		8608
ENV	ELFRPGGGDM	544	11	20	31		8609
ENV	LIFSQQNQEK	740	11	20	31		8610
ENV	GGLEITHH	426	8	21	33		8611
ENV	VLKSGILA	427	8	21	33		8612
ENV	VLKSGILA	426	8	21	33		8613
ENV	GGLEITHH	426	9	21	33		8614
ENV	DLEITHSF	428	9	21	33		8615
ENV	LGLRIVA	787	9	21	33		8616
ENV	GVAPTKAKR	571	10	21	33		8617
ENV	PLGVAPTKAK	571	10	21	33		8618
ENV	LGLRIVA	786	10	21	33		8619
ENV	SFEPIHYCA	254	11	21	33		8620
ENV	GGLEITHSF	426	11	21	33		8621
ENV	EPFYCNISGLF	443	11	21	33		8622
ENV	GVAPTKAKR	571	11	21	33		8623
ENV	GVAPTKAKR	571	11	21	33		8624
ENV	LGLRIVA	788	8	22	34		8625
ENV	RIVELGR	878	8	22	34		8626
ENV	IVELGR	879	8	22	34	0.0550	8627
ENV	RIVELGR	878	9	22	34		8628
ENV	NTIRNNITR	344	10	22	34		8629
ENV	GVAPTKAKR	571	10	22	34		8630
ENV	PWKKEATTL	54	11	22	34		8631
ENV	TTTLFCASDA	60	11	22	34		8631

Table XVI
HIV-A13 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A *D301	SEQ ID NO.
ENV	KLEPLGVA	568	8	23	37		8632
ENV	LOVAPTKA	572	8	23	36		8633
ENV	TVQCTTIGR	290	9	23	36		8634
ENV	PLQVAPTGA	571	9	23	36	0.0008	8635
ENV	STVQCTHGR	289	10	23	36		8636
ENV	STVQCTHGR	289	10	23	36		8637
ENV	OSNLRAEFA	638	10	23	36		8638
ENV	ATITLFCASD	59	11	23	36		8639
ENV	VSTVQCTHGR	288	11	23	36		8640
ENV	KVRIEPLGVA	565	11	23	36		8641
ENV	ATITLCA	59	8	24	38		8642
ENV	STVQCTHGR	289	10	24	38		8643
ENV	TTTLGASDA	60	10	24	38		8644
ENV	TRFGGDMR	545	10	25	39		8645
ENV	ALAWDDL	851	8	25	39		8646
ENV	LALAWDDL	850	9	25	39		8647
ENV	IVQQSNLLR	850	10	25	39		8648
ENV	IVQQSNLLR	850	10	25	39		8649
ENV	IVQQSNLLR	850	11	25	39	0.0024	8650
ENV	IVQQSNLLR	850	11	25	39		8651
ENV	GLALAWDDL	848	11	25	39		8652
ENV	ITLPCRK	483	8	26	41		8653
ENV	IVQQSNLLR	850	8	26	41		8654
ENV	LAVRYLK	667	8	26	41		8655
ENV	IVQQSNLLR	850	10	26	41		8656
ENV	IVQQSNLLR	850	11	26	41		8657
ENV	IVQQSNLLR	850	11	26	41		8658
ENV	IVQQSNLLR	850	11	26	41		8659
ENV	LDRWASLWN	738	11	27	42		8660
ENV	IVQQSNLLR	850	10	27	42		8661
ENV	ESNQDEK	743	8	27	42		8662
ENV	PHYCAPAGF	260	10	27	42		8663
ENV	PHYCAPAGFA	260	11	27	42		8664
ENV	VGGLGLGRVF	784	11	27	42		8665
ENV	IVQQSNLLR	850	8	28	44		8666
ENV	IVQQSNLLR	850	9	28	44	0.0021	8667
ENV	TVQCTHGR	290	9	28	44		8668
ENV	CTRINNIR	345	9	28	44		8669
ENV	ASLITVQA	619	9	28	44		8670
ENV	VSEPIPHY	253	10	28	44		8671
ENV	STVQCTHGR	289	10	28	44		8672
ENV	ASLITVQA	619	10	28	44		8673
ENV	ASLITVQAR	619	10	28	44		8674
ENV	KVSEPIPHY	252	11	28	44		8675
ENV	YCAPAGFALLK	263	11	28	44		8676
ENV	VSTVQCTHGR	288	11	28	44		8677
ENV	IVQQSNLLR	850	11	28	44		8678
ENV	ASLITVQAR	618	11	28	44		8679
ENV	GLGRIVF	787	8	29	45		8680
ENV	VSEPIPHY	253	9	29	45		8681
ENV	GLGRIVF	786	9	29	45		8682

Table XVI
HIV-1 A3 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consistency (%)	A*0101	SEQ ID NO
ENV	ITQAPKVSF	245	10	29	45		8682
ENV	KVSEPPPHI	252	10	29	45		8683
ENV	CAPAGPAUK	264	10	29	45		8684
ENV	QVSEPPPHI	265	10	29	45		8685
ENV	RSLEPKVKV	558	11	29	45		8686
ENV	IGDIROA	377	8	30	47		8687
ENV	WASLWVWF	761	8	30	40		8688
ENV	AVLSVNR	795	8	31	48		8689
ENV	AVLSVNR	928	8	31	48		8690
ENV	AVLSVNR	928	8	31	48		8691
ENV	AVLSVNR	928	8	31	48		8692
ENV	SEFPHIY	254	9	31	48		8693
ENV	FAVLSVNR	794	9	31	48		8694
ENV	SLCLFSYIR	859	9	31	48	0.0004	8695
ENV	JAVAEQDTR	927	9	31	48		8696
ENV	AVLSVNR	101	10	31	48		8697
ENV	AVLSVNR	795	10	31	48		8698
ENV	RSCLFSYIR	858	10	31	48		8699
ENV	AIATAUGTDR	926	10	31	48		8700
ENV	FAVLSVNR	794	11	31	48		8701
ENV	DQLRSCLFSY	855	11	31	48		8702
ENV	AVLSVNR	559	11	31	48		8703
ENV	AVLSVNR	559	11	31	48		8704
ENV	AVLSVNR	559	11	31	48		8705
ENV	VVEREKA	587	8	32	50		8706
ENV	VVEREKA	588	8	32	50		8707
ENV	SITLTVQA	620	8	32	50		8708
ENV	SITLTVQA	621	8	32	50		8709
ENV	SITLTVQA	621	8	32	50		8710
ENV	VVEREKA	587	9	32	50		8711
ENV	SITLTVQA	620	9	32	50		8712
ENV	RSCLFSYII	858	9	32	50		8713
ENV	DQLRSCLFSYII	856	11	32	50		8714
ENV	SEFPHIY	254	8	33	52		8715
ENV	QARVAVR	663	9	33	52	0.0009	8716
ENV	QARVAVR	663	9	33	52		8717
ENV	QARVAVR	663	9	33	52		8718
ENV	QARVAVR	663	9	33	52		8719
ENV	QARVAVR	663	9	33	52		8720
ENV	QARVAVR	663	9	33	52		8721
ENV	QARVAVR	663	9	33	52		8722
ENV	QARVAVR	663	9	33	52		8723
ENV	QARVAVR	663	9	33	52		8724
ENV	QARVAVR	663	9	33	52		8725
ENV	QARVAVR	663	9	33	52		8726
ENV	QARVAVR	663	9	33	52		8727
ENV	QARVAVR	663	9	33	52		8728
ENV	QARVAVR	663	9	33	52		8729
ENV	QARVAVR	663	9	33	52		8730
ENV	QARVAVR	663	9	33	52		8731

Table XVI
 HIV-1 A101 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1031	SEQ ID NO
ENV	NIIGLLTR	519	9	35	55	0.0064	8732
ENV	EVINWATHIA	77	10	35	55		8733
ENV	ISFNGGGEFF	434	10	35	55		8734
ENV	ISFNGGGEFF	434	10	35	55		8735
ENV	DIISLCLSS	856	10	35	55		8736
ENV	ISFNGGGEFF	434	11	35	55		8737
ENV	SPNCGGLE	437	8	36	56		8738
ENV	ISFNGGGEFF	434	9	36	56		8739
ENV	PIPIHYCAPA	258	10	36	56		8740
ENV	PIPIHYCAPA	258	10	36	56		8741
ENV	MAVIGLGLR	782	10	36	56		8742
ENV	SIVNRVROGY	798	10	36	56	0.0068	8743
ENV	PGGDMRDN	548	11	36	56		8744
ENV	PIHYCAVA	260	8	37	58		8745
ENV	ITGLLLTR	520	8	37	58		8746
ENV	PGGDMRDN	548	11	37	58		8747
ENV	PIHYCAPA	260	8	38	59		8748
ENV	LSIVNRVR	797	8	38	59		8749
ENV	DLISLCLF	856	8	38	59		8750
ENV	VLSIVNRVR	796	9	38	59		8751
ENV	INVRVROGY	799	9	38	59		8752
ENV	INVRVROGY	799	9	38	59	0.0410	8753
ENV	DIISLCLSS	856	11	39	59		8754
ENV	GDMDRDNR	551	8	39	61		8755
ENV	GDMDRDNR	550	9	39	61		8756
ENV	QACTPKVSF	248	8	40	63		8757
ENV	PIPIHYCAPA	258	8	40	63		8758
ENV	PIPIHYCAPA	258	8	40	63	0.0063	8759
ENV	RDNRWSELVK	554	10	40	63	0.0068	8760
ENV	TLFCASDAKA	64	11	40	63		8761
ENV	RDNRWSELVK	554	11	40	63		8762
ENV	GKLOQARVLA	658	11	40	63		8763
ENV	QLOQARVLA	661	8	41	64		8764
ENV	QLOQARVLA	661	8	41	64	3.8090	8765
ENV	VTYYGVGVW	47	11	41	64	0.8640	8766
ENV	CASDAKAY	67	8	42	66		8767
ENV	LCLPSYHR	860	8	42	66		8768
ENV	PCASDAKAY	66	9	42	66		8769
ENV	IVGLIGLRL	783	9	42	66		8770
ENV	IVGLIGLRL	783	9	42	66		8771
ENV	LFASDAKAY	61	10	42	66	0.0064	8772
ENV	GAAGSTMGA	610	10	42	66		8773
ENV	LCLPSYHR	860	10	42	66		8774
ENV	LGAAAGSTMGA	609	11	42	66		8775
ENV	VGLIGLRL	784	8	43	67		8776
ENV	QLOQARVLA	661	8	43	67		8777
ENV	LCLPSYHR	862	8	44	69		8778
ENV	RIRQGLR	953	8	44	69		8779
ENV	TLFCASDAK	61	9	44	69		8780
ENV	GAAGSTMGA	611	9	45	70		8781

Table XVI
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SIQ IDNO
ENV	TLFCASDAKA	64	10	46	72		8782
ENV	SLWDQSLK	123	8	47	75		8783
ENV	SLWDQSLK	124	8	47	75		8784
ENV	WDSKLPVK	125	10	47	73	0.0048	8785
ENV	RVRQGYSLSF	802	11	47	73		8786
ENV	QSLKPCVK	127	8	48	75		8787
ENV	FLGLGAA	604	8	48	75		8788
ENV	QGYSLPSF	805	8	48	75		8789
ENV	SLWDQSLK	124	8	48	75		8790
ENV	GIKQLDQ	658	8	49	77		8791
ENV	WGKQLQAR	657	9	49	77	0.0004	8792
ENV	TVWGKQLQA	655	10	49	77		8793
ENV	LTVMGRQLQ	654	11	49	77		8794
ENV	FLCSDAKA	66	8	50	78		8795
ENV	SLWDQSLK	124	8	50	78		8796
ENV	WLVYKIE	773	8	50	78		8797
ENV	FLCSDAKA	65	9	50	78		8798
ENV	LGWGCGRK	679	9	50	78	0.0097	8799
ENV	TLFLCSDAK	61	10	50	78	0.0920	8800
ENV	LLGWGCGRK	678	10	50	78		8801
ENV	SLWDQSLK	124	10	50	78		8802
ENV	QLLWGCGRK	677	11	50	78		8803
ENV	VSTVQCTII	288	8	51	80		8804
ENV	NLLRAIEA	640	8	51	80		8805
ENV	RAFAAQHI	643	8	51	80		8806
ENV	WGKQLQA	657	8	51	80		8807
ENV	SLWDQSLK	124	8	51	80		8808
ENV	LLRAIAQHI	641	10	51	80		8809
ENV	GIWGCGRK	680	8	52	81		8810
ENV	TLFLCSDA	61	9	52	81		8811
ENV	TLFLCSDAK	64	9	52	81	0.0930	8812
ENV	TLFLCSDA	64	8	54	84		8813
ENV	LLGLSLA	306	8	55	86		8814
ENV	QLLNGSLA	305	9	55	86		8815
ENV	GAAGSTMGA	610	9	55	86		8816
ENV	LGAGSTMGA	609	10	55	86		8817
ENV	QLLNGSLA	303	11	55	86		8818
ENV	SLWDQSLK	124	11	55	86		8819
ENV	FLCSDAK	65	8	57	89		8820
ENV	AAAGSTMGA	611	8	58	91		8821
GAG	EDTSARQA	133	8	01	33		8822
GAG	AAAMMQK	405	8	01	25		8824
GAG	SAIMMQK	405	8	01	25		8825
GAG	ETDKDELY	535	8	01	25		8826
GAG	ETDKDELY	537	8	01	25		8827
GAG	NSATIMMQK	404	9	01	33		8828
GAG	PTAPPESEF	507	9	01	33		8829
GAG	TAPPESEF	508	9	01	33		8830
							8831

Table XVI
HIV-1 Modif. Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1001	SEQ ID NO.
GAG	NGKQANFLK	461	10	01	25		8832
GAG	NGKQANFLK	461	10	01	25		8833
GAG	PTAPAESFR	507	10	01	25		8834
GAG	PTAPAESFR	508	10	01	33		8835
GAG	TIDKDLVPLA	538	10	01	25		8836
GAG	AAMIMQKSN	405	11	01	25		8837
GAG	SATIMMQGN	405	11	01	25		8838
GAG	NGKQANFLK	461	11	01	25		8839
GAG	PTAPAESFR	507	11	01	25		8840
GAG	PTAPAESFR	507	11	01	25		8841
GAG	KDKDKELVPL	535	11	01	25		8842
GAG	ETIDKDLVPLA	537	11	01	25		8843
GAG	PAADKKEK	123	8	01	50		8844
GAG	ASAQDLKGG	392	8	01	50		8845
GAG	PTAPAESFR	507	9	01	50		8846
GAG	PAPIAPPA	492	9	01	50		8847
GAG	AADKGVSONY	130	10	01	50		8848
GAG	SAQDLKGGY	393	10	01	50		8849
GAG	TAQDLKGGY	393	10	01	50		8850
GAG	GTHRNYYOK	480	10	01	50		8851
GAG	ETIDKDLVPLA	535	10	01	50		8852
GAG	ITSLPQDOK	526	10	01	50		8853
GAG	PAADKDKPS	123	11	01	50		8854
GAG	GANSIPVEDY	276	11	01	50		8855
GAG	ASAQDLKGG	392	11	01	50		8856
GAG	TAQDLKGGY	392	11	01	50		8857
GAG	ETIDKDLVPLA	535	11	01	50		8858
GAG	YTAVMGR	465	8	02	50		8859
GAG	TAPPAESF	508	8	02	67		8860
GAG	PTAPAESF	507	9	02	67		8861
GAG	TAPPAESF	508	9	02	67		8862
GAG	PTAPAESFR	507	10	02	67		8863
GAG	PTAPAESFR	507	10	02	67		8864
GAG	PTAPAESFR	507	11	02	67		8865
GAG	EGHQANFLK	462	10	02	100		8866
GAG	AADKGVSON	129	11	02	18		8867
GAG	EADKGVSONY	129	10	04	36		8868
GAG	AADKGVSONY	129	8	04	19		8869
GAG	AAMIMQKSN	406	10	06	15		8870
GAG	AAMIMQKSN	406	11	06	15		8871
GAG	KTYKCFNCK	421	10	08	16		8872
GAG	NIMMQGNF	407	9	10	17		8873
GAG	GARASILR	2	8	10	16		8874
GAG	GNQVSR	483	8	10	16		8875
GAG	NTLQRIK	483	9	10	16		8876
GAG	KWIPSSKGR	472	9	10	16		8877
GAG	TGNSSQVSON	139	11	10	16		8878
GAG	NFLGRWIPSSK	468	11	10	16		8879
GAG	NFLQNRPEPTA	485	11	10	16		8880
GAG	PVATQQR	243	8	10	16		8881

Table XVI
HIV-1 Gag Motif Topologies with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1000	SEQ ID NO.
GAG	MMQKSNFK	409	8	10	16		8882
GAG	MMQKSNFK	409	8	10	16		8883
GAG	KLDKWEKIRL	12	9	10	16		8884
GAG	GGKKKKYKLLK	24	9	10	16		8885
GAG	RDTEKALDK	167	9	10	16	0.0001	8886
GAG	MMQKSNFK	408	9	10	16		8887
GAG	MMQKSNFK	408	9	10	16		8888
GAG	LKQWTSKK	470	9	10	16		8889
GAG	GGKKKKYKLLK	23	10	10	16		8890
GAG	GGKKKKYKLLK	24	10	10	16		8891
GAG	QALSPKTLNA	166	10	10	16		8892
GAG	AGPAPGQMR	241	10	10	16		8893
GAG	GASLEHNSKIA	469	10	10	16		8894
GAG	MMQKSNFK	408	10	10	16		8895
GAG	FLNRHETPA	486	10	10	16		8896
GAG	TAPPAESFGT	496	10	10	16		8897
GAG	KLDKWEKIRL	12	11	10	16		8898
GAG	PGKKKKYKLLK	23	11	10	16		8899
GAG	LKQWTSKKGR	470	11	10	16		8900
GAG	MMQKSNFK	408	11	10	16		8901
GAG	ATMMQKSNFK	406	11	11	28		8902
GAG	ATMMQKSNFK	406	11	11	28		8903
GAG	PSQKQIPDK	528	11	11	18		8904
GAG	SSKGRGNE	476	9	11	18		8905
GAG	TTSTLQEQIA	260	10	11	17		8906
GAG	DKVDTEA	365	8	11	17		8907
GAG	MMQKSNFK	408	8	11	17		8908
GAG	MMQKSNFK	391	8	11	17		8909
GAG	MMQKSNFK	408	8	11	17		8910
GAG	MMQKSNFK	408	8	11	17		8911
GAG	MMQKSNFK	408	9	11	17		8912
GAG	ASLENNMTA	365	9	11	17		8913
GAG	AMSQVNTSA	400	9	11	17		8914
GAG	MMQKSNFK	408	9	11	17		8915
GAG	MMQKSNFK	408	9	11	17		8916
GAG	MMQKSNFK	408	9	11	17		8917
GAG	MMQKSNFK	408	9	11	17		8918
GAG	MMQKSNFK	408	9	11	17		8919
GAG	MMQKSNFK	408	9	11	17		8920
GAG	MMQKSNFK	408	9	11	17		8921
GAG	MMQKSNFK	408	9	11	17		8922
GAG	MMQKSNFK	408	9	11	17		8923
GAG	MMQKSNFK	408	9	11	17		8924
GAG	MMQKSNFK	408	9	11	17		8925
GAG	MMQKSNFK	408	9	11	17		8926
GAG	MMQKSNFK	408	9	11	17		8927
GAG	MMQKSNFK	408	9	11	17		8928
GAG	MMQKSNFK	408	9	11	17		8929
GAG	MMQKSNFK	408	9	11	17		8930
GAG	MMQKSNFK	408	9	11	17		8931

Table XVI
HIV-1 M10T Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consistency (%)	A*0301	SEQ ID NO.
GAG	UTSLRSLF	549	8	12	19		8932
GAG	GTSEELSLY	73	9	12	19		8933
GAG	ATLYCYVIQK	85	9	12	19		8934
GAG	KDTKEALEK	97	9	12	19		8935
GAG	NMLIVGGH	207	9	12	19		8936
GAG	TSILGIIQVA	266	9	12	19		8937
GAG	PLTSLKSLF	548	9	12	19		8938
GAG	PLTSLRSLF	548	9	12	19		8939
GAG	GTSEELSLY	72	10	12	19		8940
GAG	VATLYCYVIQK	84	10	12	19		8941
GAG	NAGQNVHQA	158	10	12	19		8942
GAG	TSILGIIQVA	266	10	12	19		8943
GAG	NMLIVGGH	207	10	12	19		8944
GAG	PLTSLKSLF	548	10	12	19		8945
GAG	YSLTSLDR	301	10	12	19		8946
GAG	RAHQAQEVK	329	10	12	19		8947
GAG	RLRGGKKKY	20	11	12	19		8948
GAG	TVATLYCYVIQK	83	11	12	19		8949
GAG	NMLIVGGH	207	11	12	19		8950
GAG	TSILGIIQVA	266	11	12	19		8951
GAG	TSILDRGQPK	308	11	12	19		8952
GAG	TIMMORGNE	407	9	13	22		8953
GAG	PGNLFQNR	483	8	13	21		8954
GAG	IARNCRAPR	434	9	13	21		8955
GAG	KIWSNKGK	472	9	13	21		8956
GAG	INRSGHAR	427	10	13	21		8957
GAG	INRSGHAR	427	10	13	21		8958
GAG	IARNCRAPRK	434	10	13	21		8959
GAG	NFLGKIWFNSK	468	11	13	21		8960
GAG	KQNGNLFQNR	478	11	13	21		8961
GAG	KLKIHWVA	31	8	13	20		8962
GAG	RIEVKDTK	93	8	13	20		8963
GAG	KLKIHWVA	31	8	13	20		8964
GAG	UTSLRSLF	549	8	13	20		8965
GAG	IVKFNCKQ	428	9	13	20		8966
GAG	CGKEGHAR	431	9	13	20		8967
GAG	EGHIANCR	431	9	13	20		8968
GAG	LOKIWSNKG	470	9	13	20		8969
GAG	KLKIHWVA	31	10	13	20		8970
GAG	KLKIHWVA	31	10	13	20		8971
GAG	TLRALGCEA	356	10	13	20		8972
GAG	EGHIANCR	431	10	13	20		8973
GAG	IARNCRAPR	433	10	13	20		8974
GAG	FLGKIWSNKG	469	10	13	20		8975
GAG	EYKDTKEALD	95	11	13	20		8976
GAG	PSYEVIMPTA	185	11	13	20		8977
GAG	KLKIHWVA	31	11	13	20		8978
GAG	KLKIHWVA	31	11	13	20		8979
GAG	KLKIHWVA	31	11	13	20		8980
GAG	KLKIHWVA	31	11	13	20		8981

Table XVI
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*0101	SIQ ID NO.
GAG	NSQVSNQY	144	9	14	31		8982
GAG	KSXKAQDA	112	9	14	22		8983
GAG	IAKNCAPRKK	414	10	14	22		8984
GAG	EVPMFTA	188	8	14	22		8985
GAG	RGFNRNOKK	412	9	14	22		8986
GAG	CGKEGHIAK	428	9	14	22		8987
GAG	EGHIAKNCR	431	9	14	22		8988
GAG	EGHIAKNCRA	431	10	14	22		8989
GAG	NSQVSNQY	428	10	14	22		8990
GAG	TAPEESFE	496	10	14	22		8991
GAG	TVAILCYHIQ	83	11	14	22		8992
GAG	IVQNAQGMV	155	11	14	22		8993
GAG	PIAPEESFE	495	11	14	22		8994
GAG	SSQVSNQY	145	8	15	31		8995
GAG	VSQNTIVQNA	149	11	15	30		8996
GAG	NSQVSNQY	149	11	15	30		8997
GAG	TVAILCYHIQ	86	8	15	23		8998
GAG	FLXLSIGA	193	8	15	23		8999
GAG	AAEWDVRVH	230	8	15	23		9000
GAG	WDRVIPVH	233	8	15	23		9001
GAG	RGFNRNQR	412	8	15	23		9002
GAG	TAPEESF	496	8	15	23		9003
GAG	TAPEESF	507	8	15	23		9004
GAG	VSQGLIDA	7	8	15	23		9005
GAG	LFNTVATLY	80	9	15	23		9006
GAG	ATLYCVHOR	85	9	15	23	0.0150	9007
GAG	MTALSEGA	192	9	15	23		9008
GAG	EAAEWDVRH	229	9	15	23		9009
GAG	WDRVIPVH	233	9	15	23		9010
GAG	TAPEESF	496	9	15	23		9011
GAG	PIAPEESF	496	9	15	23		9012
GAG	PLASLSKF	548	9	15	23		9013
GAG	SVLSGGKIDA	6	10	15	23		9014
GAG	SGGKLDAWEK	9	10	15	23		9015
GAG	ELRSLYNTYA	76	10	15	23		9016
GAG	VSQNTIVQNA	149	10	15	23		9017
GAG	WDRVIPVH	84	10	15	23		9018
GAG	KIEEQNSKK	105	10	15	23		9019
GAG	PMFTALSEGA	191	10	15	23		9020
GAG	RAEQATQDVK	329	10	15	23		9021
GAG	PIAPEESF	495	10	15	23		9022
GAG	ASVLSGGKID	5	11	15	23		9023
GAG	LSQGLDAWE	8	11	15	23		9024
GAG	WDRVIPVH	50	11	15	23		9025
GAG	KIEEQNSKK	105	11	15	23		9026
GAG	RLIPVHAGPIA	235	11	15	23		9027
GAG	MMQRGNFRN	409	11	15	23		9028
GAG	IAKNCAPRKK	434	10	16	25		9029
GAG	LSQGLIDA	8	8	16	25		9030
GAG							9031

Table XVI
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LDWKEIR	13	8	16	25		9032
GAG	NAQGMVH	138	8	16	25		9033
GAG	YSILDIR	357	8	16	25		9034
GAG	LDWKEIR	357	8	16	25		9035
GAG	KLDWKEIR	357	9	16	25		9036
GAG	GGKKKYRLK	24	9	16	25		9037
GAG	TKLALGPA	356	9	16	25		9038
GAG	ILKALGPA	357	9	16	25		9039
GAG	VLAEMSSQA	386	9	16	25		9040
GAG	LDWKEIRLLK	23	10	16	25	0.0003	9041
GAG	GGKKKYRLK	23	10	16	25		9042
GAG	GGKKKYRLKII	24	10	16	25		9043
GAG	GLLETSIEGR	51	10	16	25		9044
GAG	YSIVSILDIR	301	10	16	25		9045
GAG	TKLALGPA	355	10	16	25		9046
GAG	TKLALGPA	356	10	16	25		9047
GAG	AAILEEMHQA	385	10	16	25		9048
GAG	VLAEMSSQA	385	10	16	25		9049
GAG	GGKLDWKEIR	10	11	16	25		9050
GAG	KLDWKEIRL	12	11	16	25		9051
GAG	PGGKKKYRLK	23	11	16	25		9052
GAG	VSILDIRQGP	304	11	16	25		9053
GAG	TKLALGPA	355	11	16	25		9054
GAG	PGATLEEMHQA	353	11	16	25		9055
GAG	GGKLDWKEIR	413	11	16	25		9056
GAG	VLAEMSSQA	387	8	17	27		9057
GAG	RLKILVWA	31	8	17	27		9058
GAG	LSPTLNA	168	8	17	27		9059
GAG	PIPPQMR	243	8	17	27		9060
GAG	GGKLDWKEIR	10	9	17	27		9061
GAG	GGKLDWKEIR	52	9	17	27		9062
GAG	RLKILVWASR	31	10	17	27		9063
GAG	LKIHIEQNK	103	10	17	27		9064
GAG	AGPIPPQMR	241	10	17	27		9065
GAG	ALDKIEEQNK	102	11	17	27		9066
GAG	LSPTLNAWASR	246	11	17	27		9067
GAG	GGKLDWKEIR	246	11	17	27		9068
GAG	PIPPQMEPR	243	11	17	27		9069
GAG	PGATLEEMHQA	363	11	17	27		9070
GAG	RSLYNTVA	78	8	18	29	0.0009	9071
GAG	IAKNCRAPR	434	9	18	29		9072
GAG	LDWKEIR	13	8	18	28		9073
GAG	PGDITYKR	281	8	18	28		9074
GAG	PGDITYKR	353	8	18	28		9075
GAG	DOCKTILRA	433	8	18	28		9076
GAG	IAKNCRRA	433	8	18	28		9077
GAG	PDCKTILRA	352	9	18	28		9078
GAG	ILRALGPGA	357	9	18	28		9079
GAG	LDWKEIRLR	13	10	18	28		9080
							9081

Table XVI
HIV-1 gp120 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.01$	SEQ ID NO.
GAG	SILDKQPK	305	10	18	28		9082
GAG	HIANKCRAPR	413	10	18	28		9083
GAG	IIAGPIAPQOM	240	11	18	28		9084
GAG	IVANPXTLKR	409	11	18	28		9085
GAG	IVANPXTLKR	414	11	18	28		9086
GAG	PIIAGPIA	238	8	19	30		9087
GAG	PIIAGQMR	243	8	19	30		9088
GAG	ILDIKQPK	307	8	19	30		9089
GAG	ILDIKQPK	306	8	19	30		9090
GAG	PSIKARVLA	380	9	19	30		9091
GAG	PSIKARVLA	381	9	19	30		9092
GAG	IAFGMR	244	10	19	30		9093
GAG	IAFGMR	244	10	19	30		9094
GAG	DIKQPK	308	10	19	30		9095
GAG	RLRPGKKKY	20	11	19	30		9096
GAG	IVASRELER	35	11	19	30		9097
GAG	PIIAGMR	243	11	19	30		9098
GAG	PIIAGMR	243	11	19	30		9099
GAG	DIKQPK	308	11	19	30		9100
GAG	GFPSIKARVL	378	11	19	30		9101
GAG	PSIKARVLA	380	11	19	30		9102
GAG	LAIRCRAPR	434	9	20	32		9103
GAG	LAIRCRAPR	434	10	20	32		9104
GAG	LAIRCRAPR	434	10	20	32		9105
GAG	TAPPAESF	495	8	20	31		9106
GAG	IMMQGNFR	408	9	20	31		9107
GAG	PTAPPAESF	495	9	20	31		9108
GAG	IVASRELER	35	10	20	31	0.0099	9109
GAG	ILANRCRATP	413	10	20	31		9110
GAG	ILANRCRATP	413	11	20	31		9111
GAG	ILANRCRATP	413	11	20	31		9112
GAG	ILANRCRATP	413	8	21	33		9113
GAG	EGILARNCR	431	9	21	33		9114
GAG	NLQGMVHQA	158	10	21	33		9115
GAG	NLQGMVHQA	431	10	21	33		9116
GAG	QSHETATPA	472	11	22	35		9117
GAG	KWPSIKGR	472	9	22	35		9118
GAG	EVDKEA	95	8	22	34	0.0770	9119
GAG	ETINEAA	224	8	22	34		9120
GAG	DTLLVQNA	343	8	22	34		9121
GAG	GVGSHKAR	348	9	22	34		9122
GAG	GVGSHKAR	348	9	22	34		9123
GAG	GVGSHKAR	348	9	22	34		9124
GAG	SLYNTVAILV	79	10	22	34		9125
GAG	MLKETINEA	221	10	22	34		9126
GAG	MTDILLVQNA	341	10	22	34		9127
GAG	GVGSHKAR	376	10	22	34		9128
GAG	GVGSHKAR	376	11	22	34		9129
GAG	MLKETINEAA	221	11	22	34		9130
GAG	MTDILLVQ	340	11	22	34		9131
GAG	QVGVGSHKAR	375	11	22	34		9131

Table XVI
HIV-A05 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO
GAG	LGIKIWSIRK	470	11	22	34		9132
GAG	NLGIKIWSIRK	468	11	23	37		9133
GAG	KHEQDNK	105	8	23	36		9134
GAG	YVQVGSIRK	376	8	23	36		9135
GAG	GVGGSIRK	376	8	23	36		9136
GAG	VGGSIRK	377	8	23	36		9137
GAG	MMQRGNR	409	8	23	36		9138
GAG	QVVGGSIRK	375	9	23	36		9139
GAG	GVGGSIRK	376	9	23	36		9140
GAG	YVQVGSIRK	376	9	23	36		9141
GAG	GVGGSIRK	377	10	23	36		9142
GAG	QVVGGSIRK	375	10	23	36		9143
GAG	FLGIKIWSIRK	469	10	23	36	0.0200	9144
GAG	PSIKGRPGNF	475	10	23	36		9145
GAG	TACQVGGPS	372	11	23	36		9146
GAG	ACQVGGPSII	373	11	23	36		9147
GAG	GVGGSIRK	376	10	24	38		9148
GAG	KVIEKAF	178	8	24	38		9149
GAG	CKEGILAR	428	9	24	38		9150
GAG	WKVIEKAF	176	10	24	38		9151
GAG	YSPVSDIR	301	10	24	38		9152
GAG	NLGIKIWSIRK	468	10	25	40		9153
GAG	YVQVGSIRK	376	10	25	40		9154
GAG	LGIKIWSIRK	470	8	25	39		9155
GAG	KDIEALDK	97	9	25	39		9156
GAG	WKVIEKAF	176	9	25	39		9157
GAG	FLGIKIWSIRK	469	9	25	39		9158
GAG	LYWASRELER	35	11	25	39		9159
GAG	YVQVGSIRK	376	11	25	39		9160
GAG	VSILDIRQPK	304	11	25	39		9161
GAG	LYWASRELER	35	10	26	41		9162
GAG	HLWASRELE	34	11	26	41		9163
GAG	CFNCKEGILIA	425	11	26	41		9164
GAG	NCCKEGILIA	427	9	27	43		9165
GAG	CKEGILIA	427	9	27	43		9166
GAG	REFKTLRA	323	8	27	42		9167
GAG	IMMQRGNF	408	8	27	42		9168
GAG	CKEGILIA	428	8	27	42		9169
GAG	CKEGILIA	428	8	27	42		9170
GAG	MVLIQNSPR	363	9	27	42	0.1800	9171
GAG	YVQVGSIRK	376	9	27	42		9172
GAG	QVVGGSIRK	375	10	27	42	0.0260	9173
GAG	YVDFEKLAR	320	10	27	42		9174
GAG	VDFEKLAR	321	10	27	42		9175
GAG	FFKTLRAEQ	324	10	27	42		9176
GAG	RAEQATQEVK	329	10	27	42		9177
GAG	NAWKVYVEEK	174	11	27	42		9178
GAG	YVQVGSIRK	376	11	27	42		9179
GAG	REFKTLRAEQ	323	11	27	42		9180
GAG	REFKTLRAEQ	323	11	27	42		9181

Table XVI
HIV-A3 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*Q301	SEQ ID NO
GAG	NANPCKTLTK	349	11	27	42		9183
GAG	CFNCKEGHIL	425	11	27	42		9183
GAG	KGRGNFLQS	478	11	28	44		9184
GAG	YKGRNFTATA	485	11	28	44		9185
GAG	KYVEKFAE	178	8	28	44		9186
GAG	RFYKTLRA	323	8	28	44		9187
GAG	PDCKTLTK	352	8	28	44		9188
GAG	DCKTLKA	353	8	28	44		9189
GAG	WVKVVEEKA	176	9	28	44		9190
GAG	WVKVVEEKL	177	9	28	44		9191
GAG	PDCKTLTK	352	9	28	44		9192
GAG	WVKVVEEKA	176	10	28	44		9193
GAG	PRDYVDREY	316	10	28	44	0.0003	9194
GAG	YVDREYKTLR	320	10	28	44	9195	9201
GAG	YVDREYKTLRA	321	10	28	44	9196	9202
GAG	YVDREYKTLRA	364	10	28	44	9197	9203
GAG	YVDREYKTLRA	365	10	28	44	9198	9204
GAG	PRDYVDREY	316	11	28	44	0.0005	9205
GAG	YVDREYKTLR	320	11	28	44	9206	9207
GAG	GARASVLSGG	2	11	29	46		9208
GAG	ASVLSGGK	5	8	29	45		9209
GAG	WVKVVEEKA	176	8	29	45		9210
GAG	WVKVVEEKL	177	8	29	45		9211
GAG	WDRLLPHV	233	8	29	45		9212
GAG	RDYVDREY	318	8	29	45		9213
GAG	RASVLSGGK	4	9	29	45	0.0050	9214
GAG	ASPRELNA	167	9	29	45	0.0007	9215
GAG	YVDREYKTLR	323	9	29	45		9216
GAG	PDYVDREYKTLR	324	9	29	45		9217
GAG	QASPRTLNA	166	10	29	45		9218
GAG	NWVKVVEEK	174	10	29	45		9219
GAG	YVDREYKTLR	320	11	29	45		9220
GAG	AAEWDRLLPV	230	11	29	45		9221
GAG	YVDREYKTLR	323	8	30	48		9222
GAG	NWVKVVEEK	174	11	30	47	0.0004	9223
GAG	KIRLRGGGKKK	18	11	30	47	0.0003	9224
GAG	WVKVVEEK	176	8	31	48		9225
GAG	MLKDTINEEA	221	10	32	50		9226
GAG	OMLKDTINEEA	220	11	32	50		9227
GAG	WVKVVEEKA	176	11	32	50		9228
GAG	KDTINEEA	221	8	33	52		9229
GAG	DTINEEA	224	8	33	52		9230
GAG	KDTINEEA	223	9	33	52		9231
GAG	RDYVDREYK	318	9	33	52		9232
GAG	PRDYVDREY	316	11	33	52		9233
GAG	RLRPGGKKK	20	9	34	53		9234
GAG	PRDYVDREY	316	10	34	53		9235
GAG	PHVGVYKX	279	10	34	53	0.0003	9236
GAG	PHVGVYKX	279	10	34	53		9237
GAG	RDYVDREY	318	8	35	55		9238

Table XVI
HIV-AIDS Modifying Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*Q301	SEQ ID NO.
GAG	PIPVGEYK	279	9	35	55	0.0002	9232
GAG	PGIKARVLA	380	9	35	55		9233
GAG	PHDYVIDRF	316	10	35	55		9234
GAG	WVYVYVYVYV	316	10	35	55		9235
GAG	GGGIKARVLA	378	11	35	55		9236
GAG	PGIKARVLA	380	11	35	55		9237
GAG	DTREALDK	98	8	36	56	0.0003	9238
GAG	ISPTILNA	168	8	36	56		9239
GAG	QGVGGPGHI	375	8	36	56		9240
GAG	QGVGGPGHI	375	8	36	56		9241
GAG	QGVGGPGHI	375	8	36	56	0.0004	9242
GAG	MTIELLVQNA	341	10	36	56		9243
GAG	ACQVGGPGHI	373	10	36	56		9244
GAG	QGVGGPGHI	375	10	36	56		9245
GAG	ISPTILNAWV	168	11	36	56	0.0001	9246
GAG	QGVGGPGHI	375	11	36	56		9247
GAG	ACQVGGPGHI	373	11	36	56		9248
GAG	QGVGGPGHI	375	11	36	56		9249
GAG	QGVGGPGHI	375	11	36	56		9250
GAG	QGVGGPGHI	375	11	36	56		9251
GAG	ETLLVQNA	343	8	37	58	0.0012	9252
GAG	QGVGGPGHI	375	8	37	58		9253
GAG	QGVGGPGHI	375	8	37	58		9254
GAG	QGVGGPGHI	375	8	37	58		9255
GAG	QGVGGPGHI	375	8	37	58		9256
GAG	QGVGGPGHI	375	8	37	58	0.0003	9257
GAG	QGVGGPGHI	375	8	37	58		9258
GAG	QGVGGPGHI	375	8	37	58		9259
GAG	QGVGGPGHI	375	8	37	58	0.0003	9260
GAG	QGVGGPGHI	375	8	37	58		9261
GAG	QGVGGPGHI	375	8	37	58		9262
GAG	QGVGGPGHI	375	8	37	58		9263
GAG	QGVGGPGHI	375	8	37	58	0.3100	9264
GAG	QGVGGPGHI	375	8	37	58		9265
GAG	QGVGGPGHI	375	8	37	58		9266
GAG	QGVGGPGHI	375	8	37	58		9267
GAG	QGVGGPGHI	375	8	37	58		9268
GAG	QGVGGPGHI	375	8	37	58		9269
GAG	QGVGGPGHI	375	8	37	58	0.0420	9270
GAG	QGVGGPGHI	375	8	37	58		9271
GAG	QGVGGPGHI	375	8	37	58		9272
GAG	QGVGGPGHI	375	8	37	58		9273
GAG	QGVGGPGHI	375	8	37	58		9274
GAG	QGVGGPGHI	375	8	37	58		9275
GAG	QGVGGPGHI	375	8	37	58	1.9000	9276
GAG	QGVGGPGHI	375	8	37	58		9277
GAG	QGVGGPGHI	375	8	37	58		9278
GAG	QGVGGPGHI	375	8	37	58		9279
GAG	QGVGGPGHI	375	8	37	58		9280
GAG	QGVGGPGHI	375	8	37	58		9281

Table XVI
HIV-1 Gag Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1001	SEQ ID NO.
GAG	PGQAREPR	246	8	45	70		9282
GAG	MFSAISLGA	192	9	45	70		9283
GAG	PGQAREPR	191	9	45	70		9284
GAG	PMFSAISLGA	191	10	45	70		9285
GAG	KCGKRGHOMK	448	10	45	70		9286
GAG	ASRELEHF	38	8	46	72		9287
GAG	EVPMFESA	188	8	46	72		9288
GAG	TLERAMTA	366	8	46	72		9289
GAG	WASRELER	37	8	46	72		9290
GAG	ATLEEMATA	365	9	46	72		9291
GAG	MLNTVGGH	208	8	47	73	0.0003	9292
GAG	MLNTVGGHQA	210	8	47	73		9293
GAG	TVGGHQA	211	8	47	73		9294
GAG	TVGGHQA	210	9	47	73		9295
GAG	MLNTVGGHQA	208	10	47	73	0.0005	9296
GAG	MLNTVGGHQA	208	11	47	73		9297
GAG	WASRELER	37	8	48	75		9298
GAG	GCWKCCKEGH	445	10	48	75		9299
GAG	RLPTGGRK	20	8	49	77		9300
GAG	QMKDCTER	455	8	49	77		9301
GAG	QMKDCTER	455	9	49	77		9302
GAG	EGHDMKKDCTE	452	11	49	77		9303
GAG	AFSPFVPMF	184	10	50	78	0.0007	9304
GAG	KATSPFVPMF	183	11	50	78		9305
GAG	RAPRKGCWVK	439	10	51	80		9306
GAG	KDCTERQA	457	8	52	83		9307
GAG	CTERQANF	459	10	52	83		9308
GAG	CTERQANF	459	11	52	83		9309
GAG	DCTERQANF	458	9	52	81		9310
GAG	NCRAPRKK	437	8	53	84		9311
GAG	TINEEAPEWD	225	11	53	83		9312
GAG	KTLRAEQN	326	8	54	84		9313
GAG	CTERQANF	459	10	55	84		9314
GAG	CTERQANF	459	11	55	87		9315
GAG	WILLGLNK	289	8	57	89		9316
GAG	KARVLAE	383	8	57	89		9317
GAG	CFNCKGEGH	425	9	57	89		9318
GAG	ILGLNKYR	290	10	57	89	0.0003	9319
GAG	WILLGLNKYR	289	11	57	89		9320
GAG	WILLGLNKYR	289	11	57	89		9321
GAG	ILGLNKYR	291	9	58	91		9322
GAG	ILGLNKYR	292	10	58	91	0.0008	9323
GAG	LLVQANPDG	345	11	58	91	0.0004	9324
GAG	LLVQANPDG	345	11	59	92		9325
GAG	LLVQANPDG	346	10	59	92		9326
GAG	GLNKIVRM	293	9	60	94	0.0002	9327
GAG	GLNKIVRM	293	10	60	94	0.0100	9328
GAG	QAAMQMLK	216	8	61	95		9329
GAG	QAGQAMQM	213	11	61	95		9330
GAG	RLINAAWK	171	8	63	98	0.0410	9331

Table XVI
 HIV-1 Gag-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0.001	SEQ ID NO
GAG	QGKLEPER	311	8	63	98		9332
IFRDYVDR		316	8	63	98		9333
GAG	IFRDYVDR	316	9	63	98		9334
QAEPAAGV		34	11	63	98	0.0004	9335
NEF	QAEPAAGV	34	11	63	33		9336
NEF	RAQAFPA	32	9	01	17		9337
NEF	RAQAFPA	32	9	01	17		9338
NEF	QTEPAAGV	32	11	01	17		9339
NEF	QTEPAAGV	32	11	01	17		9340
NEF	RAEPAAGV	32	11	01	17		9341
NEF	RAEPAAGV	32	11	01	17		9342
NEF	QAEPAAGV	33	11	01	17		9343
NEF	QAEPAAGV	33	11	01	17		9344
NEF	AADGVGAVSR	42	10	09	15		9345
NEF	SSVGVWPA	8	8	09	15		9346
NEF	XGWPFAIR	11	9	10	17		9347
NEF	XGWPFAIR	11	9	10	17		9348
NEF	FDRLAFH	310	8	10	16		9349
NEF	FDRLAFH	310	9	10	16		9350
NEF	DSRLAFH	311	8	10	16		9351
NEF	AVSQDLK	48	8	10	16		9352
NEF	KLRPMTEK	102	8	10	16		9353
NEF	KLRPMTEK	102	8	10	16		9354
NEF	GAFDLSIF	110	8	10	16		9355
NEF	GAVSQDLK	47	9	10	16		9356
NEF	QVLRPMTEK	100	9	10	16		9357
NEF	KGAFDLSIF	109	9	10	16		9358
NEF	MAEGLYSK	125	9	10	16		9359
NEF	MAEGLYSK	125	9	10	16		9360
NEF	VGAVSQDLK	46	10	10	16		9361
NEF	QVLRPMTEK	100	10	10	16		9362
NEF	GAFDLSIFL	110	10	10	16		9363
NEF	KGLEGLYSK	124	10	10	16		9364
NEF	QVLRPMTEK	100	10	10	16		9365
NEF	MAEGLYSK	124	10	10	16		9366
NEF	MAEGLYSK	124	10	10	16		9367
NEF	MAEGLYSK	124	10	10	16		9368
NEF	MAEGLYSK	124	10	10	16		9369
NEF	MAEGLYSK	124	10	10	16		9370
NEF	MAEGLYSK	124	10	10	16		9371
NEF	MAEGLYSK	124	10	10	16		9372
NEF	MAEGLYSK	124	10	10	16		9373
NEF	MAEGLYSK	124	10	10	16		9374
NEF	MAEGLYSK	124	10	10	16		9375
NEF	MAEGLYSK	124	10	10	16		9376
NEF	MAEGLYSK	124	10	10	16		9377
NEF	MAEGLYSK	124	10	10	16		9378
NEF	MAEGLYSK	124	10	10	16		9379
NEF	MAEGLYSK	124	10	10	16		9380
NEF	MAEGLYSK	124	10	10	16		9381

Table XVI
 HIV-1 Gag-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
NEF	GVGANSRDLE	45	11	11	17		9382
NEF	VGVANSRDLEK	46	11	11	17		9383
NEF	AVNSKLERK	48	11	11	17		9384
NEF	AVNSKLERK	49	11	11	17		9385
NEF	ATNADCAWLE	70	8	12	22		9386
NEF	EGNNCLLIH	251	9	12	19		9387
NEF	IMTYKGAF	105	8	12	19		9388
NEF	YITGPGVR	207	8	12	19		9389
NEF	YATNADCA	69	9	12	19		9390
NEF	YATNADCA	70	9	12	19		9391
NEF	NTATNAKCA	68	10	12	19		9392
NEF	QDLDLVVYH	184	10	12	19		9393
NEF	ITSSNTAATNA	64	11	12	19		9394
NEF	PLRPMYAKGA	102	11	12	19		9395
NEF	PGHRYPLTF	211	9	13	21		9396
NEF	PGHRYPLTF	212	9	13	21		9397
NEF	EGNNSLLH	251	9	13	21		9398
NEF	WVYHITQGF	191	8	13	20		9399
NEF	GRYPLTF	213	8	13	20		9400
NEF	GTRPPLTF	213	8	13	20		9401
NEF	SSNTAATNA	66	9	13	20		9402
NEF	YITGPGVR	191	9	13	20		9403
NEF	YITGPGVR	207	9	13	20		9404
NEF	ITSSNTAATNA	65	10	13	20		9405
NEF	VOLSHLEK	112	10	13	20		9406
NEF	DLVYHITQGF	188	10	13	20		9407
NEF	AVDLSHLEK	111	11	13	20		9408
NEF	DLVYHITQGF	188	11	13	20		9409
NEF	DLVYHITQGF	188	11	13	20		9410
NEF	PGHRYPLTF	209	11	13	20		9411
NEF	PGHRYPLTF	209	11	13	20		9412
NEF	VOLSHLEK	112	8	14	22		9413
NEF	VOLSHLEK	112	8	14	22		9414
NEF	VLDPK	32	8	14	22		9415
NEF	VLDPK	32	8	14	22		9416
NEF	ATSSNTAA	63	9	14	22	0.0003	9417
NEF	AVDLSHLEK	111	9	14	22	0.0740	9418
NEF	LDGLYSKK	171	9	14	22		9419
NEF	LDGLYSKK	172	9	14	22		9420
NEF	LDGLYSKK	172	9	14	22		9421
NEF	GATSSNTAA	62	10	14	22		9422
NEF	LDGLYSKK	171	10	14	22		9423
NEF	IGATSSNTAA	61	11	14	22		9424
NEF	LDGLYSKK	171	11	14	22		9425
NEF	LDGLYSKK	171	11	14	22		9426
NEF	PLDGVCA	41	8	15	23		9427
NEF	ITSSNTAA	64	8	15	23		9428
NEF	CLLHPMSQH	256	9	15	23		9429
NEF	CLLHPMSQH	255	10	15	23		9430
NEF	EAQEEFVGF	82	10	16	25		9431

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A *1001	SEQ ID NO.
NEF	RDLEKIGA	51	8	16	25		9432
NEF	LDGLYSK	171	9	16	25		9433
NEF	GLDGLYSK	125	9	16	25		9434
NEF	GGLDGLYSK	124	10	16	25		9435
NEF	KGLDGLYSK	122	11	16	25		9436
NEF	RFLPTGWCF	216	10	17	27		9437
NEF	KPLTHWCF	216	11	17	27		9438
NEF	RDLEKIGA	51	8	17	27		9439
NEF	FFPDWQNY	199	8	17	27		9440
NEF	LLIPMSQH	257	8	17	27		9441
NEF	NADCAWLEA	73	9	17	27		9442
NEF	GFDPDQNY	198	9	17	27		9443
NEF	YTPGKIRY	207	9	17	27		9444
NEF	QSTPDWQNY	112	10	17	27		9445
NEF	QSTPDWQNY	116	10	17	27		9446
NEF	AFDLSFLKEK	112	11	17	27		9447
NEF	FDLSFLK	112	8	18	28		9448
NEF	LLIPICQH	257	8	18	28		9449
NEF	AFDLSFLK	111	9	18	28		9450
NEF	GGLEGLIY	124	8	19	30		9451
NEF	LDLEWVY	185	8	20	30		9452
NEF	LDLEWVY	185	8	20	31		9453
NEF	YTPGKIR	207	8	20	31		9454
NEF	QDILDLWVY	184	9	20	31		9455
NEF	PLRIMTYKAA	102	10	20	31		9456
NEF	QPLRIMTYK	100	11	20	31		9457
NEF	LDLEWVY	184	8	21	33		9458
NEF	GGLDGLY	124	8	21	33		9459
NEF	WYVHTQCY	191	8	21	33		9460
NEF	YTPGKIR	207	8	21	33		9461
NEF	PLRIMTYKA	102	9	21	33		9462
NEF	KGLDGLY	122	9	21	33		9463
NEF	WYVHTQCY	191	9	21	33		9464
NEF	LDLEWVY	185	10	21	33		9465
NEF	LDLEWVY	187	11	21	33		9466
NEF	LDLEWVY	187	11	21	33		9467
NEF	LDLEWVY	188	11	21	33		9468
NEF	LSFLKEK	114	8	22	34		9469
NEF	ELIPEYK	324	8	22	34		9470
NEF	LDLSFLKEK	113	9	22	34		9471
NEF	LDLEWVY	187	9	22	34		9472
NEF	GLYSK	173	8	22	34		9473
NEF	PLRIMTYKGA	102	10	22	39		9474
NEF	ATSSNTA	63	8	27	42		9475
NEF	LSHELKEK	114	8	27	42		9476
NEF	GAITSSNTA	62	9	27	42		9477
NEF	LDLSHLKEK	113	9	27	42		9478
NEF	ATSSNTA	63	10	27	42		9479
NEF	ELDLWVY	185	8	33	53		9480
NEF	ALDLWVY	186	8	33	53		9481
NEF	YFPDQWNY	199	8	36	56		9482

Table XVI
 HIV A03.101 Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
NEF	QGVHDDQWNY	196	10	36	56	0.0004	9482
NEF	PLTGWGCF	219	9	39	61		9483
NEF	PLTGWGCF	219	9	43	67		9484
NEF	QVLPKPMY	100	9	46	72		9485
NEF	QVLPKPMY	100	10	46	72	0.6100	9486
NEF	QVLPKPMY	95	9	48	75		9487
NEF	QVLPKPMY	102	11	48	75		9488
NEF	PLTGWGCF	102	8	47	72		9489
NEF	STNSPTSR	32	8	01	33	0.0010	9490
POL	RANSFSSR	35	8	01	33		9491
POL	STNSPTSR	31	9	01	33		9492
POL	PLTRELQVR	36	9	01	33		9493
POL	QVLPKPMY	33	10	01	33		9494
POL	QVLPKPMY	34	11	01	33		9495
POL	QVLPKPMY	34	11	01	33		9496
POL	STNSPTSR	37	8	01	33		9497
POL	RANSPTTR	39	9	01	50		9498
POL	PLTRELQVR	39	9	01	50		9499
POL	STNSPTSR	24	10	01	50		9500
POL	PLTRELQVR	37	11	01	50		9501
POL	STNSPTSR	39	11	01	50		9502
POL	STNSPTSR	39	11	01	50		9503
POL	ADRGQGVSF	71	9	01	20		9504
POL	ADRGQGVSF	71	9	01	20		9505
POL	GADRGQGVSF	70	10	01	20		9506
POL	GADRGQGVSF	70	10	01	20		9507
POL	ADRGQGVSF	71	11	01	20		9508
POL	ADRGQGVSF	71	11	01	20		9509
POL	AGDRQGVSF	69	11	01	17		9510
POL	AGDRQGVSF	69	11	01	17		9511
POL	GTLNPPQTF	79	11	01	17		9512
POL	NLAPQGEA	5	9	10	16		9513
POL	NLAPQGEA	5	9	10	16		9514
POL	KTGKAKMRT	542	11	10	16		9515
POL	ILIEICGH	149	8	10	16		9516
POL	LIEICGH	150	8	10	16		9517
POL	YAKMRTAI	546	8	10	16		9518
POL	YAKMRTAI	546	8	10	16		9519
POL	YAKMRTAI	546	8	10	16		9520
POL	APQGEARE	543	10	10	16		9521
POL	LIEALLDTGA	106	10	10	16		9522
POL	TKGYAKMRTA	543	10	10	16		9523
POL	ETWETWMTD	588	10	10	16		9524
POL	ETWETWMTD	588	10	10	16		9525
POL	ETWETWMTD	588	10	10	16		9526
POL	VSLDTINQK	659	10	10	16		9527
POL	LAFPOGEARE	6	11	10	16		9528
POL	QLIEALLDTGA	105	11	10	16		9529
POL	MLTQLGCTIN	176	11	10	16		9530
POL	TKGYAKMRTA	543	11	10	16		9531
POL	VSLDTINQK	658	11	10	16		9531

Table XVI
 CHY A03 Modf Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (n)	A*0301	SIQ D NO.
POL	QTKELQKQIK	861	11	10	16		9532
POL	QTRANSTR	21	11	11	17		9533
POL	LDGDKAQEDH	754	11	11	17		9534
POL	IGGFHKV	137	8	11	17		9535
POL	RIGPENP	238	8	11	17		9536
POL	WPLTELA	481	8	11	17		9537
POL	YKSNVPEK	331	8	11	17		9538
POL	QLTEVQK	339	8	11	17		9539
POL	LDKAEEDH	757	8	11	17		9540
POL	WAGIQEF	884	8	11	17		9541
POL	VYRRKVK	1012	8	11	17		9542
POL	KIKDYGC	1019	8	11	17		9543
POL	GGGFHKV	136	9	11	17		9544
POL	EWLPELA	480	9	11	17		9545
POL	SLDTINQK	660	9	11	17		9546
POL	GDKAEEDH	756	9	11	17		9547
POL	KVYRRKVK	1011	9	11	17		9548
POL	GGGFHKV	135	10	11	17		9549
POL	ISRGPENP	236	10	11	17		9550
POL	SLDTEVQK	330	10	11	17		9551
POL	ESWYVNDK	433	10	11	17		9552
POL	ETTNQKLEH	663	10	11	17		9553
POL	DGDKAQEDH	755	10	11	17		9554
POL	GSNFTTVK	870	10	11	17		9555
POL	GIQEEGIPY	886	10	11	17		9556
POL	YKSNVPEK	332	10	11	17		9557
POL	IKDYGKMA	100	10	11	17		9558
POL	IGGGGFKVK	134	10	11	17		9559
POL	KISRGPENP	235	11	11	17		9560
POL	PSNNETGIR	322	11	11	17		9561
POL	STNNETGIR	323	11	11	17		9562
POL	YKSNVPEK	478	11	11	17		9563
POL	VYSLETELA	479	11	11	17		9564
POL	ETTNQKLEH	662	11	11	17		9565
POL	ETTNQKLEH	663	11	11	17		9566
POL	NGSNFTTV	869	11	11	17		9567
POL	GSNFTTVK	870	11	11	17		9568
POL	ACWAGQDE	881	11	11	17		9569
POL	GIQEEGIPY	885	11	11	17		9570
POL	IKDYGKMA	983	11	11	17		9571
POL	IMIASQWIK	953	11	11	17		9572
POL	VDIATDGT	957	11	11	17		9573
POL	ASDQTKELQK	1007	11	11	17		9574
POL	NSEKVVRKK	1019	11	11	17		9575
POL	KIKDYGKQMA	1019	11	11	17		9576
POL	NLSLADGA	60	8	12	20		9577
POL	IKDYGKMA	100	10	12	19		9578
POL	IKDKNER	969	8	12	19		9579
POL	QIVFGVK	458	9	12	19		9580
POL	QDQWLYQV	526	9	12	19		9581
POL	IKIQNFRVY	969	10	12	19		9582
POL	ASQVYGHVK	456	11	12	19		9583

Table XVI
 HIV A03 Motif Pockets with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SHQ ID NO.
POL	IKIQKRVVY	969	11	12	19		9592
POL	LAFOGEA	6	8	12	19		9583
POL	LAFOKRA	6	8	12	19		9584
POL	AFKGRAR	668	8	12	19		9585
POL	KTELQATL	670	8	12	19		9586
POL	ELQATYLA	670	8	12	19		9587
POL	QIKQKQNF	968	8	12	19		9588
POL	KDYGRQMA	1022	8	12	19		9589
POL	LAFOGEAR	6	9	12	19		9590
POL	ELNCKKWK	122	9	12	19		9591
POL	QIKQKQNLH	664	9	12	19		9592
POL	QIKQKQNF	1003	9	12	19		9593
POL	VIQDSEIK	1007	9	12	19		9594
POL	NSEIKVVR	119	10	12	19		9595
POL	VLEENLGR	119	10	12	19		9596
POL	TTNOKTELIA	664	10	12	19		9597
POL	KTELQATYLA	668	10	12	19		9598
POL	QIKQKQNLH	1002	10	12	19		9599
POL	NSEIKVVR	119	10	12	19		9600
POL	TVLEENLGR	118	11	12	19		9601
POL	ELNCKKWK	122	11	12	19		9602
POL	ELRQILLRWG	393	11	12	19		9603
POL	QGDQWYQI	524	11	12	19		9604
POL	RMGKAITNDV	548	11	12	19		9605
POL	QIKQKQNLH	968	11	12	19		9606
POL	AVIQDSEIK	1005	11	12	19		9607
POL	QDSEIKVVR	1005	11	12	19		9608
POL	ELQKQIK	964	8	13	21		9609
POL	EFSEQTRA	16	9	13	21		9610
POL	KTGRYARMR	542	9	13	21		9611
POL	NKTKGYARM	540	10	13	21		9612
POL	QIKQKQNLH	542	11	13	21		9613
POL	QIKQKQNLH	542	11	13	21		9614
POL	IVPLTEEA	481	8	13	20		9615
POL	TKGYARMAR	543	8	13	20		9616
POL	YARMRGAI	546	8	13	20		9617
POL	IGQVREQA	914	8	13	20		9618
POL	QIKQKQNLH	916	8	13	20		9619
POL	QIKQKQNLH	122	9	13	20		9620
POL	QIKQKQNLH	122	9	13	20		9621
POL	QIKQKQNLH	122	9	13	20		9622
POL	QIKQKQNLH	122	9	13	20		9623
POL	QIKQKQNLH	122	9	13	20		9624
POL	QIKQKQNLH	122	9	13	20		9625
POL	QIKQKQNLH	122	9	13	20		9626
POL	QIKQKQNLH	122	9	13	20		9627
POL	QIKQKQNLH	122	9	13	20		9628
POL	QIKQKQNLH	122	9	13	20		9629
POL	QIKQKQNLH	122	9	13	20		9630
POL	QIKQKQNLH	122	9	13	20		9631
POL	QIKQKQNLH	122	9	13	20		9632
POL	QIKQKQNLH	122	9	13	20		9633
POL	QIKQKQNLH	122	9	13	20		9634
POL	QIKQKQNLH	122	9	13	20		9635
POL	QIKQKQNLH	122	9	13	20		9636
POL	QIKQKQNLH	122	9	13	20		9637
POL	QIKQKQNLH	122	9	13	20		9638
POL	QIKQKQNLH	122	9	13	20		9639
POL	QIKQKQNLH	122	9	13	20		9640
POL	QIKQKQNLH	122	9	13	20		9641
POL	QIKQKQNLH	122	9	13	20		9642
POL	QIKQKQNLH	122	9	13	20		9643
POL	QIKQKQNLH	122	9	13	20		9644
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POL	QIKQKQNLH	122	9	13	20		9648
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POL	QIKQKQNLH	122	9	13	20		9650
POL	QIKQKQNLH	122	9	13	20		9651
POL	QIKQKQNLH	122	9	13	20		9652
POL	QIKQKQNLH	122	9	13	20		9653
POL	QIKQKQNLH	122	9	13	20		9654
POL	QIKQKQNLH	122	9	13	20		9655
POL	QIKQKQNLH	122	9	13	20		9656
POL	QIKQKQNLH	122	9	13	20		9657
POL	QIKQKQNLH	122	9	13	20		9658
POL	QIKQKQNLH	122	9	13	20		9659
POL	QIKQKQNLH	122	9	13	20		9660
POL	QIKQKQNLH	122	9	13	20		9661
POL	QIKQKQNLH	122	9	13	20		9662
POL	QIKQKQNLH	122	9	13	20		9663
POL	QIKQKQNLH	122	9	13	20		9664
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POL	QIKQKQNLH	122	9	13	20		9666
POL	QIKQKQNLH	122	9	13	20		9667
POL	QIKQKQNLH	122	9	13	20		9668
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POL	QIKQKQNLH	122	9	13	20		9670
POL	QIKQKQNLH	122	9	13	20		9671
POL	QIKQKQNLH	122	9	13	20		9672
POL	QIKQKQNLH	122	9	13	20		9673
POL	QIKQKQNLH	122	9	13	20		9674
POL	QIKQKQNLH	122	9	13	20		9675
POL	QIKQKQNLH	122	9	13	20		9676
POL	QIKQKQNLH	122	9	13	20		9677
POL	QIKQKQNLH	122	9	13	20		9678
POL	QIKQKQNLH	122	9	13	20		9679
POL	QIKQKQNLH	122	9	13	20		9680
POL	QIKQKQNLH	122	9	13	20		9681
POL	QIKQKQNLH	122	9	13	20		9682
POL	QIKQKQNLH	122	9	13	20		9683
POL	QIKQKQNLH	122	9	13	20		9684
POL	QIKQKQNLH	122	9	13	20		9685
POL	QIKQKQNLH	122	9	13	20		9686
POL	QIKQKQNLH	122	9	13	20		9687
POL	QIKQKQNLH	122	9	13	20		9688
POL	QIKQKQNLH	122	9	13	20		9689
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POL	QIKQKQNLH	122	9	13	20		9701
POL	QIKQKQNLH	122	9	13	20		9702
POL	QIKQKQNLH	122	9	13	20		9703
POL	QIKQKQNLH	122	9	13	20		9704
POL	QIKQKQNLH	122	9	13	20		9705
POL	QIKQKQNLH	122	9	13	20		9706
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POL	QIKQKQNLH	122	9	13	20		9712
POL	QIKQKQNLH	122	9	13	20		9713
POL	QIKQKQNLH	122	9	13	20		9714
POL	QIKQKQNLH	122	9	13	20		9715
POL	QIKQKQNLH	122	9	13	20		9716
POL	QIKQKQNLH	122	9	13	20		9717
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POL	QIKQKQNLH	122	9	13	20		9719
POL	QIKQKQNLH	122	9	13	20		9720
POL	QIKQKQNLH	122	9	13	20		9721
POL	QIKQKQNLH	122	9	13	20		9722
POL	QIKQKQNLH	122	9	13	20		9723
POL	QIKQKQNLH	122	9	13	20		9724
POL	QIKQKQNLH	122	9	13	20		9725
POL	QIKQKQNLH	122	9	13	20		9726
POL	QIKQKQNLH	122	9	13	20		9727
POL	QIKQKQNLH	122	9	13	20		9728
POL	QIKQKQNLH	122	9	13	20		9729
POL	QIKQKQNLH	122	9	13	20		9730
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POL	QIKQKQNLH	122	9	13	20		9732
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POL	QIKQKQNLH	122	9	13	20		9736
POL	QIKQKQNLH	122	9	13	20		9737
POL	QIKQKQNLH	122	9	13	20		9738
POL	QIKQKQNLH	122	9	13	20		9739
POL	QIKQKQNLH	122	9	13	20		9740
POL	QIKQKQNLH	122	9	13	20		9741
POL	QIKQKQNLH	122	9	13	20		9742
POL	QIKQKQNLH	122	9	13	20		9743
POL	QIKQKQNLH	122	9	13	20		9744
POL	QIKQKQNLH	122	9	13	20		9745
POL	QIKQKQNLH	122	9	13	20		9746
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POL	QIKQKQNLH	122	9	13	20		9765
POL	QIKQKQNLH	122	9	13	20		9766
POL	QIKQKQNLH	122	9	13	20		9767
POL	QIKQKQNLH	122	9	13	20		9768
POL	QIKQKQNLH	122	9	13	20		9769
POL	QIKQKQNLH	122</					

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KIGQVREQA	912	10	13	20		9632
POL	IGQVREQAHEI	914	10	13	20		9633
POL	QVQAEQHEILK	916	10	13	20		9634
POL	QVQAEQHEILK	919	10	13	20		9635
POL	TLWGRHXYTV	91	11	13	20		9636
POL	LVTRIGGOLK	97	11	13	20		9637
POL	TVLEDINLPGK	118	11	13	20		9638
POL	DINLPGKWK	122	11	13	20		9639
POL	QLIEICGKKA	148	11	13	20		9640
POL	QVQAEQHEILK	390	11	13	20		9641
POL	QVQAEQHEILK	418	11	13	20		9642
POL	LDIVPLILEA	433	11	13	20	0.0011	9643
POL	TKGYARMRGA	543	11	13	20		9644
POL	LAGRWVPKTI	856	11	13	20		9645
POL	IIGQVREQAHEI	913	11	13	20		9646
POL	DSRDPLWKGFP	981	11	13	20		9647
POL	EFVQVTRKAK	1009	11	13	20		9648
POL	EFVQVTRKAK	1011	11	13	20		9649
POL	QVQAEQHEILK	438	9	14	22		9650
POL	ASQVFGIKVR	456	9	14	22		9651
POL	IATESIVWGG	567	11	14	22		9652
POL	ILIEICGR	149	8	14	22		9653
POL	LIIEICGRK	150	8	14	22		9654
POL	EFVQVTRKAK	152	8	14	22		9655
POL	EFVQVTRKAK	872	8	14	22		9656
POL	EFVQVTRKAK	873	8	14	22		9657
POL	TSTIVKAA	874	8	14	22		9658
POL	IASDQIK	956	8	14	22		9659
POL	DSRDPLWK	981	8	14	22		9660
POL	QLIEICGR	148	9	14	22		9661
POL	ILIEICGKK	149	9	14	22		9662
POL	EFVQVTRKAK	872	9	14	22		9663
POL	EFVQVTRKAK	873	9	14	22	0.0003	9664
POL	IASDQIK	955	9	14	22		9665
POL	IASDQIK	980	9	14	22		9666
POL	RSRDPLWK	983	9	14	22		9667
POL	RDPLWKGFA	983	9	14	22		9668
POL	QLIEICGK	148	10	14	22		9669
POL	QVQAEQHEILK	388	10	14	22		9670
POL	RTKIELRQH	411	10	14	22		9671
POL	THUNNDSF	864	10	14	22		9672
POL	EFVQVTRKAK	872	10	14	22		9673
POL	TTVKAACWW	876	10	14	22	0.0006	9674
POL	AGERIVDIA	948	10	14	22		9675
POL	DIASDIQIK	954	10	14	22		9676
POL	RDPLWKGPAK	983	10	14	22		9677
POL	EFVQVTRKAK	146	11	14	22		9678
POL	YQVQIEICGR	146	11	14	22		9679
POL	ELBEILLKGG	393	11	14	22		9680
POL	KTPKFKLPQK	577	11	14	22		9681
POL	GIIDKAEHEER	756	11	14	22		9682
POL	STTVKAACW	875	11	14	22		9683

Table XVI
HIV-A03-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	SAGERIVDIA	947	11	14	22		9682
POL	QTRANSPTK	21	9	15	24		9683
POL	LVEICTEMEK	221	10	15	24	0.0002	9684
POL	FFREDLAF	1	8	15	23		9685
POL	PSSIGDTHA	17	8	15	23		9686
POL	QKQDQWY	305	8	15	23		9687
POL	QKQDQWY	524	8	15	23		9688
POL	KTELQAHII	668	8	15	23		9689
POL	AGIRKVLV	746	8	15	23		9690
POL	PIQKRWEA	584	9	15	23		9691
POL	SAGIRKVLV	745	9	15	23		9692
POL	IRKVPKRR	1099	9	15	23		9693
POL	IRKVPKRR	177	9	15	23		9694
POL	QKQDQWY	177	10	15	23		9695
POL	KTELQAHII	668	10	15	23		9696
POL	LGHOQDPR	695	10	15	23		9697
POL	VDKLVASGIR	740	10	15	23		9698
POL	VSAGIRKVLV	744	10	15	23		9699
POL	IDKAEIEHIER	757	10	15	23		9700
POL	ALVEICTHEK	220	11	15	23		9701
POL	QKQDQWY	524	11	15	23		9702
POL	ALVEICTHEK	694	11	15	23		9703
POL	LVNQHEDLIK	709	11	15	23		9704
POL	QVDKLVASGIR	739	11	15	23		9705
POL	VDKLVASGIRK	740	11	15	23		9706
POL	LVASGIRKVLV	743	11	15	23		9707
POL	IDKAEIEHIER	757	11	15	23		9708
POL	QKQDQWY	759	11	16	25		9709
POL	LVNQHEDLIK	709	9	16	25		9710
POL	KAQIEHIER	759	9	16	25		9711
POL	NLAFOQGEAR	5	10	16	25		9712
POL	KAQIEHIERVII	759	10	16	25		9713
POL	LAPQOGEA	6	8	16	25		9714
POL	QKQDQWY	7	8	16	25		9715
POL	QKQDQWY	305	8	16	25		9716
POL	QKQDQWY	179	8	16	25		9717
POL	SAHTINDVK	551	8	16	25		9718
POL	ELQAHIIA	670	8	16	25		9719
POL	ILQAOQDR	697	8	16	25		9720
POL	QVDKLVSA	739	8	16	25		9721
POL	LVNQHEDLIK	742	8	16	25		9722
POL	QKQDQWY	743	8	16	25		9723
POL	ELKVVPR	1099	8	16	25	0.0091	9724
POL	LAPQOGEAR	6	9	16	25		9725
POL	GIHQAOQDR	696	9	16	25		9726
POL	KLVSAGIRK	742	9	16	25	0.1300	9727
POL	QKQDQWY	620	10	16	25		9728
POL	QKQDQWY	26	8	17	27		9729
POL	QKQDQWY	301	8	17	27		9730
POL	ELKELLIK	301	8	17	27		9731
POL	WGKTPKFK	575	8	17	27		9732

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	TIKIGGOLK	99	9	17	27		9732
POL	VIKIGGOLK	98	9	17	27	0.2700	9733
POL	TVQHQLPEK	429	10	17	27	0.0370	9734
POL	VIWGTPEK	573	10	17	27		9735
POL	TLWQRLVTI	91	11	17	27		9736
POL	TIKIGGOLK	99	11	17	27		9737
POL	TVQHQLPEK	429	11	17	27		9738
POL	VIWGTPEK	573	11	17	27		9739
POL	ETTNQKLEQ	663	11	17	27		9740
POL	KDPRKYTAF	311	9	18	29		9741
POL	YFSPDKDF	304	10	18	29		9742
POL	YFSPDKDF	304	11	18	29		9743
POL	YFSPDKDF	304	11	18	29		9744
POL	YFSPDKDF	304	11	18	29		9745
POL	YFSPDKDF	304	8	18	28		9746
POL	YFSPDKDF	304	8	18	28		9747
POL	YFSPDKDF	304	9	18	28		9748
POL	YFSPDKDF	304	9	18	28		9749
POL	YFSPDKDF	304	10	18	28		9750
POL	YFSPDKDF	304	10	18	28		9751
POL	YFSPDKDF	304	10	18	28		9752
POL	YFSPDKDF	304	11	18	28		9753
POL	YFSPDKDF	304	11	18	28		9754
POL	YFSPDKDF	304	11	18	28		9755
POL	YFSPDKDF	304	11	18	28		9756
POL	YFSPDKDF	304	11	18	28		9757
POL	YFSPDKDF	304	8	19	30		9758
POL	YFSPDKDF	304	8	19	30		9759
POL	YFSPDKDF	304	9	19	30		9760
POL	YFSPDKDF	304	9	19	30		9761
POL	YFSPDKDF	304	11	19	30		9762
POL	YFSPDKDF	304	8	19	30		9763
POL	YFSPDKDF	304	8	19	30		9764
POL	YFSPDKDF	304	8	19	30		9765
POL	YFSPDKDF	304	8	19	30		9766
POL	YFSPDKDF	304	8	19	30		9767
POL	YFSPDKDF	304	8	19	30		9768
POL	YFSPDKDF	304	9	19	30		9769
POL	YFSPDKDF	304	9	19	30		9770
POL	YFSPDKDF	304	10	19	30		9771
POL	YFSPDKDF	304	10	19	30		9772
POL	YFSPDKDF	304	10	19	30		9773
POL	YFSPDKDF	304	10	19	30		9774
POL	YFSPDKDF	304	10	19	30		9775
POL	YFSPDKDF	304	11	19	30		9776
POL	YFSPDKDF	304	11	19	30		9777
POL	YFSPDKDF	304	11	19	30		9778
POL	YFSPDKDF	304	9	20	32		9779
POL	YFSPDKDF	304	9	20	32	0.0750	9780
POL	YFSPDKDF	304	9	20	32	0.0280	9781
POL	YFSPDKDF	304	10	20	32		

Table XVI
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*301	SEQ ID NO.
POL	KAAQWAGIK	879	10	20	32	0.0300	9782
POL	ASQYAGVAK	456	11	20	32		9783
POL	KYLAAPVPI	722	11	20	32	0.0000	9785
POL	KFKLPQK	580	8	20	31		9786
POL	GDGCVASR	1030	8	20	31		9787
POL	AGDCVASR	1029	9	20	31		9788
POL	VSLTETNQK	659	10	20	31		9789
POL	LLKAGVAPV	853	11	20	31		9790
POL	LLKAGVAPV	853	11	20	31		9791
POL	YFSVPLDK	304	8	21	33		9792
POL	KVHTDINGSNF	863	11	21	33		9793
POL	ACWVAGIK	881	8	21	33		9794
POL	WAGIKQEF	884	8	21	33		9795
POL	SLTETNQK	660	9	21	33		9796
POL	AGDCVASR	1030	9	21	33		9797
POL	DAVSGVPLDK	304	10	21	33	0.0130	9798
POL	DLEGGHRTK	381	10	21	33		9799
POL	QLCKLLRGTK	467	10	21	33		9800
POL	SDFNLPPIVA	776	10	21	33		9801
POL	LEIQGCTLNF	176	11	21	33		9802
POL	IFAIKKKIDSK	249	11	21	33		9803
POL	QVSLGQIRIK	361	11	21	33		9804
POL	SLLEGGQIRIK	380	11	21	33		9805
POL	QLCKLLRGTK	467	11	21	33		9806
POL	ASDFNLPTIVA	775	11	21	33		9807
POL	SDFNLPPIVA	776	11	21	33		9808
POL	ACWVAGIKQEF	881	11	21	33		9809
POL	AGKQEGGIPY	885	11	21	33		9810
POL	IFAIKKKIDSK	249	11	22	34		9811
POL	IFAIKKKIDSK	249	11	22	34		9812
POL	EQGQIRTK	383	8	22	34		9813
POL	RTKLEELR	388	8	22	34		9814
POL	YLAAPVPI	724	8	22	34		9815
POL	LAWVPAIK	725	8	22	34		9816
POL	YLAAPVPI	724	9	22	34	0.0770	9817
POL	NTKLEELR	383	10	22	34		9818
POL	MTKLEELR	353	10	22	34	0.0150	9819
POL	KVLAAPVPI	823	10	22	34		9820
POL	AGRWPKVPII	857	10	22	34		9821
POL	GKQEGGIPY	886	10	22	34	0.0002	9822
POL	SMKLEELR	352	11	22	34		9823
POL	KTRKLEELR	377	11	22	34		9824
POL	YLAAPVPI	722	11	22	34		9825
POL	KVLSWVPAH	722	9	23	37		9826
POL	KVLSWVPAH	722	11	23	37		9827
POL	KVLSWVPAH	722	11	23	37		9828
POL	KLEPERK	355	8	23	36		9829
POL	EKGVLVA	821	8	23	36		9830
POL	KVLAAPVPI	823	8	23	36		9831
POL	KUGQQLKEA	101	9	23	36		

Table XVI
HIV A03-Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SHQ ID NO.
POL	DNFLPPIVA	777	9	23	36		9832
POL	TVKAVHVA	824	9	23	36		9833
POL	TVKAAACWVA	877	9	23	36		9834
POL	SPQTLWQR	86	10	23	36		9835
POL	DNFLPIVAK	777	10	23	36		9836
POL	LEGRKLVVA	819	10	23	36		9837
POL	IKVQVQVVA	820	10	23	36		9838
POL	LLKNGFTTID	398	11	23	36		9839
POL	LLRWGFTTID	398	11	23	36		9840
POL	IDIATDIQIK	953	11	23	36		9841
POL	KLLRGTKA	470	8	24	38		9842
POL	NTHFAIK	246	8	24	38		9843
POL	SDIDCVAGR	1030	8	24	38		9844
POL	SPDKLIRGKA	468	9	24	38		9845
POL	LCKLLRGTK	468	9	24	38	0.0004	9846
POL	AGIDCVAGR	1029	9	24	38		9847
POL	NTHFAIKKK	246	10	24	38		9848
POL	LCKLLRGTKA	468	10	24	38		9849
POL	VHIDGNSF	864	10	24	38		9850
POL	MAIDIDCVAGR	1028	10	24	38		9851
POL	IKVQVQVVA	820	11	24	38		9852
POL	QIGQGWIYDI	524	11	24	38		9853
POL	KLGAAGYVID	643	11	24	38		9854
POL	TAYFLKLAG	849	11	24	38		9855
POL	QMAIGDDCVAG	1027	11	24	38		9856
POL	KLLRGAKA	470	8	25	40		9857
POL	QGGWYTIQY	526	9	25	40		9858
POL	QGGWYTIQY	526	9	25	40		9859
POL	PIFAIKKK	248	8	25	39	0.0004	9860
POL	QGGWYTIQY	524	8	25	39		9861
POL	FLKLKLAGR	852	8	25	39		9862
POL	QLCKLLRGA	467	9	25	39		9863
POL	IVAKEIVA	782	9	25	39		9864
POL	FLKLKLAGR	851	9	25	39		9865
POL	QLCKLLRGA	468	10	25	39		9866
POL	LGKAGYVIDR	644	10	25	39		9867
POL	IDKAEIEIK	757	10	25	39		9868
POL	SDFLNPVVA	776	10	25	39		9869
POL	PSKDLIAEQK	513	11	25	39		9870
POL	INQTELEK	763	11	25	39		9871
POL	QGGWYTIQY	524	11	25	39		9872
POL	IDKAEIEIKY	757	11	25	39		9873
POL	ASDFNLPPVVA	775	11	25	39		9874
POL	SDFLNPVVA	776	11	25	39		9875
POL	RAKIEELR	388	8	26	41		9876
POL	LCKLLRGA	468	8	26	41		9877
POL	IKVQVQVVA	820	8	26	41		9878
POL	NTHFAIK	246	8	26	41		9879
POL	IVAKEIVA	783	8	26	41		9880
POL							9881

Table XVI
HIV-A03 Motif Repeats with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	LCKLLRGAK	468	9	26	41		9882
POL	LTEAVOKIA	560	9	26	41		9883
POL	SSGGRKVLV	745	9	26	41		9884
POL	QTEAVOKIA	777	9	26	41		9885
POL	QTEAVOKIA	777	9	26	41		9886
POL	VSSGRKVLV	744	10	26	41		9887
POL	DFNLPPVAK	777	10	26	41		9888
POL	GSNFTSAAVK	870	10	26	41		9889
POL	LVSSGRKVLV	743	11	26	41		9890
POL	TGQETAYELL	845	11	26	41		9891
POL	GSNFTSAAVK	869	11	26	41		9892
POL	GSNFTSAAVK	869	11	26	41		9893
POL	KAQEDIEK	759	8	27	43		9894
POL	ASQYAGIK	456	9	27	43	0.0013	9895
POL	KAQEDIEK	759	9	27	43		9896
POL	KAQEDIEK	759	10	27	43		9897
POL	ECTEMER	223	8	27	42		9898
POL	LGQHRK	383	8	27	42		9899
POL	LGQHRK	383	8	27	42		9900
POL	SGRKKVLV	746	8	27	42		9901
POL	NLPPVAK	779	8	27	42		9902
POL	ETAYFLK	848	8	27	42	0.0037	9903
POL	TSAAVKAA	874	8	27	42		9904
POL	KLSSGRK	742	9	27	42	0.0027	9905
POL	ETAYFLK	848	9	27	42		9906
POL	ETAYFLK	848	10	27	42		9907
POL	DLGGHRK	381	10	27	42	0.0032	9908
POL	KLWASQIYA	452	10	27	42		9909
POL	WASQYAGIK	455	10	27	42		9910
POL	KYKQCKLLR	464	10	27	42		9911
POL	ETAYFLK	848	10	27	42		9912
POL	ECTEMER	223	10	27	42		9913
POL	ECTEMER	223	11	27	42		9914
POL	SDLEGGHRK	380	11	27	42		9915
POL	VKLVSGRK	740	11	27	42		9916
POL	ASQYPRK	456	9	28	44		9917
POL	KDLAEIQ	515	9	28	44		9918
POL	NKTKYAK	540	9	28	44		9919
POL	DLGGHRK	381	10	28	44		9920
POL	IVGAEFF	625	8	28	44		9921
POL	IVGAEFF	626	8	28	44		9922
POL	GSNFTSAV	870	8	28	44		9923
POL	NFTSAVR	872	8	28	44		9924
POL	FTSAVKA	873	8	28	44		9925
POL	CTEMERK	225	9	28	44	0.0002	9926
POL	IVGAEFF	625	9	28	44		9927
POL	GVKAKLEA	463	9	28	44		9928
POL	GVKAKLEA	463	9	28	44		9929
POL	QUKKEKY	716	9	28	44		9930
POL	PVVAKEIVA	782	9	28	44		9931

Table XVI
HIV-1 Gag-Mediated Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NGSNFISAA	869	9	28	44		9932
POL	NFTSAAKVA	872	9	28	44		9933
POL	ICTEMEKEGK	874	10	28	44		9934
POL	SDLEIGQIRA	880	10	28	44		9935
POL	AVAKACQW	875	10	28	44		9936
POL	AVAKACQW	876	10	28	44		9937
POL	GSDLEIGQIRA	879	11	28	44		9938
POL	VGAETFYVDG	877	11	28	44		9939
POL	TGNSGNTSA	867	11	28	44		9940
POL	SAVKAACW	875	11	28	44		9941
POL	NLTKGTAYR	840	9	29	46	0.0008	9942
POL	NSNGTKR	842	8	29	45		9943
POL	VWVTKR	843	8	29	45		9944
POL	VDKLVSSGR	740	10	29	45		9945
POL	PLTIEAELEA	483	11	29	45		9946
POL	IIVWGTIKR	572	11	29	45		9947
POL	QVDRVLSSGR	739	11	29	45		9948
POL	WGTIKR	575	8	30	47		9949
POL	ILVTVQA	861	9	30	47		9950
POL	ILVTVQA	862	9	30	47		9951
POL	ANRETKLGR	637	10	30	47	0.0007	9952
POL	IIQLIKKEK	713	10	30	47	0.0004	9953
POL	KILVAIIVA	823	10	30	47		9954
POL	GAANRETKLG	636	11	30	47		9955
POL	ANRETKLGR	637	11	30	47		9956
POL	ANRETKLGR	638	11	30	47		9957
POL	ILKAGRWV	852	11	30	47		9958
POL	ILKAGRWV	853	11	30	47		9959
POL	VVAKEIVA	783	8	31	48		9960
POL	EGKILVA	821	8	31	48		9961
POL	KILVAHI	823	8	31	48		9962
POL	ETAYHLK	848	8	31	48		9963
POL	YHLKLAGR	851	9	31	48		9964
POL	EGKILVA	821	10	31	48		9965
POL	ETAYHLKLA	848	10	31	48		9966
POL	PSINNETGIR	322	11	31	48		9967
POL	TQETAYFILK	845	11	31	48		9968
POL	TAYFILKLAGR	849	11	31	48		9969
POL	FILKLAGR	852	8	32	50		9970
POL	ETAYHLKLA	849	9	32	50		9971
POL	TAYFILKLA	849	9	32	50		9972
POL	AVKACQWVA	877	9	32	50		9973
POL	SINNETGIR	323	10	32	50		9974
POL	SINNETGIRY	323	11	32	50		9975
POL	SSMTKLEPR	351	11	32	50		9976
POL	IINDVKOLTE	553	11	32	50		9977
POL	IIINDVKOLTE	554	11	32	50		9978
POL	QTKLEQKQIK	966	11	32	50		9979
POL	DVKQLTEA	556	8	33	52	0.0050	9980
POL	NGSNFTSA	869	8	33	52		9981

Table XVI
 HIV-1 A92 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	EMEKEKISK	229	10	33	52	0.0004	9982
POL	SSMTKLELPF	351	10	33	52	0.0004	9983
POL	TDGNSFTSA	867	10	33	52		9984
POL	QSSMTKLELPF	350	11	33	52		9985
POL	DYKQLTEAVQ	356	11	33	52	0.0048	9987
POL	YDPSKGLTSS	511	11	34	53		9988
POL	YDPSKGLTSS	511	9	34	53		9989
POL	DIATDIQIK	954	11	34	53	0.0056	9990
POL	QLKQALLDYG	105	11	34	53		9991
POL	ELQKQITK	964	8	35	56		9992
POL	LKKEKVV	717	8	35	55		9993
POL	QTKIQNF	968	8	35	55		9994
POL	QTKIQNF	968	8	35	55		9995
POL	ETLKEGACY	641	9	35	55		9996
POL	HAIDQIK	955	9	35	55	0.0250	9997
POL	QTKIQNF	968	9	35	55	0.0021	9998
POL	RDSRDHWK	980	9	35	55		9999
POL	TDQIKELQK	958	10	35	55	0.0007	10000
POL	RDPWKGPAC	983	10	35	55		10001
POL	QTKIQNF	968	11	35	55	0.0051	10002
POL	QTKIQNF	968	11	35	55		10003
POL	DSRDHWKGP	981	11	35	55		10004
POL	SDIKVVRKA	1008	11	35	55		10005
POL	ITKIQNF	969	8	36	57	0.0016	10006
POL	ITKIQNF	969	10	36	57		10007
POL	ITKIQNF	969	11	36	57		10008
POL	ITKIQNF	969	8	36	57		10009
POL	ITKIQNF	969	8	36	56		10010
POL	NLPQKWKPK	124	9	36	56		10011
POL	ALFQSSMTK	347	9	36	56	1.0000	10012
POL	PAIFQSSMTK	346	10	36	56	0.0760	10013
POL	LTEAEATELA	484	10	36	56		10014
POL	PAIKKKDSTK	249	11	36	58		10015
POL	PAIKKKDSTK	249	8	37	58	0.0003	10016
POL	PVFAKKK	248	8	37	58	0.0003	10017
POL	QI TEAVOK	559	8	37	58		10018
POL	QIEQLIK	712	8	37	58		10019
POL	IEQLIK	713	8	37	58		10020
POL	YLSWVFAH	724	8	37	58		10021
POL	LSWVFAH	725	8	37	58	0.0330	10022
POL	YLSWVFAH	724	9	37	58	0.0091	10023
POL	QIEQLIK	712	9	37	58		10024
POL	YLSWVFAH	724	9	37	58		10025
POL	RDPIWKGP	983	9	37	58		10026
POL	VIQNSDIK	1003	9	37	58	0.0099	10027
POL	NPVFAKKK	246	10	37	58	0.0006	10028
POL	YQDPSDK	1002	10	37	58	0.0006	10029
POL	YQDPSDK	1002	11	37	58	0.0006	10030
POL	YQDPSDK	1002	8	38	59	0.0055	10031
POL	IFSSMTK	348	8	38	59		10032
POL	ILKEPVHGVV	498	11	38	59		10033

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1301	SEQ ID NO.
POL	LDGDKAQEEII	754	11	39	63		10013
POL	HSNWRAMA	768	8	39	61		10013
POL	AGVYTDGR	647	9	39	61		10034
POL	YVTDGRGK	649	9	39	61	0.0011	10035
POL	KAGVYTDGR	646	10	39	61		10036
POL	QVYTDGRGK	645	10	39	61	0.0007	10037
POL	DGDKAQEEII	755	10	39	61		10038
POL	DKVYPRKA	1009	10	39	61		10039
POL	PVIGVYVDF	505	11	39	61		10040
POL	AGVYTDGRGQ	647	11	39	61		10041
POL	ALGIQAQPK	694	11	39	61		10042
POL	DKVYPRKAK	1009	11	39	61	0.0090	10043
POL	TDGRGK	650	8	40	63		10044
POL	HSNWRAMA	768	9	40	63	0.0009	10045
POL	HSNWRAMA	768	9	40	63		10046
POL	GKQADPK	696	9	40	63		10047
POL	GDKAQEEII	756	9	40	63		10048
POL	NSDKVYPR	1007	9	40	63		10049
POL	ILKEPVIGVY	498	10	40	63	0.0007	10050
POL	NSDKVYPR	1007	10	40	63		10051
POL	ILKEPVIGVY	497	11	40	63	0.9300	10052
POL	WYQVDFKAL	532	11	40	63	0.2800	10053
POL	WYQVDFKAL	532	11	40	63		10054
POL	SAGERIDIA	947	11	40	63		10055
POL	QNSDKVYPR	1005	11	40	63		10056
POL	NSDKVYPR	1007	11	40	63		10057
POL	ESVWGRITPK	570	11	41	65		10058
POL	ESVWGRITPK	570	8	41	64		10059
POL	QVQDFPK	532	8	41	64	0.0010	10060
POL	QVQDFPK	532	8	41	64		10061
POL	QVQDFPK	532	8	41	64		10062
POL	QVQDFPK	532	8	41	64		10063
POL	QVQDFPK	532	8	41	64	0.0081	10064
POL	QVQDFPK	532	8	41	64	0.0048	10065
POL	QVQDFPK	532	8	41	64		10066
POL	QVQDFPK	532	8	41	64		10067
POL	QVQDFPK	532	8	41	64		10068
POL	QVQDFPK	532	8	41	64		10069
POL	QVQDFPK	532	8	41	64		10070
POL	QVQDFPK	532	8	41	64	0.0004	10071
POL	QVQDFPK	532	8	41	64		10072
POL	QVQDFPK	532	8	41	64		10073
POL	QVQDFPK	532	8	41	64	0.0004	10074
POL	QVQDFPK	532	8	41	64		10075
POL	QVQDFPK	532	8	41	64		10076
POL	QVQDFPK	532	8	41	64		10077
POL	QVQDFPK	532	8	41	64	0.0004	10078
POL	QVQDFPK	532	8	41	64	0.0008	10079
POL	QVQDFPK	532	8	41	64	0.0004	10080
POL	QVQDFPK	532	8	41	64		10081

Table XVI
HLV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO
POL	ASCDKQLK	790	9	43	67	0.0027	10082
POL	DSWTVNDOK	439	10	43	67	0.0007	10083
POL	TFYVDGAAR	631	10	43	67	0.0003	10084
POL	VASCDKQLK	789	10	43	67	0.0004	10085
POL	KIGQVRDQA	912	10	43	67		10086
POL	KDSWTVNDQ	438	11	43	67		10087
POL	DSWTVNDQ	438	11	43	67		10088
POL	IVASCDKQLK	788	11	43	67		10089
POL	SCDKCQIKGE	791	11	43	67	0.0070	10090
POL	MTKILEPT	353	8	44	69		10091
POL	IGQVRDQA	914	8	44	69		10092
POL	SDIKVPR	1008	8	44	69		10093
POL	MAGDDICVA	1028	8	44	69		10094
POL	MDIKVPR	1008	9	44	69		10095
POL	SDIKVPR	1008	9	44	69		10096
POL	QMAHDICVA	1027	9	44	69	0.0002	10097
POL	VDGAANREK	634	10	44	69	0.0003	10098
POL	IGQVRDQA	914	10	44	69		10099
POL	QVRDQAELK	916	10	44	69	0.0089	10100
POL	SDIKVPRK	1008	10	44	69	0.0004	10101
POL	YVVDGAANREK	633	11	44	69		10102
POL	GAFTYVIGA	628	11	44	69		10103
POL	YVVDGAANREK	633	11	44	69		10104
POL	IGQVRDQA	913	11	44	69		10105
POL	VAKIVASCDK	784	11	45	71		10106
POL	GAANREK	636	8	45	71		10107
POL	EVASCDK	787	8	45	71		10108
POL	PKNLIKTKY	637	9	45	71		10109
POL	PKNLIKTKY	537	10	45	70	0.0004	10110
POL	RDQAELIKTA	918	10	45	70		10111
POL	PLVLWYQLE	613	11	45	70		10112
POL	EILKEPVII	497	8	46	72		10113
POL	KLWYQLEK	616	8	46	72		10114
POL	RDQAELIKTA	918	8	46	72		10115
POL	PLVLWYQLEK	613	9	46	72		10116
POL	DIETLEK	999	9	46	72		10117
POL	LVKLWYQLEK	614	10	46	72	0.0009	10118
POL	KVKQWPLTEE	207	11	46	72	0.0560	10119
POL	VIWGRKTKF	573	9	47	73	0.0750	10120
POL	VIWGRKTKF	572	10	47	73		10121
POL	VIWGRKTKF	573	8	47	73		10122
POL	QVRDQAELK	916	8	48	75		10123
POL	DIKVVPR	1009	8	48	75		10124
POL	VIWGRKTKF	572	9	48	75	0.0850	10125
POL	DIKVVPRK	1009	9	48	75	0.0002	10126
POL	GAFTYVIGA	628	10	48	75		10127
POL	KVILLIDGDK	750	10	48	75	0.3600	10128
POL	CCKQLKGE	752	10	48	75		10129
POL	QVRDQAELK	916	10	48	75		10130
POL	VYTSNKLK	792	10	48	75		10131

Table XVI
HIV-1 M101 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KVFLDGIKKA	750	11	48	75		10132
POL	VLFLDGIKKA	901	11	48	75		10133
POL	VVSENNKELK	902	11	48	75		10134
POL	GVVSENNK	901	8	49	77		10135
POL	RDYKQMA	1022	8	49	77		10136
POL	QGVVSENNK	900	9	49	77		10137
POL	KLKPGMDGPK	197	10	49	77	0.3900	10138
POL	IRIDYKQMA	1020	10	49	77		10139
POL	KLKPGMDGPK	800	10	49	77		10140
POL	IRIDYKQMA	1019	11	49	77		10141
POL	KIRYKQMA	1019	11	49	77		10142
POL	ESVIVGK	570	8	50	79		10143
POL	VVDGAANR	633	8	50	78	0.0003	10144
POL	LAGRWPK	856	8	50	78		10145
POL	KIRIDYK	1019	8	50	78	2.7000	10146
POL	KLGRWPK	555	9	51	80	0.0007	10147
POL	KIRIDYK	238	8	51	80		10148
POL	FTTPDKII	403	8	51	80		10149
POL	TEYVDGAA	631	8	51	80		10150
POL	HTDNGSNF	866	8	51	80	0.0004	10151
POL	PGMDGPKVK	200	9	51	80		10152
POL	GFTTPDKKII	402	9	51	80		10153
POL	FTTPDKKII	630	9	51	80		10154
POL	VLELDGDKA	751	9	51	80	0.0380	10155
POL	VIVVYMDRLY	368	10	51	80	0.0007	10156
POL	WGFTTPDKKII	401	10	51	80		10157
POL	FTTPDKKIIQK	403	10	51	80	0.0002	10158
POL	VLFLDGIKKA	751	10	51	80	0.0004	10159
POL	KSYTVLDVGD	493	11	51	80		10160
POL	QVTVPEWEF	599	10	52	83	0.0004	10161
POL	PAGLKKKK	286	8	52	81		10162
POL	SDLGQKH	380	8	52	81		10163
POL	DLEGGQIR	381	8	52	81		10164
POL	WGFTTPDK	401	8	52	81		10165
POL	GFTTPDKK	402	8	52	81		10166
POL	VLELDGDKA	750	8	52	81		10167
POL	VASGYLEA	831	8	52	81		10168
POL	KIQNFVY	971	8	52	81		10169
POL	KVVRPKKA	1011	8	52	81		10170
POL	VVPRKAK	1012	8	52	81	0.0027	10171
POL	ETPRYQY	327	9	52	81		10172
POL	GSDLEQKH	327	9	52	81		10173
POL	GSDLEQKH	380	9	52	81		10174
POL	WGFTTPDK	401	9	52	81	0.0003	10175
POL	ATWPEWEF	600	9	52	81	0.0004	10176
POL	IIVASGVIEA	830	9	52	81	0.0003	10177
POL	KIQNFVY	971	9	52	81	0.0003	10178
POL	KVVRPKAK	1011	9	52	81	0.0200	10179
POL	VGSLEIGQHI	378	10	52	81		10180
POL	VGSLEIGQHI						10181

Table XVI
HIV-1 gp120 Motif Peptides with Bleeding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.01$	SEQ ID NO.
POL	GSDELIGQIR	379	10	52	81		10182
POL	KIQNERVYVR	971	10	52	81	0.0320	10183
POL	NERYVYRDSR	974	10	52	81		10184
POL	IGGIGGFKVR	134	11	52	81		10185
POL	VQPTVNIQIR	164	11	52	81		10186
POL	IGGIGGFKVR	379	11	52	81		10187
POL	VGSDLEIGQIR	378	11	52	81		10188
POL	AVIVASGVYEA	828	11	52	81		10189
POL	SGVIEAEVPA	833	11	52	81		10190
POL	GIPIHAGLKKK	282	11	53	84		10191
POL	IGGFKVR	137	8	53	83		10192
POL	GHKVRQY	139	8	53	83		10193
POL	ELVPAKIK	190	8	53	83		10194
POL	ETVPAKIK	192	8	53	83	0.0049	10195
POL	ELVPAKIK	489	8	53	83		10196
POL	QLKGEAMII	796	8	53	83		10197
POL	ESMNKELK	904	8	53	83		10198
POL	SMNRELKK	905	8	53	83		10199
POL	GGGFKVR	136	9	53	83	0.0008	10200
POL	GGGFKVR	137	9	53	83	0.0008	10201
POL	YIEAEVPA	835	9	53	83	0.0003	10202
POL	ESMNKELK	904	9	53	83		10203
POL	GGGFKVR	135	10	53	83	0.0004	10204
POL	IGGFKVRQY	137	10	53	83		10205
POL	ISPIETVPAK	188	10	53	83	0.0003	10206
POL	PIETVPAK	190	10	53	83	0.0002	10207
POL	LVAVHVASGY	489	10	53	83		10208
POL	LVAVHVASGY	826	10	53	83		10209
POL	GGGFKVRQY	136	11	53	83		10210
POL	ISPIETVPAK	187	11	53	83		10211
POL	LVAVHVASGY	825	11	53	83		10212
POL	FVNTPIELK	608	9	54	86	0.0120	10213
POL	GIPIHAGLKK	282	10	54	86	0.0110	10214
POL	GIPIHAGLKK	283	11	54	86		10215
POL	LVAVHVASGY	825	8	54	84		10216
POL	PTVNIQIR	166	9	54	84	0.0008	10217
POL	PLTEKKA	212	9	54	84		10218
POL	LAENRELK	492	9	54	84	0.0002	10219
POL	EVQLGIPIPA	278	10	54	84		10220
POL	ELAENRELK	493	10	54	84	0.0002	10221
POL	ISPIETVPAK	607	8	55	86		10222
POL	PLTEKKA	212	8	55	86		10223
POL	ETTYVDGA	630	8	55	86		10224
POL	FLDGDIDK	752	8	55	86		10225
POL	FLDGDIDK	753	8	55	86		10226
POL	FLDGDIDK	752	9	55	86		10227
POL	QLGHIIIPA	280	8	56	89	0.2300	10228
POL	KGIGGVSA	940	9	56	89		10229
POL	KGIGGVSA	940	9	56	89		10230
POL	LGIIHPIAGLK	281	10	56	89	0.0370	10231

Table XVI
HIV-1 Amino Acid Sequences with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	OLQHHPAGLK	280	11	56	89		10232
POL	LTEREKA	213	8	56	88		10233
POL	VTYLDVGDY	295	10	56	88	0.0001	10234
POL	ELKKIGQVR	909	10	56	88		10235
POL	DFEVEVLGPII	275	11	56	88		10236
POL	SVTVLDVGDY	294	11	56	88		10237
POL	VTYLDVGDY	842	11	56	88		10238
POL	VTYLDVGDY	842	11	56	88		10239
POL	VTYLDVGDY	842	11	56	88		10240
POL	KTAVQMAVFI	925	11	56	88		10241
POL	TGQETAYF	845	8	57	89	0.0017	10242
POL	AIKKAKDSTK	251	9	57	89		10243
POL	ELNKRTQDF	268	9	57	89		10244
POL	VTYLDVGDY	295	9	57	89		10245
POL	VTYLDVGDY	296	9	57	89	0.0002	10246
POL	VTYLDVGDY	404	9	57	89		10247
POL	ETGQETAYF	844	9	57	89		10248
POL	ILKTAIVOMA	923	9	57	89	0.0003	10249
POL	KTAVQMAVFI	925	9	57	89	0.0003	10250
POL	FAIKKKDSTK	250	10	57	89	0.0004	10251
POL	SVTVLDVGDY	294	10	57	89	0.0004	10252
POL	VTYLDVGDY	296	10	57	89	0.0004	10253
POL	VTYLDVGDY	296	10	57	89	0.0002	10254
POL	AIKKAKDSTK	251	11	57	89		10255
POL	ILKTAIVOMA	923	11	57	89		10256
POL	MAVTHINFRK	930	11	57	89		10257
POL	GGGGYSAGER	941	11	57	89		10258
POL	NLKTGKYA	540	8	58	92		10259
POL	VLPGQWKQSP	377	11	58	91		10260
POL	VTYLDVGDY	296	8	58	91		10261
POL	EVQLGPII	278	8	58	91		10262
POL	TVLDVGDY	296	8	58	91		10263
POL	YALGIQA	693	8	58	91		10264
POL	GGNEQYDK	735	8	58	91		10265
POL	HINIKRKK	933	8	58	91		10266
POL	GGYSAGER	944	8	58	91		10267
POL	VTYLDVGDY	976	8	58	91	0.0004	10268
POL	IGGNEQYDK	734	9	58	91		10269
POL	PAETGQETA	842	9	58	91		10270
POL	VEHINFRKK	932	9	58	91	0.0004	10271
POL	IGGYSAGER	943	9	58	91	0.0004	10272
POL	STKWRKLVDF	757	10	58	91	0.0005	10273
POL	GGNEQYDK	735	10	58	91		10274
POL	PAETGQETA	842	10	58	91	0.6600	10275
POL	AVEHINFRKK	931	10	58	91	0.0013	10276
POL	GGGYSAGER	942	10	58	91		10277
POL	DSTKWRKLVDF	256	11	58	91		10278
POL	STKWRKLVDF	257	11	58	91		10279
POL	DSQYALGIQA	690	11	58	91		10280
POL	KGIGGNEQYDK	732	11	58	91		10281
POL	VPAETGQETA	840	11	58	91		10282

Table XVI
HIV-1 Main Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QGWKGSFA	140	8	59	92		10282
POL	AVIVASGY	828	8	59	92		10283
POL	ETGQETAY	844	8	59	92		10284
POL	QAEILKTA	920	8	59	92		10285
POL	GGGGYSA	941	8	59	92		10286
POL	QVQLDCTH	827	9	59	92		10287
POL	VAVVAVDY	827	9	59	92		10288
POL	KGPALKLWK	988	9	59	92	0.0004	10289
POL	QGWKGSFAF	140	10	59	92	0.0021	10290
POL	EVNIVTSQY	684	10	59	92	0.0004	10291
POL	PGVQLDCTH	810	10	59	92		10292
POL	TAVQMAVFIH	926	10	59	92		10293
POL	QKLNLSQY	684	11	59	92		10294
POL	EVNIVTSQY	684	11	59	92		10295
POL	NFKKGGGGY	916	11	59	92		10296
POL	PAKLWKGGG	990	11	59	92		10297
POL	QLXCITILEGK	814	10	60	95	0.0010	10298
POL	DFRELNKR	265	8	60	94		10299
POL	VLDVGDAY	297	8	60	94		10300
POL	MAVHFNKR	297	8	60	94		10301
POL	VLDVGDAY	265	9	60	94		10302
POL	MGVELIPDK	297	9	60	94		10303
POL	KLNWSQIY	419	9	60	94	0.0640	10304
POL	AVQMAVFIH	452	9	60	94	0.1200	10305
POL	QMAVFIHNF	927	9	60	94		10306
POL	MAVHFNKR	929	9	60	94	0.0010	10307
POL	KLVDFELNKR	992	9	60	94	0.0010	10308
POL	QVQLDCTH	992	9	60	94	0.0003	10309
POL	LYDFELNKR	263	10	60	94		10310
POL	WMGYELIPDK	418	10	60	94		10311
POL	QMAVFIHNF	929	10	60	94	0.0005	10312
POL	MAVHFNKR	930	10	60	94	0.0068	10313
POL	KLVDFELNKR	262	11	60	94		10314
POL	QVQLDCTH	927	11	60	94		10315
POL	QMAVFIHNF	927	11	60	94		10316
POL	QMAVFIHNF	929	11	60	94		10317
POL	EALLDTGA	108	8	61	95		10318
POL	LDVGDAYF	298	8	61	95		10319
POL	LVGKLNWA	449	8	61	95		10320
POL	IVTDSQYA	687	8	61	95		10321
POL	QVQLDCTH	444	9	61	95		10322
POL	NIDQLVGGK	444	9	61	95		10323
POL	KLVGKLNWA	448	9	61	95		10324
POL	NIVTDSQYA	686	9	61	95	0.0003	10325
POL	LDCTILEGK	815	9	61	95		10326
POL	TVNDIQLVGGK	442	11	61	95	0.0400	10327
POL	MIGGIGGF	113	8	62	97		10328
POL	QVQLDCTH	444	8	62	97		10329
POL	NTVLDVGGK	441	8	62	97	0.0003	10330
POL	DQLVGGK	445	8	62	97		10331

Table XVI
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NVLDSOV	686	8	62	97		10332
POL	DCILHGGK	816	8	62	97		10333
POL	AVHIHFK	931	8	62	97	0.0280	10334
POL	VHINIKR	932	8	62	97		10335
POL	LLWKGGA	933	8	62	97		10336
POL	KMGIGGFG	132	9	62	97	0.0004	10338
POL	LVDFRLNK	132	9	62	97	0.0100	10339
POL	LVDFRLNK	133	10	62	97	0.0009	10340
POL	MGIGGFGK	133	10	62	97	0.5100	10341
POL	KLVDRELK	262	10	62	97	2.3000	10342
POL	KMGIGGFGK	132	11	62	97	0.0003	10343
POL	NVLPQGWK	336	8	63	100	0.0004	10344
POL	IGGGHFK	134	9	63	100		10345
POL	GGGGHFK	135	9	64	100		10346
POL	PLWAGYELI	416	9	64	100		10347
POL	PLWAGYELI	417	10	64	100		10348
REV	GTROTNRK	37	9	01	50		10349
REV	TTRQARRNR	37	9	01	50		10350
REV	GTROTNRK	37	10	01	50		10351
REV	TTRQARRNR	37	10	01	50		10352
REV	GTROTNRK	37	11	01	50		10353
REV	TTRQARRNR	37	11	01	50		10354
REV	GTGEGGGR	103	8	06	19		10355
REV	QGTETGGR	102	9	06	19		10356
REV	LLKTVRLK	12	9	10	16		10357
REV	GDSDELLK	6	9	11	17		10358
REV	PLQIPPER	76	9	11	17		10359
REV	SGDSDELLK	6	10	11	17		10360
REV	PLQIPPER	74	11	11	17		10361
REV	RAKORQIR	50	8	12	19		10362
REV	DSDELLK	7	8	12	19		10363
REV	ILSTCLGR	63	8	12	19		10364
REV	RLSTCLGR	9	9	12	19		10365
REV	SVARLLYK	17	9	13	20		10366
REV	PSDEGQAR	31	9	13	20		10367
REV	QPLPLERLI	78	9	13	20		10368
REV	PSPEGTQAR	31	10	13	20		10369
REV	PSPEGTQAR	31	11	13	20		10370
REV	PLQPLERLI	76	11	13	20		10371
REV	GTROAKNRK	36	11	14	22		10372
REV	RAKORQIR	50	15	15	24		10373
REV	GTROAKNRK	36	9	15	23		10374
REV	GTROAKNRK	36	10	15	23		10375
REV	QARKNRKR	40	9	16	25		10376
REV	QARKNRKR	40	11	16	25		10377
REV	QARKNRKR	40	8	17	27		10378
REV	IKILYQSNPY	20	11	18	28		10379
REV	IKILYQSNPY	22	9	26	41		10380
REV	IKILYQSNPY	22	8	27	42		10381

Table XVI
HIV A13-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta^*0.001$	SEQ ID NO.
REV	EGTQARRR	35	8	27	42		10382
REV	EGTQARRR	35	10	27	42		10383
REV	EGTQARRR	35	11	27	42		10384
REV	GTRQARRR	36	9	34	53		10385
REV	GTRQARRR	36	10	34	53		10386
REV	GTRQARRR	36	11	34	53		10387
REV	PVLQLPLR	36	11	34	53		10388
REV	PVLQLPLR	76	9	35	55		10389
REV	QARRRR	40	11	37	58		10390
REV	QARRRR	40	8	38	59		10391
REV	QARRRR	40	9	38	59		10392
TAT	PGGYPRK	104	8	01	50		10393
TAT	AGPGGYPR	102	9	01	50		10394
TAT	TGSGQFCH	102	9	01	50		10395
TAT	AGPGGYPR	101	10	01	50		10396
TAT	AGPGGYPR	101	10	01	50		10397
TAT	AGPGGYPR	102	10	01	50		10398
TAT	KAGPGGYPR	101	11	01	50		10399
TAT	GGYPRKGC	105	11	01	50		10400
TAT	PGSQPRTA	17	8	10	16		10402
TAT	ACTNCCYK	23	9	10	16		10403
TAT	YKSKCCYH	29	8	11	17		10404
TAT	YKSKCCYH	29	8	11	17		10405
TAT	CHICVCF	34	8	11	17		10406
TAT	VDPLPWP	4	9	11	17		10407
TAT	ACNNCCYCK	24	9	11	17		10408
TAT	CFHCQVCF	33	9	11	17		10409
TAT	VDPLPWP	3	10	11	17	0.0005	10410
TAT	TACNNCCYCK	23	10	11	17		10411
TAT	PVDRLPWP	3	11	11	17		10412
TAT	RGDPTGPESK	84	11	11	17		10413
TAT	GDTGPESK	85	11	11	17		10414
TAT	ESKGVESK	85	9	12	19		10415
TAT	ESKGVESK	85	10	12	19		10416
TAT	TPGPKESKK	88	10	12	19		10417
TAT	TPGPKESKK	89	9	12	19		10418
TAT	FLNKGGLGSH	41	10	14	20		10419
TAT	PVDNLPWP	3	11	14	22		10420
TAT	FLNKGGLGSH	40	11	14	22		10421
TAT	RGDPTGPESK	4	8	16	25		10422
TAT	RGDPTGPESK	4	10	16	25		10423
TAT	ACNNCCYK	24	8	17	27		10424
TAT	TACNNCCYK	23	9	17	27		10425
TAT	PTGPKESKK	88	9	18	28		10426
TAT	PTGPKESKK	89	8	19	28		10427
TAT	PTGPKESK	88	8	20	31		10428
TAT	YGRKKRQR	10	11	22	34		10429
TAT	PGSQPRTA	17	8	26	41		10430
TAT	PGSQPRTA	17	8	26	41		10431

Table XVI
HIV-1 gp120 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO
TAT	YGRKKRQRR	50	10	38	59		10432
TAT	ISYGRKKRQRR	48	11	39	61		10433
TAT	YGRKKRQRR	50	9	41	64		10434
TAT	GISYGRKKRR	47	10	45	70	0.0003	10435
TAT	LGISYGRKKRR	46	11	45	70		10436
TAT	YGRKKRQRR	49	9	46	72		10437
TAT	LGISYGRKKRR	45	11	54	86	0.0008	10438
TAT	GLGISYGR	45	8	55	87		10439
TAT	GLGISYGRK	45	9	55	87	0.0340	10440
TAT	GLGISYGRKK	45	10	55	87		10441
TAT	KGLGISYGR	44	9	55	86	0.0006	10442
TAT	KGLGISYGRK	44	10	55	86	0.0100	10443
TAT	YGRKKRQRR	47	11	55	86		10444
TAT	LGISYGRKKRR	47	9	57	89	0.0008	10445
TAT	LGISYGRK	46	8	58	91		10446
TAT	LGISYGRKK	47	8	58	91		10447
TAT	ISYGRKKR	48	8	58	91		10448
TAT	LGISYGRKK	46	9	58	91	0.0004	10449
VIF	YGRKKRQRR	49	8	58	91		10450
VIF	YGRKKRQRR	49	8	58	91		10451
VIF	YGRKKRQRR	49	8	58	91		10452
VIF	LGISYGRK	46	8	58	91		10453
VIF	KGWYFRIHYY	36	9	10	16		10454
VIF	ALIKPKKIK	157	9	10	16		10455
VIF	VDRMRINTWK	13	10	10	16		10456
VIF	GVSEWRLRR	87	10	10	16		10457
VIF	GVSEWRLRR	87	10	10	16		10458
VIF	GVSEWRLRR	87	10	10	16		10459
VIF	GVSEWRLRR	87	10	10	16		10460
VIF	GVSEWRLRR	87	10	10	16		10461
VIF	IDPLADQLII	103	11	10	16		10462
VIF	YEDRWNRKQ	178	11	10	16		10463
VIF	YSTQIDPDLA	99	10	11	17		10464
VIF	YSTQIDPDLA	99	10	11	17		10465
VIF	YSTQIDPDLA	99	10	11	17		10466
VIF	STEWRLRR	89	8	11	17		10467
VIF	TALIKPKK	156	8	11	17		10468
VIF	LVEDRWNK	178	8	11	17		10469
VIF	VSIEWRLRR	88	9	11	17		10470
VIF	STQVDDGLA	99	9	11	17		10471
VIF	STQVDDGLA	99	9	11	17		10472
VIF	STQVDDGLA	99	9	11	17		10473
VIF	TALIKPKK	155	9	11	17		10474
VIF	KLVEDRWNK	177	9	11	17		10475
VIF	VSIEWRLRR	88	10	11	17		10476
VIF	GLADQLIIMI	106	10	11	17		10477
VIF	IVSTRCEYQA	133	10	11	17		10478
VIF	GSGLYLAKKA	148	10	11	17		10479
VIF	IVSTRCEYQA	133	10	11	17		10480
VIF	IVSTRCEYQA	133	10	11	17		10481
VIF	GLADQLIIMI	106	11	11	17		10482

Table XVI
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	$\Delta Q_0 J_0 I$	SEQ ID NO.
VIF	VGSLOYLAK	147	11	11	17		10482
VIF	WYRIHMYESR	153	11	11	17		10483
VIF	WYRIHMYESR	153	11	11	17		10484
VIF	KGWYRIH	36	8	12	19		10485
VIF	WGLQTGER	72	8	12	19		10486
VIF	QTDGERDWI	75	8	12	19		10487
VIF	SDSAIRKA	121	8	12	19		10488
VIF	SLQYLALA	147	8	12	19		10489
VIF	WYRIHMYESR	149	9	12	19		10490
VIF	STQDPLA	9	9	12	19		10491
VIF	FSDSAIRKA	120	9	12	19		10492
VIF	FSDSAIRKA	120	9	12	19		10493
VIF	GSLOYLALA	148	9	12	19		10494
VIF	SLQYLALA	147	9	12	19		10495
VIF	KIRTWNSLVK	77	10	12	19		10496
VIF	WYRIHMYESR	149	10	12	19		10497
VIF	GLQIGRIDWI	73	10	12	19		10498
VIF	TGTRDWILGH	77	10	12	19		10499
VIF	HGVSLWRLH	86	10	12	19		10500
VIF	CFDSAIRKA	119	10	12	19		10501
VIF	CFDSAIRKA	119	10	12	19		10502
VIF	VGSLOYLALA	147	10	12	19		10503
VIF	WYRIHMYESR	149	10	12	19		10504
VIF	IWQVDRBK	148	10	12	19		10505
VIF	KIRTWNSLVK	9	11	12	19		10506
VIF	SLVKIIMYVS	17	11	12	19		10507
VIF	SLVKIIMYVS	23	11	12	19		10508
VIF	LVKIHIMYVS	24	11	12	19		10509
VIF	WGLQTGERD	72	11	12	19		10510
VIF	CFDSAIRKA	118	11	12	19		10511
VIF	CFDSAIRKA	118	11	12	19		10512
VIF	KVGSLOYLAL	146	11	12	19		10513
VIF	VGSLOYLALA	147	11	12	19		10514
VIF	WYRIHMYESR	147	11	12	19		10515
VIF	QYDRBKIR	12	8	13	20		10516
VIF	HIMYSKKA	28	8	13	20		10517
VIF	WYRIHMYESR	149	8	13	20		10518
VIF	ADQLIIMI	108	8	13	20		10519
VIF	CFDSAIR	119	8	13	20		10520
VIF	FSDSAIRK	120	8	13	20		10521
VIF	SLQYLAL	149	8	13	20		10522
VIF	LTALIKPK	155	8	13	20		10523
VIF	LADQLIHMH	107	9	13	20		10524
VIF	ADQLIIMI	108	9	13	20		10525
VIF	CFDSAIRK	119	9	13	20		10526
VIF	FSDSAIRKA	120	9	13	20		10527
VIF	GSLOYLAL	148	9	13	20		10528
VIF	ALTALIKPK	154	9	13	20		10529
VIF	SVKLTEDR	174	9	13	20		10530
VIF	EVHPLGDAR	54	10	13	20		10531
VIF	LADQLIHMH	107	10	13	20		10532

Table XVI
HIV-1 gp120 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO
VIF	ADQLIMHYF	108	10	13	20		10332
VIF	ADQLIMHYF	118	10	13	20		10333
VIF	CFSSARKA	119	10	13	20		10334
VIF	VGSIQYLAIA	147	10	13	20		10335
VIF	LALITALPKP	153	10	13	20		10336
VIF	PSVKILTEDR	173	10	13	20		10337
VIF	LADQLIMHYF	107	11	13	20		10338
VIF	QLHLYYDF	117	11	13	20		10339
VIF	QLHLYYDF	117	11	13	20		10340
VIF	YALITALPKP	152	11	13	20		10341
VIF	QLHLYYF	110	8	14	22		10342
VIF	QLIMHYF	110	8	14	22		10343
VIF	FSESARKA	120	8	14	22		10344
VIF	INSRCEY	133	8	14	22		10345
VIF	GVSEWRLR	87	9	14	22		10346
VIF	GVSEWRLR	87	9	14	22		10347
VIF	CFSSARKA	119	9	14	22		10348
VIF	VDMRRTWK	13	10	14	22		10349
VIF	LADQLILYY	107	10	14	22		10350
VIF	ADQLILYYF	108	10	14	22		10351
VIF	RCDYQAGHKK	137	10	14	22		10352
VIF	QVDMRRTWK	2	11	14	22		10353
VIF	QVDMRRTWK	2	11	14	22		10354
VIF	LADQLILYYF	107	11	14	22		10355
VIF	QLHIMHYDFCF	110	11	14	22		10356
VIF	RMRTWK	15	8	15	23		10357
VIF	RTWKSIVK	19	8	15	23		10358
VIF	VSEWRLR	88	8	15	23		10359
VIF	ADQLILYY	107	8	15	23		10360
VIF	RTWKSIVK	113	8	15	23		10361
VIF	RTWKSIVKH	19	9	15	23		10362
VIF	QGVSEWRK	86	9	15	23		10363
VIF	LADQLILYY	107	9	15	23		10364
VIF	AIKCALGII	124	9	15	23		10365
VIF	CDYQAGHKK	138	9	15	23		10366
VIF	RTWKSIVK	17	10	15	23		10367
VIF	RTWKSIVK	17	10	15	23		10368
VIF	RTWKSIVKHII	19	10	15	23		10369
VIF	LHIMHYDFCF	111	10	15	23		10370
VIF	SAIKCALGII	123	10	15	23		10371
VIF	RIKTKSLVK	17	11	15	23		10372
VIF	LGQGVSEWR	84	11	15	23		10373
VIF	GVSEWRLR	85	11	15	23		10374
VIF	ITTYWGLII	68	8	16	25		10375
VIF	GVSEWRK	87	8	16	25		10376
VIF	ILLYYDFCF	113	8	16	25		10377
VIF	RCDYQAGH	137	8	16	25		10378
VIF	LALITALIK	153	8	16	25		10379
VIF	VITTYWGLII	67	9	16	25		10380
VIF	YALITALIK	152	9	16	25		10381

Table XVI
HIV-1 A32 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*301	SEQ ID NO.
VIF	KTKGRGSH	188	9	16	25	0.0004	10582
VIF	LVITTYWGLI	66	10	16	25		10583
VIF	HLILKLPDCT	111	10	16	25		10584
VIF	ESLAKHIMY	180	11	17	27		10585
VIF	KSLAKHIMY	22	9	18	28		10586
VIF	EDRWKPKT	180	11	18	28		10587
VIF	RCEYQAGINK	137	10	19	30		10588
VIF	IUPLIGEAR	56	8	20	31		10589
VIF	EVHPLGEAR	54	10	20	31		10590
VIF	ITIGROWH	106	8	21	33		10591
VIF	PLADQLIH	106	8	21	33		10592
VIF	VSPICEYA	134	9	21	33		10593
VIF	GLITIGERDWH	73	10	21	33		10594
VIF	WGLITIGERD	72	11	21	33		10595
VIF	VSPICEYQAG	134	11	21	33		10596
VIF	LTIDRWKPKQ	194	11	21	33		10597
VIF	RGSDITNGH	193	8	22	34		10598
VIF	TYTYWGLITGE	69	9	22	34	0.0390	10599
VIF	ILHIGVSEW	83	11	22	34		10600
VIF	SSEVIHPLGDA	52	11	22	34		10601
VIF	NSLXKIHIMY	22	9	23	35		10602
VIF	EVHPLGDA	54	9	24	36		10603
VIF	EVHPLGEA	54	8	24	38		10604
VIF	EVHPLGEA	54	9	25	39		10605
VIF	LGQGVSEWR	84	10	25	39		10606
VIF	SSEVIHPLGEA	52	11	25	39		10607
VIF	ILHIGVSEW	83	11	25	39		10608
VIF	RCEYQAGH	137	9	26	41		10609
VIF	RTWSLVKIH	19	6	26	41		10610
VIF	RTWSLVK	19	10	26	41		10611
VIF	IGVSEWR	86	8	27	42		10612
VIF	GLADQLIH	106	8	27	42		10613
VIF	PLADQLIH	105	9	27	42		10614
VIF	LGQGVSEWR	84	10	27	42		10615
VIF	RTWSLVK	19	10	27	42		10616
VIF	WGLITIGER	72	8	27	42		10617
VIF	YFCTSESIA	116	8	28	44		10618
VIF	DCFSSESAR	117	9	28	44		10619
VIF	DCFSSESAR	117	10	28	44		10620
VIF	DCFSSESAR	117	10	28	44		10621
VIF	DCFSSESAR	117	9	29	45		10622
VIF	EDRWKPKT	180	8	29	45		10623
VIF	EDRWKPKT	180	9	29	45		10624
VIF	YFCTSESIA	116	8	30	47	0.0130	10625
VIF	YFCTSESIA	116	11	30	47		10626
VIF	EDRWKPKT	180	8	31	48	0.0003	10627
VIF	EDRWKPKT	180	9	31	48		10628
VIF	SLQYLAITA	148	9	31	48		10629
VIF	SLQYLAITA	148	10	31	48		10630
VIF	IYVQVDRMR	9	11	33	52		10631

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*Q301	SEQ ID NO.
VIF	QVDMREIR	12	8	34	53		10632
VIF	QVDMREIR	13	9	39	61		10633
VIF	QVDMREIR	17	11	41	64		10634
VIF	QVDMREIR	6	10	43	67		10635
VIF	QVDMREIR	8	10	43	67	0.0062	10636
VIF	QVDMREIR	142	11	43	67		10637
VIF	QVDMREIR	23	8	43	67		10638
VIF	QVDMREIR	7	8	44	69		10639
VIF	QVDMREIR	9	8	46	72	0.0034	10640
VIF	QVDMREIR	146	9	47	73		10641
VIF	QVDMREIR	147	9	52	81	0.0008	10642
VIF	QVDMREIR	147	9	58	91	0.0036	10643
VPR	QVDMREIR	85	8	01	50		10644
VPR	QVDMREIR	85	8	01	50		10645
VPR	QVDMREIR	85	8	01	50		10646
VPR	QVDMREIR	85	8	01	50		10647
VPR	QVDMREIR	85	8	01	50		10648
VPR	QVDMREIR	85	8	01	50		10649
VPR	QVDMREIR	85	8	01	50		10650
VPR	QVDMREIR	85	8	01	50		10651
VPR	QVDMREIR	85	8	01	50		10652
VPR	QVDMREIR	85	8	01	50		10653
VPR	QVDMREIR	85	8	01	50		10654
VPR	QVDMREIR	85	8	01	50		10655
VPR	QVDMREIR	85	8	01	50		10656
VPR	QVDMREIR	85	8	01	50		10657
VPR	QVDMREIR	85	8	01	50		10658
VPR	QVDMREIR	85	8	01	50		10659
VPR	QVDMREIR	85	8	01	50		10660
VPR	QVDMREIR	85	8	01	50		10661
VPR	QVDMREIR	85	8	01	50		10662
VPR	QVDMREIR	85	8	01	50		10663
VPR	QVDMREIR	85	8	01	50		10664
VPR	QVDMREIR	85	8	01	50		10665
VPR	QVDMREIR	85	8	01	50		10666
VPR	QVDMREIR	85	8	01	50		10667
VPR	QVDMREIR	85	8	01	50		10668
VPR	QVDMREIR	85	8	01	50		10669
VPR	QVDMREIR	85	8	01	50		10670
VPR	QVDMREIR	85	8	01	50		10671
VPR	QVDMREIR	85	8	01	50		10672
VPR	QVDMREIR	85	8	01	50		10673
VPR	QVDMREIR	85	8	01	50		10674
VPR	QVDMREIR	85	8	01	50		10675
VPR	QVDMREIR	85	8	01	50		10676
VPR	QVDMREIR	85	8	01	50		10677
VPR	QVDMREIR	85	8	01	50		10678
VPR	QVDMREIR	85	8	01	50		10679
VPR	QVDMREIR	85	8	01	50		10680
VPR	QVDMREIR	85	8	01	50		10681

Table XVI
HIV-1 A3 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPR	WAGVEAIR	54	9	16	25		10682
VPR	ELLEELKNEA	21	10	16	25		10683
VPR	ELLEELKSEA	21	10	16	25		10684
VPR	YGDWTWAGVEA	50	10	16	25		10685
VPR	ELLEELKSEAYR	52	11	16	25		10686
VPR	WAGVEAIR	54	9	16	25		10687
VPR	ELLEELKNEA	21	8	17	27		10688
VPR	ELLEELKNEA	22	9	17	27		10689
VPR	ELKNEAVRH	25	9	17	27		10690
VPR	LGQHYETY	42	9	17	27		10691
VPR	ELKNEAVRHIF	25	10	17	27		10692
VPR	ELLEELKNEAVR	22	11	17	27		10693
VPR	FGKNEAIR	52	8	18	28		10694
VPR	WAGVEAIR	54	11	18	28		10695
VPR	RANRGAIR	93	8	19	30		10696
VPR	WLGIGLQHI	38	8	20	31		10697
VPR	IGLGQHIY	40	8	20	31		10698
VPR	WLGIGLQHIY	38	10	20	31		10699
VPR	DIWIGVNEA	52	8	23	36		10700
VPR	WAGVEAIR	54	9	23	36		10701
VPR	YGDWTWAGVEA	50	10	23	36		10702
VPR	LEHFRIGCOII	68	11	29	45		10703
VPR	FHFRIGCOII	69	10	30	47		10704
VPR	FHFRPWLI	33	8	31	49		10705
VPR	AVRIIPRPWL	30	11	31	49		10706
VPR	RILOQLLIHIF	62	10	34	53		10707
VPR	RILOQLLIHIF	63	10	35	55		10708
VPR	RILOQLLIHIF	62	11	35	55	0.0130	10709
VPR	RILOQLLIHIF	63	10	36	56		10710
VPR	EDGQPOREPY	63	9	37	58		10711
VPR	AIIRILOQLLF	6	10	37	58		10712
VPR	AIIRILOQLLF	59	11	38	58		10713
VPR	QNPEDQGPQR	60	10	39	62		10714
VPR	WAGVEAIR	54	10	41	64		10715
VPR	WTLLEELK	18	10	42	69		10716
VPR	OGPOREPY	8	8	43	68		10717
VPR	QLFHIFR	66	8	44	69		10718
VPR	HFIRGCOII	71	8	44	69		10719
VPR	TLELEELK	19	9	44	69		10720
VPR	HFIRGCOII	71	10	44	69		10721
VPR	RIEGLQSK	62	8	45	70		10722
VPR	RIEGLQSK	74	8	47	73		10723
VPR	EAVRIIPR	29	8	59	92		10724
VPU	IDYRLGVGA	9	9	01	33		10725
VPU	VDYRIVVA	9	9	01	33		10726
VPU	VDYRLGVGA	9	9	01	33		10727
VPU	KYDRIIVVA	7	10	01	33		10728
VPU	VDYRLGVGA	7	10	01	33		10729
VPU	VDYRLGVGA	7	10	01	33		10730
VPU	VDYRIVVAF	9	10	01	33		10731

Table XVI
HIV-1 Gag-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VP1	KVDYRIVAF	7	11	01	33		10732
VP1	LVQRKQDR	43	8	01	50		10733
VP1	GVEMGHIA	91	8	01	50		10734
VP1	VTLSSSK	94	8	01	50		10735
VP1	LVQRKQDR	43	9	01	50		10736
VP1	VTLSSSK	64	9	01	50		10737
VP1	RIEGRDSY	64	11	01	50		10738
VP1	RIEGRDSY	64	11	01	50		10739
VP1	LAIV/ALVVA	13	9	09	15		10740
VP1	WTIVFEYR	34	9	10	16		10741
VP1	TIIVFEYR	35	8	10	16		10742
VP1	IDRLDRIR	54	9	10	16		10743
VP1	KLDRIR	56	9	10	16		10744
VP1	WTIVFEYR	52	10	10	16		10745
VP1	VVWTVIVFEYR	31	11	10	16		10746
VP1	ESGQDELSA	77	11	10	16		10747
VP1	EGQDELSA	77	9	11	17		10748
VP1	WTIVFEY	34	8	12	19		10749
VP1	ALVALVA	14	8	12	19		10750
VP1	IVHETRK	26	8	12	19		10751
VP1	LIBRERA	58	8	12	19		10752
VP1	LIBRERA	58	9	12	19		10753
VP1	VVWTVIVFEY	31	10	12	19		10754
VP1	IVVWTVIVFEY	30	11	12	19		10755
VP1	GDQDELSA	78	8	14	22		10756
VP1	LIDRRER	58	8	14	22		10757
VP1	ALVWTVIVFEY	20	9	14	22		10758
VP1	ALVWTVIVFEY	20	8	15	23		10759
VP1	KIDRLDR	52	8	15	23		10760
VP1	KLQRKQDR	46	9	15	23		10761
VP1	KLQRKQDR	45	10	15	23	0.0039	10762

Table XVII
HIV X11-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
ENV	IGPQQIFY	361	8	01	25		10763
ENV	IGSQQAIF	361	8	01	25		10764
ENV	IGSQQAIF	375	8	01	33		10765
ENV	NNTSPRSR	375	8	01	33		10766
ENV	ADNLWVTV	42	9	01	33		10767
ENV	GIGPQIFY	360	9	01	33		10768
ENV	SIGSQAFY	360	9	01	33		10769
ENV	ADNLWVTV	42	10	01	33		10770
ENV	IGKNEIDY	376	10	01	33		10771
ENV	IGKNEIDY	376	10	01	33		10772
ENV	TAGSSBAAY	376	10	01	33		10773
ENV	GIAGNSSRAA	375	11	01	33		10774
ENV	NNTSPSRVA	375	11	01	33		10775
ENV	KLREIQFENK	405	11	01	25		10776
ENV	KNTETNK	535	8	01	50		10777
ENV	IGKNEIDY	376	8	01	50		10778
ENV	IGKNEIDY	376	8	01	50		10779
ENV	IGKNEIDY	376	8	01	50		10780
ENV	IGKNEIDY	376	8	01	50		10781
ENV	IGKNEIDY	376	8	01	50		10782
ENV	IGKNEIDY	376	8	01	50		10783
ENV	IGKNEIDY	376	8	01	50		10784
ENV	IGKNEIDY	376	8	01	50		10785
ENV	IGKNEIDY	376	8	01	50		10786
ENV	IGKNEIDY	376	8	01	50		10787
ENV	IGKNEIDY	376	8	01	50		10788
ENV	IGKNEIDY	376	8	01	50		10789
ENV	IGKNEIDY	376	8	01	50		10790
ENV	IGKNEIDY	376	8	01	50		10791
ENV	IGKNEIDY	376	8	01	50		10792
ENV	IGKNEIDY	376	8	01	50		10793
ENV	IGKNEIDY	376	8	01	50		10794
ENV	IGKNEIDY	376	8	01	50		10795
ENV	IGKNEIDY	376	8	01	50		10796
ENV	IGKNEIDY	376	8	01	50		10797
ENV	IGKNEIDY	376	8	01	50		10798
ENV	IGKNEIDY	376	8	01	50		10799
ENV	IGKNEIDY	376	8	01	50		10800
ENV	IGKNEIDY	376	8	01	50		10801
ENV	IGKNEIDY	376	8	01	50		10802
ENV	IGKNEIDY	376	8	01	50		10803
ENV	IGKNEIDY	376	8	01	50		10804
ENV	IGKNEIDY	376	8	01	50		10805
ENV	IGKNEIDY	376	8	01	50		10806
ENV	IGKNEIDY	376	8	01	50		10807
ENV	IGKNEIDY	376	8	01	50		10808
ENV	IGKNEIDY	376	8	01	50		10809
ENV	IGKNEIDY	376	8	01	50		10810
ENV	IGKNEIDY	376	8	01	50		10811
ENV	IGKNEIDY	376	8	01	50		10812

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
ENV	LORGEWALK	833	10	09	15		10813
ENV	RLGWEALK	834	11	09	15		10814
ENV	RLGWEGLK	894	8	10	32		10815
ENV	ENLWVTVY	892	10	10	32		10816
ENV	ENLWTVY	43	8	17	17		10817
ENV	ENLWTVY	43	9	10	17		10818
ENV	DIQDQRAH	372	10	10	16		10819
ENV	NTNRSHR	350	8	10	16		10820
ENV	ENLWTVY	43	8	10	16		10821
ENV	DTNLAWY	769	8	10	16		10822
ENV	DTLDAAR	870	8	10	16		10823
ENV	STHQACTK	243	9	10	16		10824
ENV	FDITNLWY	768	9	10	16		10825
ENV	RDFLIAR	869	9	10	16		10826
ENV	FAILKNDKK	269	10	10	16		10827
ENV	FAILKNDKK	269	10	10	16		10828
ENV	RLAVERYLR	665	10	10	16		10829
ENV	WFDITNLWY	767	10	10	16		10830
ENV	EGHEEGGER	828	10	10	16		10831
ENV	GFALKNDKK	268	11	10	16		10832
ENV	GDIGIRQAH	371	11	10	16		10833
ENV	NYWSSWSN	973	11	10	16		10834
ENV	WFDITNLWY	725	11	10	16		10835
ENV	LAALVAEGLDR	925	11	10	16		10836
ENV	RGWEALYK	886	8	11	18		10837
ENV	KLWTVTVY	44	8	11	17		10838
ENV	WSSWSNR	696	8	11	17		10839
ENV	TITQACTK	244	8	11	17		10840
ENV	IGQGTQY	558	8	11	17		10841
ENV	LAALVAEGLDR	665	8	11	17		10842
ENV	SNWLWYK	771	8	11	17		10843
ENV	NCLFSYII	859	8	11	17		10844
ENV	RGRGQTFY	357	9	11	17		10845
ENV	ITTHSNCR	431	9	11	17		10846
ENV	NILPCKIK	482	9	11	17		10847
ENV	LAALVAEGLDR	665	9	11	17		10848
ENV	NCLFSYII	770	9	11	17		10849
ENV	NCLFSYII	858	9	11	17		10850
ENV	NCLFSYII	859	9	11	17		10851
ENV	ETTHSNCR	430	10	11	17		10852
ENV	RNCLFSYII	858	10	11	17		10853
ENV	YATGDIGDIR	368	11	11	17		10854
ENV	NCLFSYII	858	11	11	17		10855
ENV	NCLFSYII	859	11	11	17		10856
ENV	ENLWTVY	43	12	12	20		10857
ENV	GNLWTVY	43	9	12	20		10858
ENV	TGDIGDIR	370	9	12	19		10859
ENV	EAQQUILLK	646	8	12	19		10860
ENV	ILKNDKK	271	8	12	19		10861
ENV	TTTHSNCR	432	8	12	19		10862

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*1101	SEQ ID NO.
ENV	MTWMEWER	721	8	12	19		10863
ENV	GGEGDNR	829	8	12	19		10864
ENV	LAEEVVR	312	9	12	19		10865
ENV	LAEEVVR	312	9	12	19	0.0002	10866
ENV	INMWQEVGK	493	9	12	19		10867
ENV	NM1WMEWER	720	9	12	19		10868
ENV	GIEEGGER	829	9	12	19		10869
ENV	EGGERDNR	833	9	12	19		10870
ENV	SLAEEVVR	311	10	12	19		10871
ENV	SLAEEVVR	310	10	12	19		10872
ENV	INMWQEVGK	492	10	12	19		10873
ENV	ALFAQQUILLK	644	10	12	19		10874
ENV	LLQVWSQELK	906	10	12	19		10875
ENV	ALLHPRR	946	10	12	19		10876
ENV	PIRROGLER	951	10	12	19		10877
ENV	KITLCASDA	60	11	12	19		10878
ENV	QINNAWQVGR	313	11	12	19		10879
ENV	QINNAWQVGR	491	11	12	19		10880
ENV	KNFQELLELDK	750	11	12	19		10881
ENV	GIEEGGERDNR	829	11	12	19		10882
ENV	NLLQVWSQEL	905	11	12	19		10883
ENV	RAILLHPRR	945	11	12	19		10884
ENV	SVLNCNR	340	8	13	20		10885
ENV	SVLNCNR	339	8	13	20		10886
ENV	KLTVWGK	653	8	13	20		10887
ENV	RAILLHPR	945	8	13	20		10888
ENV	RAILLHPR	946	8	13	20		10889
ENV	KARRVQR	579	9	13	20	0.0002	10890
ENV	RAILLHPR	945	9	13	20		10891
ENV	RAILLHPR	946	9	13	20		10892
ENV	TUSTSTVTH	286	10	13	20		10893
ENV	SGGDEPNVH	425	10	13	20		10894
ENV	LLKLTWVGK	651	10	13	20		10895
ENV	NTSVTHQATPK	241	11	13	20		10896
ENV	NTSVTHQATPK	285	11	13	20		10897
ENV	SSGDELETH	424	11	13	20		10898
ENV	SSGDELETH	424	11	13	20		10899
ENV	PTKARRVQR	576	11	13	20		10900
ENV	KARRVQR	579	11	13	20		10901
ENV	HLKLTWVG	650	11	13	20		10902
ENV	KNEDLLALD	750	11	13	20		10903
ENV	TGEIGDIR	370	9	14	23		10904
ENV	ATQACPK	244	8	14	22		10905
ENV	GGDEPNVH	425	8	14	22		10906
ENV	GGDEPNVH	753	8	14	22		10907
ENV	SALTQACPK	243	9	14	22		10908
ENV	FAILKCNDR	269	9	14	22		10909
ENV	GGDEPNVH	426	9	14	22	0.0002	10910
ENV	GGDEPNVH	482	9	14	22		10911
ENV	TITLPCRIK	482	9	14	22		10912
ENV	TSATQACPK	242	10	14	22		10913

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
ENV	TSVTOACPK	242	10	14	22		10913
ENV	GFALIKCNDR	208	10	14	22		10914
ENV	NSATQACPK	243	10	14	22		10915
ENV	NSATQACPK	243	11	14	22		10916
ENV	AGFALIKCNDR	267	11	14	22		10917
ENV	IFFAVLINVR	792	11	14	22		10918
ENV	KIEPLGVAPTK	568	11	15	24		10919
ENV	FDPPHY	255	8	15	23		10920
ENV	PAGYALLK	266	8	15	23		10921
ENV	NSATQACPK	243	8	15	23		10922
ENV	TSVTOACPK	771	8	15	23		10923
ENV	ITNWLWYIK	770	9	15	23		10924
ENV	SGGDLLEITH	425	10	15	23		10925
ENV	IFPRGGEDMR	545	10	15	23		10926
ENV	NMWQEVOKA	494	11	15	23		10927
ENV	IFPRGGEDMR	544	11	15	23		10928
ENV	DLNRLCLFV	856	11	15	23		10929
ENV	DLNRLCLFV	856	16	16	25		10930
ENV	FNLTGK	279	8	16	25		10931
ENV	RNLCLFV	858	8	16	25		10932
ENV	ITKWLWYIK	770	9	16	25		10933
ENV	SNCRGEFF	437	10	16	25		10934
ENV	DLNRLCLFV	856	10	16	25		10935
ENV	ISFNCRGFF	434	11	16	25		10936
ENV	NSATQACPK	243	8	17	27		10937
ENV	KAYDTEV	73	8	17	27		10938
ENV	KAYDTEV	244	8	17	27		10939
ENV	RVVQREKR	587	8	17	27	0.0001	10940
ENV	SVTQACPK	243	9	17	27	0.0002	10941
ENV	VAPTAKRR	574	9	17	27		10942
ENV	DKAYDTEV	70	10	17	27		10943
ENV	VAPTAKRR	573	10	17	27		10944
ENV	VFAVLINVR	793	10	17	27		10945
ENV	SDAKAYDTEV	69	11	17	27		10946
ENV	DTIEVINWA1	75	11	17	27		10947
ENV	NTIRNNNR	344	11	17	27		10948
ENV	LGVAPTAKR	572	11	17	27		10949
ENV	VFAVLINVR	792	11	17	27		10950
ENV	WNSVQREKR	692	11	18	29		10951
ENV	ENVLENNMW	100	8	18	29		10952
ENV	VLAVERYLK	666	9	18	28		10953
ENV	RVLAVERYLK	665	10	18	28		10954
ENV	NCRGEFF	439	8	19	30		10955
ENV	GVAPTAKR	573	8	19	30		10956
ENV	VFAVLINVR	793	9	19	30		10957
ENV	FGGDLLEITH	438	9	19	30		10958
ENV	LGVAPTAKR	572	9	19	30		10959
ENV	GVAPTAKR	573	9	19	30		10960
ENV	PLGVAPTAKR	571	10	19	30		10961
ENV	LGVAPTAKR	572	10	19	30		10962
ENV	SSNTGLLTR	516	11	19	30		

Table XVII
HIV-1_{env} Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
ENV	PLGVATKAK	571	11	19	30		10963
ENV	ALKCNKDK	270	8	20	31		10964
ENV	ETFRGGGDM	544	11	20	31		10965
ENV	LIEESONQEK	740	11	20	31		10966
ENV	GDLEITH	427	8	21	33		10967
ENV	GGDLEITH	426	9	21	33		10968
ENV	TAMVAEGTDR	925	11	21	33		10969
ENV	IVELGK	878	8	22	34		10970
ENV	IVELGK	878	8	22	34		10971
ENV	IVELGK	878	9	22	34	0.0100	10972
ENV	NCTRPNNTK	344	10	22	34		10973
ENV	CTRPNNTRK	345	10	22	34		10974
ENV	TITLFCASDA	60	11	22	34		10975
ENV	ICTRPNNTK	343	11	22	34		10976
ENV	STVQCTIGIR	289	9	22	36	0.0008	10977
ENV	STVQCTIGIR	288	10	23	36		10978
ENV	STVQCTIGIR	288	11	23	36		10979
ENV	TFRPGGDMR	545	10	24	38		10980
ENV	ALAWDDL	851	8	25	39		10981
ENV	LALAWDDL	850	9	25	39		10982
ENV	KNSTVQCTII	286	10	25	39		10983
ENV	KNSTVQCTII	286	11	25	39		10984
ENV	FLAWDDL	849	10	25	39	0.0190	10985
ENV	GIVQGNLLR	633	11	25	39		10986
ENV	GELALAWDDL	848	11	25	39		10987
ENV	ITLPCRK	483	8	26	41		10988
ENV	PLGVATK	571	8	26	41		10989
ENV	LAVERYLK	667	8	26	41		10990
ENV	KNSTVQCTII	286	11	26	41		10991
ENV	IVQGSNLLR	634	10	26	41		10992
ENV	IVQGSNLLR	633	11	26	41		10993
ENV	IGDIRQAI	377	9	27	44		10994
ENV	ESQNOQEK	743	8	27	42		10995
ENV	IGDIRQAI	378	8	28	44		10996
ENV	NNVLEQMI	11	9	28	44		10997
ENV	CTRPNNTRK	345	9	28	44	0.0460	10998
ENV	CTRPNNTRK	345	9	28	44		10999
ENV	VSEPIPIH	253	10	28	44		11000
ENV	STVQCTHGIR	289	10	28	44		11001
ENV	ASTLTVQAR	619	10	28	44		11002
ENV	KVSEPIPIH	252	11	28	44		11003
ENV	VCAVNGFALK	263	11	28	44		11004
ENV	VCAVNGFALK	263	11	28	44		11005
ENV	ASTLTVQAR	618	11	28	44		11006
ENV	VSEPIPIH	253	9	29	45		11007
ENV	KVSEPIPIH	252	10	29	45		11008
ENV	CAPAGFALK	264	10	29	45		11009
ENV	RSELYKYV	558	11	29	45		11010
ENV	AVLSIVNR	795	8	31	48		11011
ENV	AVAEGTR	928	8	31	48		11012

Table XVII
HIV-1 M1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*100	SEQ ID NO.
ENV	VTEFNFWK	102	9	31	48		11013
ENV	STEDPVR	254	9	31	48		11014
ENV	FVLSVNR	794	9	31	48		11015
ENV	SLCLFSYIIR	859	9	31	48		11016
ENV	IAVAEGTDR	927	9	31	48	0.0003	11017
ENV	NTVENFMW	101	10	31	48		11018
ENV	AVLSVNR	795	10	31	48		11019
ENV	RSCLFSYIR	928	10	31	48		11020
ENV	SLCLFSYIR	928	10	31	48		11021
ENV	FVLSVNR	794	11	31	48		11022
ENV	DLRSCLFSY	855	11	31	48		11023
ENV	SLCLFSYIIR	859	11	31	48		11024
ENV	ELYKVK	560	9	32	51		11025
ENV	RVERKER	387	8	32	50		11026
ENV	SLCLFSYIIR	859	8	32	50		11027
ENV	SLCLFSYIIR	859	8	32	50		11028
ENV	STLTYSQAR	620	9	32	50		11029
ENV	RSCLFSYIIR	858	9	32	50		11030
ENV	DLRSCLFSYIIR	856	11	32	50		11031
ENV	SFEPIPII	254	8	33	52		11032
ENV	KVLAVERY	665	8	33	52		11033
ENV	QKVLAVERY	663	8	33	52		11034
ENV	QKVLAVERY	663	10	33	52	0.0003	11035
ENV	QKVLAVERY	661	11	33	52		11036
ENV	IMVGLGLR	781	11	34	54		11037
ENV	LIQLTVWGK	651	10	34	53	0.0110	11038
ENV	ILLQLTVWGK	650	11	34	53		11039
ENV	VLVNRVROGY	797	11	34	53		11040
ENV	SLCLFSYIIR	859	11	35	55		11041
ENV	NCGGEFFY	439	8	35	55		11042
ENV	RSCLFSYIIR	858	8	35	55		11043
ENV	EVINVAWII	77	9	35	55		11044
ENV	FNCGGEFFY	438	9	35	55		11045
ENV	NTGLLLR	519	9	35	55	0.0001	11046
ENV	FNCGGEFFY	437	10	35	55		11047
ENV	SLCLFSYIIR	859	10	35	55	0.0014	11048
ENV	DLRSCLFSYIIR	856	11	35	55		11049
ENV	HSFNCGGEFFY	434	11	35	55		11050
ENV	GGGDMRDNW	549	10	36	56		11051
ENV	MIVGGLGLR	782	10	36	56	0.0008	11052
ENV	SLVNRVROGY	798	10	36	56		11053
ENV	PGGDMRDN	548	11	36	56		11054
ENV	SLVNRVROGY	797	11	37	58		11055
ENV	DMEDVWSEL	552	11	37	58		11056
ENV	PAGEFALK	266	8	38	59		11057
ENV	SLVNRVROGY	797	8	38	59		11058
ENV	VLVNRVROGY	796	9	38	59		11059
ENV	IVNRVROGY	799	9	38	59		11060
ENV	ISLWDQSLK	121	10	38	59	0.0540	11061
ENV	DISLWDQSLK	120	11	38	59		11062

Table XVII
HIV-1_{CRF01_AG} Motif Equivalents with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SIQ ID NO.
ENV	GDMDANVR	551	8	39	61		11063
ENV	GDMDANVR	550	9	39	61		11064
ENV	RDNWSELYK	554	10	40	63	0.0001	11065
ENV	RDNWSELYK	554	11	40	63	0.0028	11066
ENV	TLFCASDAKA	64	11	40	63		11067
ENV	RDNWSELYK	554	11	40	63		11068
ENV	TVYGGPPWVK	48	10	41	64	7.8000	11069
ENV	TVYGGPPWVK	47	11	41	64	4.1000	11070
ENV	CLFCASDAKAY	67	8	42	66		11071
ENV	LCLEFSYIIR	860	8	42	66		11072
ENV	FCASDAKAY	66	9	42	66		11073
ENV	IVGGLIGLR	783	9	42	66		11074
ENV	CLFSYIIRLR	861	9	42	66		11075
ENV	LCFCASDAKAY	65	10	42	66	0.0002	11076
ENV	CLFSYIIRLR	861	10	42	66		11077
ENV	VGGLIGLR	784	8	43	67		11078
ENV	QLTVWGRK	653	8	44	69		11079
ENV	LTYSYIIRLR	862	8	44	69		11080
ENV	RIRQGLER	953	8	44	69		11081
ENV	VNRVRQGY	800	8	45	71		11082
ENV	SLWDOSLR	123	8	47	73		11083
ENV	QSLKPCVK	125	9	47	73		11084
ENV	QSLKPCVK	127	10	47	73	0.0090	11085
ENV	QSLKPCVK	127	8	48	75		11086
ENV	TVWGHKQLOA	655	11	48	75		11087
ENV	DNWSELYK	555	8	49	77		11088
ENV	GKIQLOAR	658	8	49	77		11089
ENV	DNWSELYK	555	9	49	77	0.0014	11090
ENV	DNWSELYK	555	9	49	77	0.0001	11091
ENV	DNWSELYK	555	11	49	77	0.0001	11092
ENV	LGHWGCSGK	679	10	50	78		11093
ENV	TLFCASDAK	61	10	50	78	0.0023	11094
ENV	LLGWGCSGK	678	10	50	78	0.2200	11095
ENV	NLGNLGAQHH	670	11	50	80	0.0120	11096
ENV	TVYGGPPWVK	677	11	50	78		11097
ENV	VSTVQCTII	288	8	51	80		11098
ENV	RALEAQHI	643	8	51	80		11099
ENV	NVSTVQCTII	287	51	51	80		11100
ENV	LERAEQAQHI	641	10	51	80		11101
ENV	GIWGCSCGK	680	9	52	81		11102
ENV	TLFCASDAK	65	8	54	84	0.5300	11103
ENV	LCFCASDAK	65	8	54	84		11104
ENV	LCFCASDAK	65	8	57	89		11105
GAG	AAAIMMQK	405	8	01	25		11106
GAG	SATMMQK	405	8	01	25		11107
GAG	KDKDKELY	535	8	01	25		11108
GAG	ETDKDKELY	537	8	01	25		11109
GAG	NSATIMMQK	404	9	01	33		11110
GAG	TATPHEPR	508	9	01	33		11111
							11112

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
GAG	NGQANFLGK	461	10	01	25		11113
GAG	NGHQANFLGK	461	10	01	25		11114
GAG	PTAPPESEK	507	10	01	33		11115
GAG	NGQANFLGK	461	11	01	25		11116
GAG	NGQANFLGK	461	11	01	25		11117
GAG	PTAPPESEK	507	11	01	33		11118
GAG	ASAQDLK	392	8	01	50		11119
GAG	ATAQDLK	392	8	01	50		11120
GAG	AADKGVSONY	130	10	01	50		11121
GAG	SAQDLKGGY	393	10	01	50		11122
GAG	TAQDLKGGY	393	10	01	50		11123
GAG	GTRGNYVOK	480	10	01	50		11124
GAG	TAQDLKGGY	393	10	01	50		11125
GAG	ITSIPKQEK	526	10	01	50		11126
GAG	PAAADKEKIS	123	11	01	50		11127
GAG	GANSIPVGDHY	276	11	01	50		11128
GAG	PNQPIVGDHY	276	11	01	50		11129
GAG	ASAQDLKGG	392	11	01	50		11130
GAG	ATAQDLKGG	392	11	01	50		11131
GAG	TAQDLKGGY	393	11	01	50		11132
GAG	YTAVMGR	406	8	02	30		11133
GAG	TAAPAESR	508	9	02	67		11134
GAG	PTAPPAESR	507	10	02	67		11135
GAG	EGROANFLGK	462	10	02	100		11136
GAG	AADKGVSONY	129	11	02	18		11137
GAG	EADKGVSONY	129	10	04	36		11138
GAG	TAQDLKGGY	393	10	04	36		11139
GAG	AAMMKNSK	406	11	06	15		11140
GAG	KTVKGNCKOK	421	10	08	16		11141
GAG	GARASILR	2	8	10	16		11142
GAG	PGNFTQSR	483	8	10	16		11143
GAG	MGARASILR	1	9	10	16		11144
GAG	LGKIPWSSK	12	9	10	16		11145
GAG	TONKGVSONY	131	11	10	16		11146
GAG	NEIGKWPSSK	468	11	10	16		11147
GAG	PVAPGQMR	243	8	10	16		11148
GAG	MMQKSNFK	409	8	10	16		11149
GAG	MMQKSNFK	409	8	10	16		11150
GAG	KLDKWEKIR	12	10	10	16	0.0001	11151
GAG	GGKKKYKLIK	24	9	10	16		11152
GAG	GGKKKYKLIK	24	9	10	16		11153
GAG	MMQKSNFK	408	9	10	16		11154
GAG	LGKIPWSSK	470	9	10	16		11155
GAG	GGKKKYKLIK	23	10	10	16		11156
GAG	GGKKKYKLIK	24	10	10	16		11157
GAG	AGPVAPGQMR	241	10	10	16		11158
GAG	LGKIPWSSK	469	10	10	16		11159
GAG	KLDKWEKIR	12	11	10	16		11160
GAG	GGKKKYKLIK	23	11	10	16		11161
GAG	LGKIPWSSKIR	470	11	10	16		11162

Table XVII
HIV-1 M1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Concurrence (%)	A*101	SEQ ID NO.
GAG	ATIMKRGKGF	406	11	11	28		11163
GAG	ATIMKRGK	407	10	11	18		11164
GAG	PIVGDY	279	8	11	17		11165
GAG	TKCFNCK	422	9	11	17		11166
GAG	1VKCFNCK	422	9	11	17		11167
GAG	GNSQVSNQ	140	10	12	23		11168
GAG	TIMKRGKGF	407	10	12	21		11169
GAG	QTSGLK	420	8	11	17		11170
GAG	1VKCFNCK	422	9	12	19		11171
GAG	KGKKKKYK	23	8	12	19		11172
GAG	TYLYCVIQ	86	8	12	19		11173
GAG	DIKALEK	98	8	12	19		11174
GAG	MLNVGGH	208	8	12	19		11175
GAG	PISLDR	103	8	12	19		11176
GAG	GSSELSLY	73	9	12	19		11177
GAG	1VKCFNCK	422	9	12	19		11178
GAG	KDIKALEK	97	9	12	19		11179
GAG	MLNVGGH	207	9	12	19		11180
GAG	TGSELSLY	72	10	12	19		11181
GAG	VATLYCVIQ	84	10	12	19		11182
GAG	NMLNVGGH	206	10	12	19		11183
GAG	YSPISLDR	101	10	12	19		11184
GAG	1VKCFNCK	422	9	12	19		11185
GAG	RLRGKKKY	20	11	12	19		11186
GAG	1VATLYCVIQ	83	11	12	19		11187
GAG	LNMLNVGG	205	11	12	19		11188
GAG	SNPIPYGEY	273	11	12	19		11189
GAG	TSILDRQPK	304	11	12	19		11190
GAG	1VKCFNCK	422	9	12	21		11191
GAG	KWPSNCKR	433	9	13	21		11192
GAG	1VKCFNCK	422	9	13	21		11193
GAG	NCQEGHAR	427	10	13	21		11194
GAG	IARNCRAPRK	434	10	13	21		11195
GAG	1VKCFNCK	422	9	13	21		11196
GAG	1VKCFNCK	422	9	13	21		11197
GAG	1VKCFNCK	422	9	13	21		11198
GAG	1VKCFNCK	422	9	13	21		11199
GAG	1VKCFNCK	422	9	13	21		11200
GAG	CGKEGHAR	428	9	13	20		11201
GAG	EGHARNC	431	9	13	20		11202
GAG	LGKIWPSN	470	9	13	20		11203
GAG	KLKHWASR	31	10	13	20		11204
GAG	1VKCFNCK	422	9	13	20		11205
GAG	FLGKIPSN	469	10	13	20		11206
GAG	EVDKTEALD	95	11	13	20		11207
GAG	AAEWRVHFV	230	11	13	20		11208
GAG	IARNCRAPRK	433	11	13	20		11209
GAG	LGKIWPSN	470	11	13	20		11210
GAG	NSSVSNQ	144	9	14	31		11211
GAG	NCQEGHAR	427	10	14	22		11212

Table XVII
HIV-XII Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*100	SEQ ID NO.
GAG	FNGCKGIIIAK	426	11	14	22		11213
GAG	IAKCKAPRRK	434	11	14	22		11214
GAG	QNAQQQWVI	417	9	14	22		11215
GAG	QNAQQQWVI	417	9	14	22		11216
GAG	CKGKGIIAK	428	9	14	22		11217
GAG	EGHIAKCKR	431	9	14	22		11218
GAG	FNIVATLYCV	81	11	14	22		11219
GAG	TVATLYCVIIQ	83	11	14	22		11220
GAG	IVQMAQGMV	135	11	14	22		11221
GAG	SSQSQSNV	175	9	14	22		11222
GAG	SSQSQSNV	175	9	14	22		11223
GAG	FNIVATLY	81	11	15	24		11224
GAG	FNIVATLY	81	11	15	23		11225
GAG	TLVYCVIQR	86	8	15	23		11226
GAG	AAEWDVII	220	8	15	23		11227
GAG	WDRVIPIII	233	8	15	23		11228
GAG	RGNFRNQR	412	8	15	23		11229
GAG	FNIVATLY	81	9	15	23		11230
GAG	AAEWDVII	229	9	15	23	0.7100	11231
GAG	TAPPEESR	496	9	15	23		11232
GAG	SGGKLDWEK	9	10	15	23		11233
GAG	SLFNIVATLY	79	10	15	23		11234
GAG	VATLYCVIQR	84	10	15	23		11235
GAG	KHEEQKSK	325	10	15	23		11236
GAG	SGGKLDWEK	9	10	15	23		11237
GAG	PTAPPEESR	495	10	15	23		11238
GAG	LSGGKLDWE	8	11	15	23		11239
GAG	PGLLETSEGR	50	11	15	23		11240
GAG	KHEEQKSKK	105	11	15	23		11241
GAG	MMQGNFRN	409	11	15	23		11242
GAG	IAKCKAPRR	434	11	15	23		11243
GAG	LAWEKIRL	13	8	16	25		11244
GAG	NAQGMVII	158	8	16	25		11245
GAG	PVSILDIK	303	8	16	25		11246
GAG	GNERNQRK	413	8	16	25		11247
GAG	KLDWEKIRK	12	9	16	25		11248
GAG	GKRRKYRLK	24	9	16	25		11249
GAG	LAWEKIRL	13	9	16	25		11250
GAG	PGKRRYRLK	23	10	16	25		11251
GAG	GKRRKYRLK	24	10	16	25		11252
GAG	GLLFTSEGR	51	10	16	25		11253
GAG	YSPVSILDIK	301	10	16	25		11254
GAG	GGKLDWEKI	10	11	16	25		11255
GAG	KLDWEKIRL	12	11	16	25		11256
GAG	YSGKRRKYRLK	22	11	16	25		11257
GAG	YSGKRRKYRLK	304	11	16	25		11258
GAG	HAKNCRAPRK	433	11	16	25		11259
GAG	PIPFQGMIR	243	8	17	27		11260
GAG	GGKLDWEK	10	9	17	27		11261
GAG	DAWEKIRL	14	9	17	27		11262

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
GAG	LEITSDGR	52	9	17	27		11263
GAG	RLKIKKQGR	103	10	17	27		11264
GAG	RLKIKKQGR	103	10	17	27		11265
GAG	APPPQGR	241	10	17	27		11266
GAG	ALDKIEEQNK	102	11	17	27		11267
GAG	LSPTLNWV	168	11	17	27		11268
GAG	IIAGPIPGQMR	240	11	17	27		11269
GAG	PIPGQMR	243	11	17	27		11270
GAG	IIAKKCRAPR	434	11	18	28	0.0003	11271
GAG	IIAKKCRAPR	434	11	18	28		11272
GAG	IIAKKCRAPR	434	11	18	28		11273
GAG	IIAKKCRAPR	434	11	18	28		11274
GAG	IIAKKCRAPR	434	11	18	28		11275
GAG	IIAKKCRAPR	434	11	18	28		11276
GAG	IIAKKCRAPR	434	11	18	28		11277
GAG	IIAKKCRAPR	434	11	18	28		11278
GAG	IIAKKCRAPR	434	11	18	28		11279
GAG	IIAKKCRAPR	434	11	18	28		11280
GAG	IIAKKCRAPR	434	11	18	28		11281
GAG	IIAKKCRAPR	434	11	18	28		11282
GAG	IIAKKCRAPR	434	11	18	28		11283
GAG	IIAKKCRAPR	434	11	18	28		11284
GAG	IIAKKCRAPR	434	11	18	28		11285
GAG	IIAKKCRAPR	434	11	18	28		11286
GAG	IIAKKCRAPR	434	11	18	28		11287
GAG	IIAKKCRAPR	434	11	18	28		11288
GAG	IIAKKCRAPR	434	11	18	28		11289
GAG	IIAKKCRAPR	434	11	18	28		11290
GAG	IIAKKCRAPR	434	11	18	28		11291
GAG	IIAKKCRAPR	434	11	18	28		11292
GAG	IIAKKCRAPR	434	11	18	28		11293
GAG	IIAKKCRAPR	434	11	18	28		11294
GAG	IIAKKCRAPR	434	11	18	28		11295
GAG	IIAKKCRAPR	434	11	18	28	0.0066	11296
GAG	IIAKKCRAPR	434	11	18	28		11297
GAG	IIAKKCRAPR	434	11	18	28		11298
GAG	IIAKKCRAPR	434	11	18	28		11299
GAG	IIAKKCRAPR	434	11	18	28		11300
GAG	IIAKKCRAPR	434	11	18	28	0.0005	11301
GAG	IIAKKCRAPR	434	11	18	28		11302
GAG	IIAKKCRAPR	434	11	18	28		11303
GAG	IIAKKCRAPR	434	11	18	28		11304
GAG	IIAKKCRAPR	434	11	18	28		11305
GAG	IIAKKCRAPR	434	11	18	28		11306
GAG	IIAKKCRAPR	434	11	18	28		11307
GAG	IIAKKCRAPR	434	11	18	28		11308
GAG	IIAKKCRAPR	434	11	18	28		11309
GAG	IIAKKCRAPR	434	11	18	28		11310
GAG	IIAKKCRAPR	434	11	18	28		11311
GAG	IIAKKCRAPR	434	11	18	28		11312

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1001	SEQ ID NO.
GAG	GVGGPSHK	376	8	23	36		11313
GAG	GVGGPSHK	476	8	23	36		11314
GAG	GVGGPSHK	375	9	23	36		11315
GAG	GVGGPSHK	470	9	23	36		11316
GAG	ACQGVGPSII	373	10	23	36		11317
GAG	FLGRKPSHK	469	10	23	36	0.0013	11318
GAG	YNTVATLYCV	81	11	23	36		11319
GAG	TACQGVGPS	372	11	23	36		11320
GAG	ACQGVGPSII	472	11	23	36		11321
GAG	NCQGVGPSII	427	10	24	38		11322
GAG	NCQGVGPSII	427	10	24	38		11323
GAG	ENCQGVGPSII	426	11	24	38		11324
GAG	CGKGVGPSII	428	9	24	38		11325
GAG	YSPVSLDIR	301	10	24	38		11326
GAG	NELGKIPSH	468	10	25	40		11327
GAG	PVSLDIR	303	8	25	40		11328
GAG	GVGGPSHK	375	9	25	39		11329
GAG	FLGRKPSHK	469	9	25	39		11330
GAG	VSLDIRQPK	304	9	25	39		11331
GAG	ANFLGRKPSH	467	11	25	39		11332
GAG	LYWASRELER	35	10	26	41		11333
GAG	ILYWASRELE	14	11	26	41		11334
GAG	YVDFEFTLR	321	9	27	42	0.0070	11335
GAG	QAVHQMSPR	162	10	27	42	0.0010	11336
GAG	YVDFEFTLR	320	10	27	42		11337
GAG	RAEQATQEVK	329	10	27	42		11338
GAG	ANPDKTLK	350	10	27	42	0.0002	11339
GAG	NANPDKTLK	349	11	27	42		11340
GAG	LYWASRELER	352	11	28	44		11341
GAG	POCKTLK	352	8	28	44		11342
GAG	YVDFEFTLR	321	9	28	44		11343
GAG	PERDYVDRFY	316	10	28	44		11344
GAG	YVDFEFTLR	320	10	28	44		11345
GAG	PERDYVDRFY	316	11	28	44		11346
GAG	GARASVLSGG	2	8	28	46		11347
GAG	YVDFEFTLR	321	8	29	45		11348
GAG	NLOQGVII	158	8	29	45		11349
GAG	WYKVEEK	176	8	29	45		11350
GAG	WDLHPVH	233	8	29	45		11351
GAG	RDYVDRFY	318	8	29	45		11352
GAG	RASVLSGGK	4	9	29	45		11353
GAG	QNLGGQVH	17	9	29	45		11354
GAG	QNLGGQVH	318	9	29	45	0.0400	11355
GAG	NAWVKVEEK	174	10	29	45		11356
GAG	IVNQLGOMV	155	11	29	45		11357
GAG	LNAAVYKVEE	173	11	29	45		11358
GAG	LNAAVYKVEE	230	11	29	45		11359
GAG	AAEWDLIIPV	483	11	29	45		11360
GAG	PNGLQSR	483	8	30	48		11361
GAG	NAWVKVVEEK	174	10	30	47	0.0002	11362

Table XVII
HIV-1 Nef Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
GAG	KRLRPGGKK	18	11	30	47		11363
GAG	WKKVVEK	173	11	30	47		11364
GAG	WKKVVEK	176	8	31	48	0.0001	11365
GAG	RNYVDRFFK	318	9	33	52		11366
GAG	RNYVDRFFK	318	9	33	52		11367
GAG	PRDYVDRFF	316	11	33	53		11368
GAG	RNYVDRFFK	316	9	33	53		11369
GAG	RNYVDRFFK	316	9	34	53		11370
GAG	RLRIGRKKK	20	10	34	53		11371
GAG	RLRIGRKKK	20	10	34	53		11372
GAG	PIVGEYK	279	10	34	53	0.0001	11373
GAG	PIVGEYK	279	8	35	55		11374
GAG	PIVGEYK	279	9	35	55	0.0012	11375
GAG	DTKEALDK	98	8	36	56	0.0001	11376
GAG	QVGGGPGII	375	8	36	56		11377
GAG	QVGGGPGII	375	8	36	56		11378
GAG	ISPTLSAVV	168	10	36	56	0.0001	11379
GAG	TACQVGGPG	373	11	36	56	0.0001	11380
GAG	ACQVGGGPGH	373	11	36	56		11381
GAG	QVGGGPGIIA	375	11	36	56		11382
GAG	GVGGPGHK	376	8	37	58	0.0018	11383
GAG	GVGGPGHK	376	8	37	58		11384
GAG	GVGGPGHK	376	9	37	58		11385
GAG	GVGGPGHK	376	10	37	58	0.0001	11386
GAG	GVGGPGHK	376	10	37	58		11387
GAG	GVGGPGHK	376	10	37	58		11388
GAG	GVGGPGHK	376	10	37	58		11389
GAG	GVGGPGHK	376	10	37	58		11390
GAG	GVGGPGHK	376	10	37	58		11391
GAG	GVGGPGHK	376	10	37	58	0.7100	11392
GAG	GVGGPGHK	376	10	37	58		11393
GAG	GVGGPGHK	376	10	37	58		11394
GAG	GVGGPGHK	376	10	37	58		11395
GAG	GVGGPGHK	376	10	37	58	0.0048	11396
GAG	GVGGPGHK	376	10	37	58		11397
GAG	GVGGPGHK	376	10	37	58		11398
GAG	GVGGPGHK	376	10	37	58		11399
GAG	GVGGPGHK	376	10	37	58		11400
GAG	GVGGPGHK	376	10	37	58		11401
GAG	GVGGPGHK	376	10	37	58	0.0010	11402
GAG	GVGGPGHK	376	10	37	58		11403
GAG	GVGGPGHK	376	10	37	58		11404
GAG	GVGGPGHK	376	10	37	58		11405
GAG	GVGGPGHK	376	10	37	58		11406
GAG	GVGGPGHK	376	10	37	58		11407
GAG	GVGGPGHK	376	10	37	58		11408
GAG	GVGGPGHK	376	10	37	58		11409
GAG	GVGGPGHK	376	10	37	58		11410
GAG	GVGGPGHK	376	10	37	58		11411
GAG	GVGGPGHK	376	10	37	58		11412

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
GAG	RAPKKGWCK	439	10	51	80		11413
GAG	CTERQANTLG	439	11	52	83		11414
GAG	CTERQANTLG	437	8	53	84		11415
GAG	TINEEAWEVD	225	11	53	83		11416
GAG	INEEAAWEVD	226	10	55	86		11417
GAG	FNCCKEGH	426	8	57	90		11418
GAG	WILGLNK	289	3	57	89		11419
GAG	FNCCKEGH	425	9	57	89		11420
GAG	ILGLNKIVR	290	10	57	89		11421
GAG	FNCCKEGH	424	10	57	89	0.0006	11422
GAG	WILGLNKIVR	289	11	57	89		11423
GAG	ILGLNKIVRMV	291	11	57	89		11424
GAG	ILGLNKIVR	291	10	58	91	0.0001	11425
GAG	LGLNKIVRMV	292	10	58	91	0.0002	11426
GAG	LLVQNANPDC	345	11	58	92		11427
GAG	LGLNKIVRMV	292	10	59	92		11428
GAG	LLVQNANPDC	344	10	59	92	0.0110	11429
GAG	LGLNKIVRMV	294	10	60	94		11430
GAG	LNKIVRMV	293	9	60	94	0.0002	11431
GAG	GLNKIVRMV	293	8	61	95		11432
GAG	QANQMMLK	216	8	61	95		11433
GAG	QANPDC	348	8	61	95		11434
GAG	GLNQAMQM	213	11	62	98	0.0560	11435
GAG	RGLNKIVR	311	8	62	98		11436
GAG	GLNKIVR	311	8	63	98		11437
GAG	PRDYDVR	316	8	63	98		11438
GAG	QPKPEPHDY	311	10	63	98	0.0002	11439
NEF	AADGVGVSR	42	10	09	15		11440
NEF	ANEGNNSLLI	249	11	09	15		11441
NEF	VGWPAIRER	9	10	10	16		11442
NEF	VGWPAIRER	310	9	10	16		11443
NEF	FDSLAFHII	311	8	10	16		11444
NEF	DSKLAFLII	311	8	10	16		11445
NEF	AVSQDLDK	48	8	10	16		11446
NEF	PLRMTFK	102	8	10	16		11447
NEF	AVSQDLDK	47	9	10	16		11448
NEF	GLIEGLYSK	325	10	10	16		11449
NEF	VGWPAIRER	321	9	10	16		11450
NEF	VGWPAIRER	321	9	10	16		11451
NEF	VGWPAIRER	321	9	10	16		11452
NEF	QVPLRMTFK	109	10	10	16		11453
NEF	GAFDLSFLK	110	10	10	16		11454
NEF	GGLEGLYSK	124	10	10	16		11455
NEF	CKLVPVDPK	226	10	10	16		11456
NEF	HMARELIPEY	320	10	10	16		11457
NEF	HMARELIPEY	320	10	10	16		11458
NEF	GVGAVSQDL	45	11	10	16		11459
NEF	KGAFDLSFLK	109	11	10	16		11460
NEF	KGLEGLYSK	122	11	10	16		11461
NEF	WCKLVPVDP	225	11	10	16		11462
NEF	NNSLLHPVDP	254	11	10	16		11463
NEF	HMARELIPEY	320	11	10	16		11464

Table XVII
HIV-1 X1-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*101	SIQ ID NO.
NEF	MARELIPYY	321	11	10	16		11463
NEF	AGEENNCLL	269	11	11	18		11464
NEF	VSRLDKL	48	8	11	17		11465
NEF	VSRLDKL	49	8	11	17		11466
NEF	KLVPDPR	228	8	11	17		11467
NEF	AVSRDLK	47	9	11	17		11468
NEF	AVSRDLK	48	9	11	17		11469
NEF	AVSRDLK	46	10	11	17		11470
NEF	AVSRDLK	47	10	11	17		11471
NEF	AVSRDLK	48	10	11	17		11472
NEF	AVSRDLK	49	10	11	17		11473
NEF	NSLLHPCOH	255	10	11	17		11474
NEF	GVGAVSRDLK	45	11	11	17		11475
NEF	GVGAVSRDLK	46	11	11	17		11476
NEF	EGENNCLLI	251	9	12	19		11477
NEF	YTPGVYR	207	8	12	19		11478
NEF	DLDLWYTH	184	9	12	19		11479
NEF	EGENNCLLI	251	10	12	19		11480
NEF	VDSLSFLK	112	9	13	21		11481
NEF	VDSLSFLK	111	10	13	20		11482
NEF	VDSLSFLK	112	11	13	20		11483
NEF	VDSLSFLK	113	11	13	20		11484
NEF	VDSLSFLK	114	11	13	20		11485
NEF	VDSLSFLK	115	11	13	20		11486
NEF	VDSLSFLK	116	11	13	20		11487
NEF	VDSLSFLK	117	11	13	20		11488
NEF	VDSLSFLK	118	11	13	20		11489
NEF	VDSLSFLK	119	11	13	20		11490
NEF	VDSLSFLK	120	11	13	20		11491
NEF	VDSLSFLK	121	11	13	20		11492
NEF	VDSLSFLK	122	11	13	20		11493
NEF	VDSLSFLK	123	11	13	20		11494
NEF	VDSLSFLK	124	11	13	20		11495
NEF	VDSLSFLK	125	11	13	20		11496
NEF	VDSLSFLK	126	11	13	20		11497
NEF	VDSLSFLK	127	11	13	20		11498
NEF	VDSLSFLK	128	11	13	20		11499
NEF	VDSLSFLK	129	11	13	20		11500
NEF	VDSLSFLK	130	11	13	20		11501
NEF	VDSLSFLK	131	11	13	20		11502
NEF	VDSLSFLK	132	11	13	20		11503
NEF	VDSLSFLK	133	11	13	20		11504
NEF	VDSLSFLK	134	11	13	20		11505
NEF	VDSLSFLK	135	11	13	20		11506
NEF	VDSLSFLK	136	11	13	20		11507
NEF	VDSLSFLK	137	11	13	20		11508
NEF	VDSLSFLK	138	11	13	20		11509
NEF	VDSLSFLK	139	11	13	20		11510
NEF	VDSLSFLK	140	11	13	20		11511
NEF	VDSLSFLK	141	11	13	20		11512

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
NEF	QNTVPGIR	205	10	18	28		11513
NEF	GGLEGLY	124	8	19	30		11514
NEF	GGLEGLY	122	9	19	30		11515
NEF	DILDVWY	185	8	20	31		11516
NEF	YTPGIR	207	31	20	31		11517
NEF	QDLDLWY	184	9	21	31		11518
NEF	QNTVPGIR	205	10	20	31		11519
NEF	QNTVPGIR	205	10	21	31		11520
NEF	WYVITQY	191	8	21	33		11521
NEF	YTPGIR	207	8	21	33		11522
NEF	KGDLGLY	122	9	21	33		11523
NEF	DLWVYITQY	188	10	21	33		11524
NEF	LDLWVYITQY	187	11	21	33		11525
NEF	LSFLKK	114	8	22	34		11526
NEF	LSFLKK	113	8	22	34		11527
NEF	LSFLKK	113	8	22	34		11528
NEF	ELDLWY	185	9	22	34		11529
NEF	ELDLWY	185	9	22	34		11530
NEF	GLYSKKR	173	8	23	36		11531
NEF	LSFLKK	114	8	27	42		11532
NEF	LSFLKK	113	9	27	42		11533
NEF	ELDLWY	185	8	33	53		11534
NEF	ELDLWY	185	8	34	53		11535
NEF	YTPWQNY	196	8	36	56		11536
NEF	QNTVPGIR	205	10	36	56		11537
NEF	LTFCWCFC	221	8	39	61	0.0017	11538
NEF	PLTFGWCFK	219	9	39	61		11539
NEF	QVPLRMITY	100	9	46	72	0.6300	11540
NEF	QVPLRMITY	100	10	46	72		11541
NEF	QVPLRMITY	100	11	48	75		11542
NEF	GFPRVQPLR	91	11	48	75		11543
NEF	PLRMITYK	102	8	49	77	0.0003	11544
POL	STNSPTR	32	8	01	33		11545
POL	RANSPTSR	35	8	01	33		11546
POL	STNSPTSR	31	9	01	33		11547
POL	PSRELQVR	33	10	01	33		11548
POL	QTRNSPTR	35	10	01	33		11549
POL	NSPTSRELQVR	34	11	01	33		11550
POL	RANSPTSR	37	8	01	50		11551
POL	PSRELQVR	39	9	01	50		11552
POL	PSRNSPTR	24	10	01	50		11553
POL	NSPSRELQVR	39	11	01	50		11554
POL	NSPSRELQVR	39	11	01	50		11555
POL	NSLSEAGD	5	10	05	25		11556
POL	NLAFTQGEAR	5	10	10	16		11557
POL	ILIEFGII	149	8	10	16		11558
POL	LIEICGII	150	8	10	16		11559
POL	YAKMRTAH	546	8	10	16		11560
POL	RSMTINDYK	580	8	10	16		11561
POL	ETETWWTID	588	10	10	16		11562

Table XVII
HIV-XII Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
POL	ETWETWATE	588	10	10	16		11563
POL	VSLIDTINOK	659	10	10	16		11564
POL	ENLAPQGEAR	4	11	10	16		11565
POL	TGKYARMRIA	543	11	10	16		11566
POL	VVSLDTTNO	658	11	10	16		11567
POL	QTKELQKQIK	901	11	10	16		11568
POL	YVNSRARR	324	10	11	18		11569
POL	TNNETGHR	324	9	11	17		11570
POL	TNNETGHR	324	10	11	17		11571
POL	LDGDKAQEDH	754	11	11	17		11572
POL	IGGFKVK	137	8	11	17		11573
POL	RIGPENPY	238	8	11	17		11574
POL	TAHTNDVK	551	8	11	17		11575
POL	YVNSRARR	324	8	11	17		11576
POL	DKAQEDH	757	8	11	17		11577
POL	VVPRKVK	1012	8	11	17		11578
POL	KIKDYK	1019	8	11	17		11579
POL	GGGFKVK	136	9	11	17		11580
POL	SLDITINOK	660	9	11	17		11581
POL	GDKAQEDH	756	9	11	17		11582
POL	YVNSRARR	324	9	11	17		11583
POL	KVPRKVK	1011	9	11	17		11584
POL	GGGFKVK	135	10	11	17		11585
POL	ISRGPENPY	236	10	11	17		11586
POL	STNNETGHR	323	10	11	17		11587
POL	ESWTVNDQK	439	10	11	17		11588
POL	ETNQRTELH	463	10	11	17		11589
POL	GGGFKVK	755	10	11	17		11590
POL	GSNSTTVK	820	10	11	17		11591
POL	GQGEFGPY	886	10	11	17		11592
POL	SDQIKLEQK	958	10	11	17		11593
POL	FNFPQLWQR	85	11	11	17		11594
POL	IGGFKVK	134	11	11	17		11595
POL	KSRGPEK	235	11	11	17		11596
POL	STNNETGHR	323	11	11	17		11597
POL	STNNETGHR	323	11	11	17		11598
POL	VVSLTETNO	658	11	11	17		11599
POL	NGSNFTSTV	869	11	11	17		11600
POL	AGIQEQGIPY	885	11	11	17		11601
POL	ADIASDQTK	953	11	11	17		11602
POL	VQIADQTK	953	11	11	17		11603
POL	YVNSRARR	957	11	11	17		11604
POL	NSKVKPRK	1007	11	11	17		11605
POL	OTRANSFTR	21	10	12	19		11606
POL	IKQNFR	969	8	12	19		11607
POL	QYFGRVK	458	9	12	19		11608
POL	QDQWTQY	526	9	12	19		11609
POL	IKQNFRVK	969	10	12	19		11610
POL	YVNSRARR	969	11	12	19		11611
POL	IKQNFRVYY	969	11	12	19		11612

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*101	SEQ ID NO.
POL	AFQGEAR	7	8	12	19		11613
POL	TNQTLEI	465	8	12	19		11614
POL	KTQLOVYAR	668	9	12	19		11615
POL	ELNLRGKWK	122	9	12	19		11616
POL	TTNQTLEI	664	9	12	19		11617
POL	QIKIQNER	968	9	12	19		11618
POL	VIQDNSEIK	1003	9	12	19		11620
POL	NSEIKVPR	1007	9	12	19		11621
POL	VTLEINRQK	1002	9	12	19		11622
POL	VIQDNSEIK	1006	10	12	19		11623
POL	DNSEIKVPR	1007	10	12	19		11624
POL	NSEIKVPR	1007	10	12	19		11625
POL	TVLEINLRGK	118	11	12	19		11626
POL	ELNLRGKWKPK	122	11	12	19		11627
POL	QGDQWTYQI	524	11	12	19		11628
POL	TKRGKHTINDY	648	11	12	19		11629
POL	TKRGKHTINDY	648	11	12	19		11630
POL	QIKIQNER	968	11	12	19		11631
POL	AVIQDNSEIK	1000	11	12	19		11632
POL	QDNSEIKVPR	1005	11	12	19		11633
POL	DNSEIKVPR	1006	11	12	19		11634
POL	ELQKQIR	964	8	13	21		11635
POL	KTQYARMAR	542	9	13	21		11636
POL	KTQYARMAR	542	9	13	21		11637
POL	KTQYARMAR	542	9	13	21		11638
POL	EDINLPK	121	8	13	20		11639
POL	TKQYARMAR	543	8	13	20		11640
POL	YARMRGAI	546	8	13	20		11641
POL	QVREQAEH	916	8	13	20		11642
POL	DNINLRGKWK	122	9	13	20		11643
POL	EDINLPKWK	121	10	13	20		11644
POL	RAKIEELREH	388	10	13	20		11645
POL	TVQPIVLPK	429	10	13	20	5.6000	11646
POL	AGRWPKVTH	857	10	13	20		11647
POL	IQVREQAEH	914	10	13	20		11648
POL	QVREQAEHLK	916	10	13	20		11649
POL	QVREQAEHLK	916	10	13	20		11650
POL	LVTKLGGQK	97	11	13	20		11651
POL	TVLEINLRGK	118	11	13	20		11652
POL	DNINLRGKWK	122	11	13	20		11653
POL	KIEELREHLK	390	11	13	20		11654
POL	WTVQPIVLPK	428	11	13	20		11655
POL	TKQYARMAR	543	11	13	20		11656
POL	QVREQAEHLK	916	11	13	20		11657
POL	IQVREQAEH	913	11	13	20		11658
POL	EKQVPRKAK	1009	11	13	20		11659
POL	ESSEQIR	16	8	14	22	0.0510	11660
POL	QIVTGKVR	458	9	14	22		11661
POL	ASQIVGKVR	456	11	14	22		11662

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SIQ ID NO.
POL	MTESVWVGK	567	11	14	22		11663
POL	LEIEGCK	149	8	14	22		11664
POL	LEIEGCK	150	8	14	22		11665
POL	QNPDIIV	363	8	14	22		11666
POL	NFISTIVK	872	8	14	22		11667
POL	IASDIQTK	956	8	14	22		11668
POL	DSIDPLWK	981	8	14	22		11669
POL	LEIEGCK	149	9	14	22		11670
POL	LEIEGCK	149	9	14	22		11671
POL	IASDIQTK	955	9	14	22		11672
POL	RDSRDLWK	980	9	14	22		11673
POL	QLIEGCK	148	10	14	22		11674
POL	QNPDIIVQY	363	10	14	22		11675
POL	RTKIELRLQI	388	10	14	22		11676
POL	QNPDIIVQY	363	10	14	22		11677
POL	QNPDIIVQY	363	10	14	22		11678
POL	DIASDIQTK	954	10	14	22		11679
POL	RPIAWGTPAK	983	10	14	22		11680
POL	FSHQILWQR	85	11	14	22		11681
POL	YDQIEGCK	146	11	14	22		11682
POL	KTPKFLIQK	577	11	14	22		11683
POL	GDKAQEHER	756	11	14	22		11684
POL	YDQIEGCK	146	11	14	22		11685
POL	LVETCTEMK	221	10	15	24	0.0120	11686
POL	ELRQILLR	393	8	15	23		11687
POL	QGDQWTV	524	8	15	23		11688
POL	KTELQALI	668	8	15	23		11689
POL	EKVVRPK	1009	9	15	23		11690
POL	VGHQIQPDR	695	10	15	23		11691
POL	VDKLSAGIR	746	10	15	23		11692
POL	IKAQEHER	757	10	15	23		11693
POL	ALVECTEMK	220	11	15	23		11694
POL	KIELRQILLR	390	11	15	23		11695
POL	TNQTQLQAH	665	11	15	23		11696
POL	ALHQIQPDR	694	11	15	23		11697
POL	VDKLSAGIR	746	11	15	23		11698
POL	VDKLSAGIR	739	11	15	23		11699
POL	VDKLSAGIR	740	11	15	23		11700
POL	IKAQEHERY	757	11	15	23		11701
POL	KAQEHER	759	8	16	25		11702
POL	KAQEHERY	759	9	16	25		11703
POL	NLAPOGEAR	5	10	16	25		11704
POL	KAQEHERYH	7	10	16	25		11705
POL	KAQEHER	7	8	16	25		11706
POL	RANSIR	26	8	16	25		11707
POL	SAITNDVK	551	8	16	25		11708
POL	IIQAQDR	697	8	16	25		11709
POL	KLVSAGIR	742	8	16	25		11710
POL	LVSAGIR	743	8	16	25		11711
POL	EKVVRPK	1009	8	16	25	0.0054	11712
POL	LATQGEAR	6	9	16	25		

Table XVII
HLV-AH Motif Peptides with Binding Information

Protein	Sequence	Position	No of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO
POL	GHQAQDFR	696	9	16	25		11713
POL	KLNSAGIRK	742	9	16	25		11714
POL	ENLAFQGEA	4	11	16	25	0.0770	11715
POL	KLNSAGIRK	36	8	17	27		11716
POL	KIEELRQI	393	8	17	27		11717
POL	ELREILLL	393	8	17	27		11718
POL	WGKTPKFK	575	8	17	27		11719
POL	TKIGGGOLK	99	9	17	27		11720
POL	VTIKGGOLK	98	10	17	27	0.0330	11721
POL	VTIKGGOLK	98	10	17	27	0.2100	11722
POL	VTIKGGOLK	429	10	17	27		11723
POL	VTIKGGOLK	575	10	17	27		11724
POL	TLWBRILYTI	91	11	17	27		11725
POL	WTVPQIQLPEK	428	11	17	27		11726
POL	VTWVGKTPKFK	572	11	17	27		11727
POL	YFSPVLKDFR	304	11	18	29		11728
POL	NKTKTKYAKM	540	11	18	29		11729
POL	YFSPVLKDFR	306	9	18	28		11730
POL	SVPLDKDFR	305	10	18	28		11731
POL	SVPLDKDFR	306	10	18	28		11732
POL	AGIKVQQLCK	461	10	18	28		11733
POL	VNQHIEQLIK	710	10	18	28		11734
POL	VNQHIEQLIK	710	10	18	28		11735
POL	SVPLDKDFR	306	11	18	28		11736
POL	VAGIKVQQLCK	460	11	18	28		11737
POL	LVSQIEQLIK	709	11	18	28		11738
POL	VNQHIEQLIK	710	11	18	28		11739
POL	PLDKDFR	308	8	19	30		11740
POL	PLDKDFR	309	9	19	30		11741
POL	KTKGYAKMR	542	8	19	30		11742
POL	LDKDFRKY	309	8	19	30		11743
POL	KIEELREI	390	8	19	30		11744
POL	TKGYAKMR	543	8	19	30		11745
POL	GAHTTNVYK	551	8	19	30		11746
POL	PLWKGPAK	985	8	19	30		11747
POL	PLWKGPAK	985	8	19	30		11748
POL	GKIVQQLCK	462	9	19	30		11749
POL	RGATINDVYK	550	9	19	30		11750
POL	KVRQLCKLLR	464	10	19	30		11751
POL	ATLSEYVWGR	568	10	19	30		11752
POL	MAQEDCVASR	1028	10	19	30		11753
POL	VSNHIEQLIK	710	11	19	30		11754
POL	QMAQDDCVAS	1027	11	19	30		11755
POL	QIYAGIKVYK	458	9	20	32		11756
POL	KVYLAQWPAH	722	10	20	32	0.0036	11757
POL	KVYLAQWPAH	722	10	20	32	0.0740	11758
POL	ASQIYAGIKVYK	459	11	20	32		11759
POL	KVYLAQWPAH	722	11	20	32		11760
POL	KFKLMQK	580	8	20	31	2.3000	11761

Table XVII
HIV-1 N-Modi Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO
POL	GDGVASR	1030	8	20	31		11763
POL	AGDCVSR	1029	9	20	31		11764
POL	VSLTETNOK	659	10	20	31		11765
POL	LLLAGRWIV	853	11	20	31		11766
POL	YESVPLDK	304	8	21	33		11767
POL	ACWAGIK	881	9	21	33		11768
POL	VSLTETNOK	880	9	21	33		11769
POL	YESVPLDK	880	9	21	33		11770
POL	DAYSVPDK	302	10	21	33	0.0470	11771
POL	DLEGIQIRTK	381	10	21	33		11772
POL	QLCKLLRGTK	467	10	21	33		11773
POL	IFAIKKKDKTK	249	11	21	33		11774
POL	GDAYSVPDL	301	11	21	33		11775
POL	SDLEGIQIRTK	380	11	21	33		11776
POL	IFAIKKKDKTK	776	11	21	33		11777
POL	AGDKQEGIPY	885	11	21	33		11778
POL	EGGIQIRTK	383	8	22	34		11779
POL	RTKIEELR	388	8	22	34		11780
POL	YLAWVPVPI	724	8	22	34		11781
POL	YLAWVPAIR	725	8	22	34		11782
POL	YLAWVPAIR	724	8	22	34		11783
POL	MTKILEPFRK	353	10	22	34	0.0570	11784
POL	AGRWPKVVIH	857	10	22	34	0.0380	11785
POL	GRQEGFIPY	886	10	22	34		11786
POL	SMTKILEPFRK	352	11	22	34	0.0002	11787
POL	KTPKFRLLPQK	577	11	22	34		11788
POL	LAGRWPKVVIH	856	11	22	34		11789
POL	YLAWVPVPI	722	10	23	37		11790
POL	KYLWSVPVPI	722	11	23	37		11791
POL	KILEPFRK	355	8	23	36		11792
POL	KVLAVAVI	823	8	23	36		11793
POL	SFPTLLWQR	86	10	23	36		11794
POL	ENLPPVIAK	777	10	23	36		11795
POL	ECGKAVAVI	822	10	23	36		11796
POL	LLKNGETPD	398	11	23	36		11797
POL	LLRWGETPD	398	11	23	36		11798
POL	IDIATDQTK	953	11	23	36		11799
POL	NTPIFAIK	246	8	24	38		11800
POL	GDGCVAGR	1030	8	24	38		11801
POL	YNTPIFAIK	245	9	24	38		11802
POL	YNTPIFAIK	245	9	24	38		11803
POL	LCKLLRGTK	468	9	24	38	0.0001	11804
POL	AGDDCVAGR	1029	9	24	38		11805
POL	YNTPIFAIK	245	10	24	38		11806
POL	YNTPIFAIKK	246	10	24	38		11807
POL	MAGDDCVAGR	1028	10	24	38		11808
POL	YNTPIFAIKK	245	11	24	38		11809
POL	YNTPIFAIKK	244	11	24	38		11810
POL	QGQGGWYIYQI	244	11	24	38		11811
POL	KLQAGATYID	643	11	24	38		11812

Table XVII
HIV-1 CRF01_AG P-epitopes with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	TAVALLLKLAG	849	11	24	38		11813
POL	QMAAGHRCVAG	1027	11	24	38		11814
POL	QGWVTVQY	526	9	25	40	0.0001	11815
POL	PIFAKKK	248	8	25	39		11816
POL	QGGQGWY	524	8	25	39		11817
POL	FLKLGR	852	9	25	39		11818
POL	YTLKLGR	852	9	25	39		11819
POL	YTLKLGR	467	9	25	39		11820
POL	YTLKLGR	644	10	25	39		11821
POL	LDKAGVYDR	757	10	25	39		11822
POL	LDKAGVYDR	757	10	25	39		11823
POL	PSKDLAEHQ	513	11	25	39		11824
POL	GIDKAEHEIK	756	11	25	39		11825
POL	IDKAEHEIK	757	11	25	39		11826
POL	IDKAEHEIK	757	11	25	39		11827
POL	SPNLPVPVAK	778	11	26	41		11828
POL	KAKHEIK	580	8	26	41		11829
POL	KAKHEIK	779	8	26	41		11830
POL	NLPVPVAK	779	8	26	41		11831
POL	LCKLLKGAK	468	9	26	41		11832
POL	FNLPPVAK	778	9	26	41		11833
POL	SNFTSAVAK	871	9	26	41		11834
POL	DNLPVPVAK	777	10	26	41		11835
POL	SNFTSAVAK	870	10	26	41		11836
POL	TGQETATYLL	869	11	26	41		11837
POL	NGSFTSAV	869	11	26	41		11838
POL	KAQEEHEK	759	8	27	43	0.3400	11839
POL	ASQVAGIK	456	9	27	43		11840
POL	KAQEEHEKY	759	9	27	43		11841
POL	KAQEEHEKY	759	9	27	43		11842
POL	KAQEEHEKY	123	10	27	42		11843
POL	KAQEEHEKY	223	8	27	42		11844
POL	EICTEMEK	383	8	27	42		11845
POL	EIGQIRAK	743	8	27	42		11846
POL	LYSSGIRK	779	8	27	42	0.0410	11847
POL	NLPVPVAK	779	8	27	42		11848
POL	ETAYFLIK	848	8	27	42		11849
POL	KLVSQGRK	462	9	27	42		11850
POL	NLPVPVAK	778	9	27	42		11851
POL	NLPVPVAK	123	10	27	42		11852
POL	DLKQIRAK	381	10	27	42		11853
POL	WASQVAGIK	455	10	27	42		11854
POL	KVKQLCKLLR	464	10	27	42		11855
POL	EICTEMEK	223	11	27	42		11856
POL	SDLEQGRK	740	11	27	42		11857
POL	ASQVAGIK	456	9	28	44		11858
POL	KDLAEIQK	515	9	28	44		11859
POL	NLTKGKYAK	540	9	28	44		11860
POL	DLAEIQK	516	8	28	44		11861
POL	INGAETTY	626	8	28	44		11862
POL	NFTSAVAK	869	8	28	44	0.0001	11863
POL	CTEMEKGR	223	9	28	44		11864

Table XVII
 HIV-1 Mod. Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
POL	GKVKQLCK	462	9	28	44		11863
POL	PVGAQETP	625	9	28	44		11864
POL	QIKKEXYV	716	9	28	44		11865
POL	QIKKEXYV	716	9	28	44		11866
POL	WASQYDGR	455	10	28	44		11867
POL	KNLKTGYAK	539	10	28	44		11868
POL	NLKTGKVAR	540	9	29	46		11869
POL	KLVSSGIR	742	8	29	45	0.0001	11870
POL	KNLKTGYAK	539	10	29	45		11871
POL	QIKKEXYV	716	10	29	45		11872
POL	QIKKEXYV	716	10	29	45		11873
POL	YVWKLSSGIR	572	11	29	45		11874
POL	QVQKLVSSGIR	739	11	29	45		11875
POL	WGRTPKER	575	8	30	47		11876
POL	LTETTNOK	661	8	30	47		11877
POL	ANRRTKGR	638	8	30	47	0.0001	11878
POL	ANRRTKGR	638	8	30	47	0.0016	11879
POL	IEQQLKKEK	713	10	30	47	0.0005	11880
POL	GAANRETLLG	636	11	30	47		11881
POL	QIEQLKKEK	712	11	30	47		11882
POL	IKLAGRWPT	853	11	30	47		11883
POL	EGKILVAVH	821	8	31	48		11884
POL	YFLLKLAGR	851	9	31	48		11885
POL	EGKILVAVH	821	10	31	48		11886
POL	ISINNETGIR	322	11	31	48		11887
POL	TGQETAVFLK	845	11	31	48		11888
POL	YFLLKLAGR	851	11	31	48		11889
POL	INNETPGIR	324	9	32	51		11890
POL	INNETPGIR	324	10	32	51		11891
POL	PIKLALGR	852	8	32	50		11892
POL	INNETPGIR	323	10	32	50		11893
POL	SINNETGIRY	323	11	32	50		11894
POL	SINNETGIRY	323	11	32	50		11895
POL	SNMKEKPERK	869	11	32	50		11896
POL	EMEKGNISK	926	11	32	50	0.0100	11897
POL	EMEKGNISK	926	10	33	52	0.0100	11898
POL	DYKQLTEAVQ	556	11	33	52	0.0240	11899
POL	DIATDIQTK	954	10	34	53	0.0130	11900
POL	ELQKQITK	964	8	35	56		11901
POL	ELQKQITK	964	8	35	55		11902
POL	ISRDPIWK	981	10	35	55		11903
POL	ETKLGRAGY	641	9	35	55		11904
POL	IATDIQTK	955	9	35	55	0.0900	11905
POL	QIKRQNER	988	9	35	55	0.0045	11906
POL	RISRDPIWK	980	9	35	55		11907
POL	TDQTKELQK	958	10	35	55	0.0001	11908
POL	ATDIQTKELQK	957	10	35	55		11909
POL	ATDIQTKELQK	957	11	35	55	0.1800	11910
POL	ITKIQNER	968	11	35	55		11911
POL	ITKIQNER	969	8	36	57		11912

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ITKONERVY	869	10	36	57	0.0012	11913
POL	ITKONERVY	956	11	36	57		11914
POL	IATDICTK	956	8	36	56		11915
POL	PIWKGPAK	985	8	36	56		11916
POL	NLPKGWPK	124	9	36	56		11917
POL	AFQSSMTK	347	9	36	56	0.9600	11918
POL	PAFQSSMTK	346	10	36	56	0.0850	11919
POL	YVQNSNDK	1002	11	37	58		11920
POL	NTPEFAIK	246	8	37	58	0.0003	11921
POL	PVFAIKK	248	8	37	58	0.0001	11922
POL	QLTEAVQK	559	8	37	58		11923
POL	QIEQLIK	712	8	37	58		11924
POL	IIEQLIKK	713	8	37	58		11925
POL	YLSWPAIK	724	8	37	58		11926
POL	YLSWPAIK	724	8	37	58		11927
POL	YNTVFAIK	245	9	37	58		11928
POL	NTVFAIKK	246	9	37	58	0.0002	11929
POL	QIEQLIKK	712	9	37	58		11930
POL	YLSWPAIK	724	9	37	58	0.1600	11931
POL	VQNSNDK	1003	9	37	58	0.0068	11932
POL	YNTVFAIK	245	10	37	58		11933
POL	YNTVFAIK	245	10	37	58	0.0046	11934
POL	VQNSNDK	1002	10	37	58	0.0210	11935
POL	YNTVFAIKK	245	11	37	58		11936
POL	AVVQNSNDK	1000	11	37	58	0.0150	11937
POL	IFQSSMTK	348	8	38	59	0.0073	11938
POL	ILKEPVIGVY	498	11	38	59		11939
POL	LDGDKAQEEH	754	11	38	59		11940
POL	YVTRDGROK	649	9	39	61		11941
POL	KAGYVTRDGR	646	10	39	61	0.0010	11942
POL	LGIIQAQPK	695	10	39	61		11943
POL	DGDKAQEEH	755	10	39	61	0.0001	11944
POL	PVIGVYDPS	505	11	39	61		11945
POL	AGYVTRDGROK	647	11	39	61		11946
POL	AGYVTRDGROK	647	11	39	61		11947
POL	DIKSVTRERAK	1009	11	39	61		11948
POL	VTRDGROK	650	8	40	63		11949
POL	IIQAQPK	697	8	40	63	0.0065	11950
POL	GIIQAQPK	696	9	40	63		11951
POL	GIDKAQEEH	756	9	40	63	0.0400	11952
POL	NSDIKVVPR	1006	10	40	63		11953
POL	ILKEPVIGVY	498	10	40	63		11954
POL	NSDIKVVPR	1006	10	40	63		11955
POL	NSDIKVVPR	1007	10	40	63	0.0001	11956
POL	ELKEPVIGVY	497	11	40	63		11957
POL	WTYQYQEF	529	11	40	63	0.0540	11958
POL	QYQEPFNK	532	11	40	63	0.2500	11959
POL	QNSDIKVVPR	1005	11	40	63		11960
POL	QNSDIKVVPR	1006	11	40	63		11961
POL	QNSDIKVVPR	1006	11	40	63		11962

Table XVII
 HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
POL	NSDIKVPREK	1097	11	40	63		11963
POL	NSDIKVPREK	1098	11	41	65		11964
POL	QYQDEPK	532	8	41	64	0.0013	11965
POL	IDKAGEH	757	8	41	64		11966
POL	KAKIRDY	1017	8	41	64		11967
POL	KAKIRDYQK	1017	10	41	64	0.0018	11968
POL	KISKIGPENYK	235	11	41	64		11969
POL	KAGYVTDK	646	8	42	66		11970
POL	NSDIKVPREK	259	10	42	66		11971
POL	SAIKLEPR	351	10	42	66	0.0004	11972
POL	SVINGKTPK	571	10	42	66		11973
POL	IVIVQVMDLY	367	11	42	66		11974
POL	VVPRKAKIR	1012	11	42	66		11975
POL	GYVDPK	508	8	43	67		11976
POL	SCDKCQK	791	8	43	67		11977
POL	NSDIKVPREK	791	9	43	67		11978
POL	IGVYDPK	507	9	43	67	0.0160	11979
POL	ASDKCQK	790	9	43	67		11980
POL	DSWTVNDQK	439	10	43	67	0.0140	11981
POL	TFYVDGAAR	631	10	43	67	0.0002	11982
POL	VASDKCQK	789	10	43	67	0.0004	11983
POL	KDSWTVNDQ	438	11	43	67		11984
POL	NSDIKVPREK	788	11	43	67		11985
POL	IVASDKCQK	788	11	43	67		11986
POL	SDIKVVPK	1008	8	44	69	0.1000	11987
POL	SDIKVVPK	1008	9	44	69	0.0001	11988
POL	VDGAANRETK	634	10	44	69		11989
POL	IGQVRDQAEH	914	10	44	69		11990
POL	QVRDQAEHLK	916	10	44	69	0.0023	11991
POL	NSDIKVPREK	916	11	44	69	0.0001	11992
POL	INREILKEPVH	404	11	44	69		11993
POL	YVDGAANREI	633	11	44	69		11994
POL	IGQVRDQAEH	913	11	44	69		11995
POL	VAKENVASCOK	784	11	45	71		11996
POL	GAANRETK	636	8	45	70		11997
POL	IVASDKCQK	637	9	45	70		11998
POL	NSDIKVPREK	637	9	45	70		11999
POL	PKSNLKGK	537	10	45	70	0.0002	12000
POL	ELKLEPVH	613	11	45	70		12001
POL	KLWYQLEK	497	8	46	72		12002
POL	KLWYQLEK	616	8	46	72		12003
POL	RDQAEHLK	918	8	46	72		12004
POL	PRKLLTGK	537	9	46	72		12005
POL	NSDIKVPREK	537	9	46	72	0.0006	12006
POL	LKXLYQLEK	614	10	46	72		12007
POL	KVKQWPLTEE	207	11	46	72	0.0339	12008
POL	VIWGTKPK	573	8	48	75		12009
POL	QVRDQAEH	916	8	48	75		12010
POL	DIKVVPRK	1009	8	48	75		12011
POL	VIWGTKPK	572	9	48	75	0.3700	12012

Table XVII
HIV-1 H₁ Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	DIKVVPRKK	1009	9	48	75	0.0001	12013
POL	KVFLDGDK	750	10	48	75	0.7800	12014
POL	KCOLGEAMIL	794	10	48	75		12015
POL	GVVSMNKKL	902	11	48	75		12016
POL	GVVSMNKKL	901	11	48	75		12017
POL	GVVSMNKK	901	8	49	77		12018
POL	GVVSMNKK	900	9	49	77		12019
POL	GVVSMNKK	900	9	49	77		12020
POL	KLEKMDGPK	197	10	49	77	0.0760	12021
POL	KLEKMDGPK	197	10	49	77		12022
POL	GVVSMNKK	900	9	49	77		12023
POL	GVVSMNKK	900	9	49	77		12024
POL	GVVSMNKK	900	9	49	77		12025
POL	GVVSMNKK	900	9	49	77		12026
POL	GVVSMNKK	900	9	49	77		12027
POL	GVVSMNKK	900	9	49	77		12028
POL	GVVSMNKK	900	9	49	77		12029
POL	GVVSMNKK	900	9	49	77		12030
POL	GVVSMNKK	900	9	49	77		12031
POL	GVVSMNKK	900	9	49	77		12032
POL	GVVSMNKK	900	9	49	77		12033
POL	GVVSMNKK	900	9	49	77		12034
POL	GVVSMNKK	900	9	49	77		12035
POL	GVVSMNKK	900	9	49	77		12036
POL	GVVSMNKK	900	9	49	77		12037
POL	GVVSMNKK	900	9	49	77		12038
POL	GVVSMNKK	900	9	49	77		12039
POL	GVVSMNKK	900	9	49	77		12040
POL	GVVSMNKK	900	9	49	77		12041
POL	GVVSMNKK	900	9	49	77		12042
POL	GVVSMNKK	900	9	49	77		12043
POL	GVVSMNKK	900	9	49	77		12044
POL	GVVSMNKK	900	9	49	77		12045
POL	GVVSMNKK	900	9	49	77		12046
POL	GVVSMNKK	900	9	49	77		12047
POL	GVVSMNKK	900	9	49	77		12048
POL	GVVSMNKK	900	9	49	77		12049
POL	GVVSMNKK	900	9	49	77		12050
POL	GVVSMNKK	900	9	49	77		12051
POL	GVVSMNKK	900	9	49	77		12052
POL	GVVSMNKK	900	9	49	77		12053
POL	GVVSMNKK	900	9	49	77		12054
POL	GVVSMNKK	900	9	49	77		12055
POL	GVVSMNKK	900	9	49	77		12056
POL	GVVSMNKK	900	9	49	77		12057
POL	GVVSMNKK	900	9	49	77		12058
POL	GVVSMNKK	900	9	49	77		12059
POL	GVVSMNKK	900	9	49	77		12060
POL	GVVSMNKK	900	9	49	77		12061
POL	GVVSMNKK	900	9	49	77		12062

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
POL	GHIPAGLKK	282	11	51	84		12063
POL	GGFKVR	137	8	53	83		12064
POL	GFKVRQY	139	8	53	83		12065
POL	PIETVPK	192	8	53	83		12066
POL	ETVPKLLK	190	8	53	83	0.0001	12067
POL	ELAELENR	489	8	53	83		12068
POL	ELAELENH	490	8	53	83		12069
POL	SNKKELKS	904	8	53	83		12070
POL	GGFKVR	905	8	53	83		12071
POL	GGFKVRQY	136	9	53	83	0.0005	12072
POL	ESMNKELK	904	9	53	83	0.0001	12073
POL	GGGFKVRQY	135	10	53	83		12074
POL	GGGFKVRQY	135	10	53	83	0.0002	12075
POL	ISDETPVK	188	10	53	83	0.0002	12076
POL	PIETVPKLLK	190	10	53	83	0.0310	12077
POL	EAELELENR	487	10	53	83	0.0001	12078
POL	LVAIVIVASGY	826	10	53	83		12079
POL	GGGFKVRQY	136	10	53	83		12080
POL	PIETVPK	187	11	53	83		12081
POL	PIETVPK	187	11	53	83		12082
POL	LVAIVIVASGY	826	11	53	83		12083
POL	PIETVPKLLK	608	9	54	86	0.0660	12084
POL	GHIPAGLKK	282	10	54	86	0.1700	12085
POL	GHIPAGLKK	281	11	54	86		12086
POL	QNRVYVR	973	8	54	84		12087
POL	PIVNIIGR	166	9	54	84		12088
POL	LAENNELK	492	9	54	84	0.0001	12089
POL	LAENNELK	492	10	54	84	0.0003	12090
POL	LAENNELK	607	10	54	84		12091
POL	PLTEUK	212	8	55	86		12092
POL	LFEDGDK	752	8	55	86		12093
POL	GHIPAGLKK	282	9	56	89	0.0650	12094
POL	GHIPAGLKK	281	10	56	89	0.0150	12095
POL	QLGHIPAGLKK	280	11	56	89		12096
POL	ELKKHGVVR	275	10	56	88	0.0004	12097
POL	ELKKHGVVR	909	10	56	88		12098
POL	DFWEVLGPHI	275	11	56	88		12099
POL	SVTVLDGDA	294	11	56	88		12100
POL	KTAQVMVH	925	11	56	88		12101
POL	VNTPLVK	609	8	57	89		12102
POL	AIKKKDKTK	251	9	57	89	0.0066	12103
POL	AIKKKDKTK	251	9	57	89	0.0066	12104
POL	TTTDDKKHOK	404	9	57	89	0.0042	12105
POL	FAIKKKDKTK	250	10	57	89	0.0002	12106
POL	NTPPLVKLWY	610	10	57	89		12107
POL	AIKKKDKTKW	251	11	57	89	0.0002	12108
POL	VNTPLVKLW	609	11	57	89		12109
POL	MAVTHINKR	930	11	57	89		12110
POL	GGGFKVRQY	135	11	57	89		12111
POL	KSTKWRK	255	8	58	91		12112

Table XVII
HIV-1 Nucleotide Sequences with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
POL	EVQLGPIH	278	8	58	91		12113
POL	GNFQVDK	735	8	58	91		12114
POL	FIHFKRK	933	8	58	91		12115
POL	GGYSAGER	944	8	58	91		12116
POL	RYYVRSR	976	8	58	91		12117
POL	IGNEQVDR	734	9	58	91	0.0001	12118
POL	YHNRKRS	943	9	58	91	0.0003	12119
POL	IGYSAGER	943	9	58	91	0.0001	12120
POL	GGGNGFYDK	733	10	58	91	0.0001	12121
POL	PAETGQETAY	842	10	58	91		12122
POL	AVFHFNKRR	931	10	58	91	0.8500	12123
POL	GGGYSAGER	942	10	58	91	0.0001	12124
POL	SIKWRKLVDK	727	11	58	91		12125
POL	AKGNGFYDK	727	11	58	91		12126
POL	AVHNSGK	828	8	59	92		12127
POL	ETGQETAY	844	8	59	92		12128
POL	GIWQLDCTH	811	9	59	92		12129
POL	VAVHVASGY	827	9	59	92	0.0001	12130
POL	KGPAKLLWK	988	9	59	92	0.0007	12131
POL	ENNVITDSQY	684	10	59	92		12132
POL	GIWQLDCTH	811	10	59	92		12133
POL	TGQQLDCTH	926	10	59	92	0.0110	12134
POL	VGKLNWASDI	450	11	59	92		12135
POL	NFKRKGIGGY	936	11	59	92		12136
POL	QLDKCTHLEGR	814	10	60	95		12137
POL	DFRELNR	265	8	60	94	0.0003	12138
POL	VLDYGDAY	297	8	60	94		12139
POL	DFRELNR	264	8	60	94		12140
POL	VDFELNR	264	9	60	94		12141
POL	MGYELJPDK	419	9	60	94	0.0960	12142
POL	KLNWASQY	452	9	60	94	0.0006	12143
POL	AVQMAVFHII	927	9	60	94		12144
POL	MAYFIHNR	980	9	60	94	0.3000	12145
POL	VDFRELNR	263	10	60	94		12146
POL	QMAVFIHNR	929	10	60	94	0.0004	12147
POL	QMAVFIHNR	929	10	60	94	0.6400	12148
POL	MAYFIHNR	930	10	60	94	0.0083	12149
POL	KLVDRELNR	262	11	60	94		12150
POL	QMAVFIHNR	929	11	60	94		12151
POL	LNWASQY	453	8	61	95		12152
POL	NDQKLVRK	444	9	61	95		12153
POL	QMAVFIHNR	929	10	61	95		12154
POL	VNDQKLVRK	443	10	61	95		12155
POL	VNDQKLVRK	442	11	61	95	0.1700	12156
POL	VDFRELNR	264	8	62	97		12157
POL	WTYNDIQK	441	8	62	97	0.0001	12158
POL	DIQKLVRK	445	8	62	97		12159
POL	NVITDSQY	686	8	62	97		12160
POL	DIQKLVRK	445	8	62	97		12161
POL	AVTHFNK	931	8	62	97	0.0380	12162

Table XVII
HIV-1 Nucleotide Sequences with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Consensus (%)	A*101	SIQ ID NO.
POL	VFIINFKR	932	8	62	97		12163
POL	LVDFRLNK	263	9	62	97	0.0300	12164
POL	AVIINIKR	931	9	62	97		12165
POL	MIGGIGFK	133	10	62	97	1.8000	12166
POL	KLVPFRLNK	262	10	62	97	0.0550	12167
POL	KMGIGGFK	132	11	62	97	0.0900	12168
POL	NLPQGWK	336	8	62	97	0.7000	12169
POL	IGGIGGFK	134	9	63	100	0.0012	12170
POL	KLVPFRLNK	263	9	63	100	0.0172	12171
POL	GGGIGFK	135	8	63	98	0.0001	12172
POL	FLWANGYELI	416	9	64	100		12173
POL	PELWANGYELI	415	10	64	100		12174
REV	GTQTRKNR	37	9	01	50		12175
REV	TTQARRNR	37	9	01	50		12176
REV	GTQTRKNR	37	9	01	50		12177
REV	GTQTRKNR	37	10	01	50		12178
REV	GTQTRKNR	37	10	01	50		12179
REV	TTQARRNR	37	11	01	50		12180
REV	GTETGVGR	103	8	06	19		12181
REV	QGTETGVGR	102	9	06	19		12182
REV	LLKTVRLIK	12	9	10	16		12183
REV	GSDDIELLK	9	9	11	16		12184
REV	GSDDIELLK	9	9	11	17		12185
REV	GSDDIELLK	5	10	11	17		12186
REV	RSDDIELLK	4	11	11	17		12187
REV	PVPLQLPPIR	74	11	11	17		12188
REV	RARQRQR	50	8	12	19		12189
REV	DSDELLK	7	8	12	19		12190
REV	ILSTCLQR	63	8	12	19		12191
REV	SNPPSPHGR	27	11	12	19		12192
REV	AVRIKILY	17	9	13	20		12193
REV	QPLPLERLI	78	9	13	20		12194
REV	PSPEGTRQAR	31	10	13	20		12195
REV	RNRREWRER	43	10	13	20		12196
REV	PSPEGLI	31	11	13	20		12197
REV	PSPEGLI	76	11	13	20		12198
REV	GTQTRKNR	36	11	14	22		12199
REV	RARQROH	50	8	15	24		12200
REV	GTQTRKNR	36	9	15	23		12201
REV	GTQTRKNR	36	10	15	23		12202
REV	QAKNRNR	40	9	16	25		12203
REV	QAKNRNR	40	9	16	25		12204
REV	QAKNRNR	40	11	17	27		12205
REV	IKILYQSNPY	20	11	18	28		12206
REV	KNRREWRRA	43	10	19	30		12207
REV	KNRREWRRA	43	8	21	33		12208
REV	KNRREWRRA	43	10	23	36		12209
REV	KILYQSNPY	22	9	26	41		12210
REV	KILYQSNPY						12211
REV	KILYQSNPY						12212

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
REV	ILYQSNFY	23	8	27	42		12213
REV	EGTRQARRNR	35	8	27	42		12214
REV	EGTRQARRNR	35	10	27	42		12215
REV	EGTRQARRNR	36	9	27	42		12216
REV	GTRQARRNR	36	10	34	53		12217
REV	GTRQARRNR	36	11	34	53		12218
REV	GTRQARRNR	36	11	34	53		12219
REV	IVPLQLPTLLR	74	9	35	53		12220
REV	IVPLQLPTLLR	74	9	37	55		12221
REV	QARRNR	40	11	35	58		12222
REV	QARRNR	40	8	38	59		12223
REV	QARRNR	40	9	38	59		12224
REV	RNRNRNR	43	8	40	63		12225
TAT	PGGYPRK	104	8	01	50		12226
TAT	AGRGGYPR	102	9	01	50		12227
TAT	ETGSGQPCII	101	10	01	50		12228
TAT	KAGGGYPR	101	10	01	50		12229
TAT	AGPGGYPRK	102	10	01	50		12230
TAT	KAGPGGYPR	101	11	01	50		12231
TAT	GGYPRKGGSC	105	11	01	50		12232
TAT	ACTNCK	24	8	10	16		12233
TAT	ACTNCK	24	8	10	16		12234
TAT	CONCYCK	25	8	11	17		12235
TAT	YCKKCCFH	29	8	11	17		12236
TAT	YCKKCCFH	29	8	11	17		12237
TAT	VDRLPWW	4	9	11	17		12238
TAT	ACNCKYCK	24	9	11	17		12239
TAT	VDRLPWW	3	10	11	17		12240
TAT	VDRLPWW	4	10	11	17		12241
TAT	TACNCKYCK	23	10	11	17		12242
TAT	VDRLPWW	3	11	11	17		12243
TAT	RGDPTGPKES	84	11	11	17		12244
TAT	GDPTGPKES	85	11	11	17		12245
TAT	ESKAKVESK	93	9	11	19		12246
TAT	GDPTGPKES	85	10	12	19		12247
TAT	TPKSKSK	88	10	12	19		12248
TAT	TPKSKSK	89	12	12	19		12249
TAT	LNKGLGISY	42	9	13	20		12250
TAT	LNKGLGISY	41	14	14	22		12251
TAT	PVDNLEPN	3	11	14	22		12252
TAT	PVDNLEPN	40	11	14	22		12253
TAT	LNKGLGISY	42	11	14	22		12254
TAT	LNKGLGISY	42	11	14	22		12255
TAT	LNKGLGISY	44	9	15	23		12256
TAT	RGDPTGPK	84	8	16	25		12257
TAT	VDNLEPNWH	4	10	16	25		12258
TAT	PNLEPNWH	9	8	17	27		12259
TAT	ACNCKYCK	24	8	17	27		12260
TAT	TACNCKYCK	23	9	17	27		12261
TAT	PTGPKESKK	88	9	18	28		12262

0.0001

Table XVII
HIV-1 H₁ Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
TAT	TGPKESKK	89	8	10	30		12353
TAT	PTGPKESK	88	8	20	31		12364
TAT	YGRKKRRQR	50	11	22	34		12365
TAT	YGRKKRRQR	50	10	38	59		12366
TAT	ISYGRKKRRQR	48	11	39	61		12367
TAT	YGRKKRRQR	50	9	41	64		12368
TAT	YGRKKRRQR	50	10	45	65	0.0001	12369
TAT	LGISYGRKKRR	46	11	45	70		12370
TAT	ISYGRKKRR	48	9	46	72	0.0005	12371
TAT	GLGISYGRKKRR	45	11	54	86		12372
TAT	GLGISYGR	45	8	55	87		12373
TAT	GLGISYGRK	45	9	55	87	0.0006	12374
TAT	GLGISYGRK	45	10	55	87		12375
TAT	YGRKKRR	48	9	55	87	0.0180	12376
TAT	KGLGISYGRK	44	10	55	86	0.0007	12377
TAT	KGLGISYGRKK	44	11	55	86		12378
TAT	GISYGRKKRR	47	9	57	89	0.0005	12379
TAT	GISYGRKKRR	46	10	57	89		12380
TAT	GISYGRKK	46	8	58	91		12381
TAT	GISYGRKK	46	8	58	91		12382
TAT	ISYGRKKRR	48	9	58	91	0.0005	12383
TAT	LGISYGRKK	46	9	58	91		12384
VIF	LIVWQVDR	8	8	10	16		12385
VIF	RMRENTWK	15	8	10	16		12386
VIF	KRPKKRR	158	8	10	16		12387
VIF	KRPKKRR	158	9	10	16		12388
VIF	ALPKPKKK	157	9	10	16		12389
VIF	VDRRENTWK	13	10	10	16		12390
VIF	GVSEWLLRR	87	10	10	16		12391
VIF	QVDRMRINTW	12	11	10	16		12392
VIF	RLVHTYWG	65	11	10	16		12393
VIF	GVSEWLLRR	87	11	10	16		12394
VIF	GVSEWLLRR	87	11	10	16		12395
VIF	IDPLADQLIH	103	11	10	16		12396
VIF	LVEDRWKPKQ	178	11	10	16		12397
VIF	SEWLLRR	89	8	11	17		12398
VIF	TALIKPKK	156	8	11	17		12399
VIF	SEWLLRR	89	8	11	17		12400
VIF	SEWLLRR	88	9	11	17		12401
VIF	SEWLLRR	89	9	11	17		12402
VIF	LTALIKPKK	155	11	11	17		12403
VIF	KLVEDRWK	177	9	11	17		12404
VIF	VSIEWLLRR	88	10	11	17		12405
VIF	GLADQLHMH	156	10	11	17		12406
VIF	GLADQLHMH	156	10	11	17		12407
VIF	WNPQKTRGII	183	10	11	17		12408
VIF	PGLADQLHMH	105	11	11	17		12409
VIF	GLADQLHMH	106	11	11	17		12410
VIF	LALALIKPKK	153	11	11	17		12411
VIF	WNPQKTRGII	183	11	11	17		12412

Table XVII
HIV-1 Nucleocapsid Protein Peptide Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
VIF	WFRHIVYSR	38	11	12	19		12313
VIF	KGNFYRHH	36	8	12	19		12314
VIF	WGLQTGER	72	8	12	19		12315
VIF	WGLQTGER	72	8	12	19		12316
VIF	WVQVDMRK	9	9	12	19		12317
VIF	KRTWNSLVK	17	10	12	19		12318
VIF	LVRKHIMYSK	24	10	12	19		12319
VIF	GLQTGERDWH	73	10	12	19		12320
VIF	IGHRDWILGH	77	10	12	19		12321
VIF	IGHRDWILGH	77	10	12	19		12322
VIF	WVQVDMRK	9	9	12	19		12323
VIF	KRTWNSLVK	17	11	12	19		12324
VIF	SLVKHIMYS	23	11	12	19		12325
VIF	LVRKHIMYSK	24	11	12	19		12326
VIF	WGLQTGERD	72	11	12	19		12327
VIF	WFRHIVYSR	38	10	13	21		12328
VIF	WGLQTGERD	72	10	13	21		12329
VIF	WGLQTGERD	72	8	13	20		12330
VIF	WGLQTGERD	72	8	13	20		12331
VIF	ADQLIMHI	108	8	13	20		12332
VIF	CFSDSAR	119	8	13	20		12333
VIF	CFSDSAR	120	8	13	20		12334
VIF	SLQYLAK	149	8	13	20		12335
VIF	SLQYLAK	149	8	13	20		12336
VIF	ADQLIMHI	107	9	13	20		12337
VIF	ADQLIMHI	108	9	13	20		12338
VIF	CFSDSAR	119	9	13	20		12339
VIF	OSLOYLAK	148	9	13	20		12340
VIF	ALALJKPK	154	9	13	20		12341
VIF	ADQLIMHI	107	10	13	20		12342
VIF	EVIMIDGAR	54	10	13	20		12343
VIF	ADQLIMHI	107	10	13	20		12344
VIF	DCFSAR	118	10	13	20		12345
VIF	WGLQYLAK	147	10	13	20		12346
VIF	ALALJKPK	153	10	13	20		12347
VIF	ADQLIMHI	107	11	13	20		12348
VIF	DCFSAR	117	11	13	20		12349
VIF	YALALJKPK	152	11	13	20		12350
VIF	CFSDSAR	120	8	14	22		12351
VIF	INSPREY	133	8	14	22		12352
VIF	GVSEWRLR	87	9	14	22		12353
VIF	GVSEWRLR	87	9	14	22		12354
VIF	CFSDSAR	118	9	14	22		12355
VIF	VDRMRRTWK	13	10	14	22		12356
VIF	LADQLHLY	107	10	14	22		12357
VIF	RCDYQAGINK	137	10	14	22		12358
VIF	QVDRMRRTWK	12	11	14	22		12359
VIF	KRTWNSLVK	17	11	14	22		12360
VIF	RTWNSLVK	15	8	15	23		12361
VIF	RTWNSLVK	19	8	15	23		12362
VIF	VSEWRLR	88	8	15	23		12363

Table XVII
 HIV-1 Malt Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
VIF	ADQLILY	108	8	15	23		12363
VIF	RTWKSIVKH	19	9	15	23		12364
VIF	QGVSEWRK	86	9	15	23		12365
VIF	LADQLILY	107	9	15	23		12366
VIF	AIRKALGH	124	9	15	23		12367
VIF	EDYQAGH	108	9	15	23		12368
VIF	RTWKSIVKH	17	10	15	23		12369
VIF	RTWNSLVK	17	10	15	23		12370
VIF	RTWKSIVKH	19	10	15	23		12371
VIF	SAIRKALGH	123	10	15	23		12372
VIF	RTWKSIVKH	17	11	15	23		12373
VIF	LGQGVSEWR	84	11	15	23		12374
VIF	VDGLADQLH	103	11	15	23		12375
VIF	RTWNSLVK	17	8	16	25		12376
VIF	GVSIEWRK	87	8	16	25		12377
VIF	RTWYQAGH	137	8	16	25		12378
VIF	LALTALIK	153	8	16	25		12379
VIF	VITTYWGLH	67	9	16	25		12380
VIF	YLALTALIK	152	9	16	25		12381
VIF	KTKHGHOSH	108	9	16	25		12382
VIF	WNSLVKIH	108	10	16	25		12383
VIF	WNSLVKIH	183	10	16	25		12384
VIF	WNSLVKIH	183	11	16	25		12385
VIF	EDRWKTPQKT	180	11	17	27		12386
VIF	WNSLVKIH	183	8	18	28		12387
VIF	WNSLVKIH	183	8	18	28		12388
VIF	EDRWKTPQKT	180	9	18	28		12389
VIF	EDRWKTPQKT	137	10	19	30		12390
VIF	EDRWKTPQKT	137	10	20	31		12391
VIF	HPLGEAR	56	8	20	31		12392
VIF	WNSLVKIH	183	8	20	31		12393
VIF	EVHPLGEAR	54	10	20	31		12394
VIF	ITGERDWH	106	8	21	33		12395
VIF	DLADQLH	106	8	21	33		12396
VIF	WNSLVKIH	183	11	21	33		12397
VIF	WNSLVKIH	183	11	21	33		12398
VIF	WNSLVKIH	183	11	21	33		12399
VIF	VSPKCEVQAG	134	11	21	33		12400
VIF	LTEDRWKTPQ	178	11	21	33		12401
VIF	GSITMNGH	194	8	22	34		12402
VIF	RGSIITMNGH	193	9	22	34		12403
VIF	WNSLVKIH	183	11	22	34		12404
VIF	WNSLVKIH	183	11	22	34		12405
VIF	WNSLVKIH	22	9	24	38		12406
VIF	WNSLVKIH	21	10	24	38		12407
VIF	QGVSEWR	86	8	25	39		12408
VIF	LGQGVSEWR	84	10	25	39		12409
VIF	HLGGQVSEWR	83	11	25	39		12410
VIF	RCEVQAGH	137	8	26	41		12411
VIF	RTWNSLVKIH	19	9	26	41		12412
VIF	RTWNSLVKIH	19	10	26	41		12413

Table XVII
 HIV-1 C-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
VIF	RTVNSLVK	19	8	27	42		12413
VIF	HGVSEWR	86	8	27	42		12414
VIF	GLADQLH	106	8	27	42		12415
VIF	PGLADQLH	105	9	27	42		12416
VIF	LHGVSEWR	84	10	27	42		12417
VIF	WGLTGER	116	11	28	44		12418
VIF	WGLTGER	72	8	28	44		12419
VIF	DCFESAIR	118	9	28	44		12420
VIF	FDCTESAIR	117	10	28	44		12421
VIF	WNSLVKIH	21	8	29	45		12422
VIF	CFESAIR	119	8	29	45		12423
VIF	KLIEDRWK	177	9	29	45	0.2700	12424
VIF	WNSLVKIH	176	9	29	45	0.0045	12425
VIF	WNSLVKIH	177	9	33	52		12426
VIF	WNSLVKIH	178	9	33	52		12427
VIF	QVDMRIR	12	8	34	53		12428
VIF	EDRWKPKK	180	9	39	61		12429
VIF	VMVWQVDR	7	11	41	64		12430
VIF	QVMVWQVDR	6	10	43	67		12431
VIF	VMVWQVDR	182	10	43	67	0.0001	12432
VIF	WNSLVKIH	181	10	44	69		12433
VIF	SLVHIMY	23	9	44	69		12434
VIF	VMVWQVDR	7	9	44	69	0.0320	12435
VIF	VMVWQVDR	8	9	46	72		12436
VIF	VMVWQVDR	9	9	47	73	0.0007	12437
VIF	INKVGSQY	144	9	47	73		12438
VPR	ALPQRGR	83	9	51	80		12439
VPR	WNSLVKIH	181	10	50	80		12440
VPR	WALELELK	18	10	09	15		12441
VPR	QLLEVIER	66	8	10	16		12442
VPR	ISRGIRH	79	8	10	16		12443
VPR	RIGTRQR	81	8	10	16		12444
VPR	IGTRQR	82	8	10	16		12445
VPR	ALLELELK	9	8	10	16		12446
VPR	ISRGIRH	81	9	10	16		12447
VPR	ISRGIRH	79	10	10	16		12448
VPR	HSRIGTRQR	79	11	10	16		12449
VPR	WLIIGLQY	38	8	11	17		12450
VPR	HFRCGRH	71	8	11	17		12451
VPR	HSRIGTR	79	9	11	17		12452
VPR	HFRCGRH	68	10	11	17		12453
VPR	FVHFRGCH	69	10	11	17		12454
VPR	FVHFRGCH	69	10	11	17		12455
VPR	IFRFGCRISR	71	10	11	17		12456
VPR	LLFIHFRGCR	67	11	11	17		12457
VPR	LFHFRGCRH	68	11	11	17		12458
VPR	LFVHFRGCRH	68	11	11	17		12459
VPR	LFVHFRGCRH	68	12	12	19		12460
VPR	LGQVINY	9	8	13	20		12461
VPR	LGQVINY	42	9	13	20		12462

HIV-1 All Motif Peptides with Binding Information
Table XVII

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO
VPR	HPREWLII	33	8	14	22		12463
VPR	KSEAVRIIFPR	27	10	14	22		12464
VPR	AVRIIFRIWL	30	11	14	22		12465
VPR	ELKSEAVR	25	8	16	25		12466
VPR	AGVEAIR	55	8	16	25		12467
VPR	ELKSEAVRII	25	9	16	25		12468
VPR	ELKSEAVR	24	9	16	25		12469
VPR	ELKSEAVR	22	9	16	25		12470
VPR	ELKSEAVR	52	11	16	25		12471
VPR	ELKSEAVR	25	8	17	27		12472
VPR	ELKSEAVR	25	9	17	27		12473
VPR	ELKSEAVR	42	9	17	27		12474
VPR	ELKSEAVR	22	11	17	27		12475
VPR	ELKSEAVR	52	8	18	28		12476
VPR	ELKSEAVR	52	11	18	28		12477
VPR	ELKSEAVR	52	8	18	28		12478
VPR	ELKSEAVR	95	8	19	30		12479
VPR	ELKSEAVR	27	10	19	30		12480
VPR	ELKSEAVR	27	10	19	30		12481
VPR	ELKSEAVR	38	8	20	31		12482
VPR	ELKSEAVR	38	8	20	31		12483
VPR	ELKSEAVR	38	8	20	31		12484
VPR	ELKSEAVR	69	10	30	47		12485
VPR	ELKSEAVR	33	8	31	49		12486
VPR	ELKSEAVR	30	11	31	48		12487
VPR	ELKSEAVR	63	11	35	55		12488
VPR	ELKSEAVR	62	10	36	58		12489
VPR	ELKSEAVR	63	10	37	58		12490
VPR	ELKSEAVR	3	10	39	62		12491
VPR	ELKSEAVR	18	10	42	69		12492
VPR	ELKSEAVR	8	8	43	68		12493
VPR	ELKSEAVR	66	8	44	69		12494
VPR	ELKSEAVR	71	8	44	69		12495
VPR	ELKSEAVR	71	8	44	69		12496
VPR	ELKSEAVR	74	10	44	69		12497
VPR	ELKSEAVR	74	10	44	69		12498
VPR	ELKSEAVR	29	8	47	73		12499
VPR	ELKSEAVR	43	8	51	92		12500
VPR	ELKSEAVR	94	8	51	90		12501
VPR	ELKSEAVR	43	9	51	90		12502
VPR	ELKSEAVR	11	11	51	90		12503
VPR	ELKSEAVR	64	11	51	90		12504
VPR	ELKSEAVR	64	11	51	90		12505
VPR	ELKSEAVR	34	9	10	16		12506
VPR	ELKSEAVR	35	8	10	16		12507
VPR	ELKSEAVR	54	9	10	16		12508
VPR	ELKSEAVR	56	9	10	16		12509
VPR	ELKSEAVR	32	11	10	16		12510
VPR	ELKSEAVR	31	11	10	16		12511
VPR	ELKSEAVR	34	8	12	19		12512

Table XVII
HIV-1 Modf Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*101	SEQ ID NO.
VP1	WPEYRK	36	8	12	19		12513
VP1	WVTVVEY	34	10	12	19		12514
VP1	WVTVVEY	30	11	12	19		12515
VP1	WVTVVEY	30	8	14	22		12516
VP1	LDRRLR	58	8	15	23		12517
VP1	KIDRLDR	52	9	15	23		12518
VP1	ILRQRKIDR	46	10	15	23	0.0001	12519
VP1	KILRQRKIDR	45	10	15	23		12519

Table XVIII
HIV-A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	IMLQITW	650	8	10	16		12520
ENV	WFDINWL	767	8	10	16		12521
ENV	WFDINWL	767	8	10	16		12522
ENV	IXYCTAGAI	262	10	10	16		12523
ENV	IXYCTAGAI	717	10	10	16		12524
ENV	WFDINWAE	767	10	10	16		12525
ENV	WFDINWAE	767	11	10	16		12526
ENV	SYIIRLDLLI	864	11	10	16		12527
ENV	HYCTAGF	262	8	11	17		12528
ENV	HYCTAGF	717	8	11	17		12529
ENV	FYALDHGDI	367	9	12	19		12530
ENV	FYALDHGDI	723	9	12	19		12531
ENV	WMEWERI	896	8	12	19		12532
ENV	WMEWERI	896	8	12	19		12533
ENV	WMEWERI	722	9	12	19		12534
ENV	SYIIRLDLLI	864	10	12	19		12535
ENV	SYIIRLDLLI	864	11	12	19		12536
ENV	WYQELKNSA	909	11	12	19		12537
ENV	LYKYAVFI	561	11	13	20		12538
ENV	LYKYAVFI	864	9	13	20		12539
ENV	SYIIRLDIF	864	10	13	20		12540
ENV	WYHSCGGE	432	11	13	20		12541
ENV	WYHSCGGE	862	11	13	20		12542
ENV	LESYIRLDLL	862	11	14	22		12543
ENV	SYIIRLDLL	864	9	14	22		12544
ENV	KYWNLLQY	901	10	14	22		12545
ENV	WYNNLLQY	903	8	15	23		12546
ENV	WYNNLLQY	902	9	15	23		12547
ENV	WYNNLLQY	900	11	15	23		12548
ENV	WYNNLLQY	900	11	15	23		12549
ENV	SPNCGE	437	9	16	25		12550
ENV	SPNCGE	772	9	16	25		12551
ENV	KWLWYKIF	772	10	16	25		12552
ENV	KWLWYKIF	772	10	16	25		12553
ENV	KWLWYKIF	772	10	16	25		12554
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ENV	KWLWYKIF	772	10	16	25		12577
ENV	KWLWYKIF	772	10	16	25		12578
ENV	KWLWYKIF	772	10	16	25		12579
ENV	KWLWYKIF	772	10	16	25		12580
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ENV	KWLWYKIF	772	10	16	25		12583
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ENV	KWLWYKIF	772	10	16	25		12585
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ENV	KWLWYKIF	772	10	16	25		12591
ENV	KWLWYKIF	772	10	16	25		12592
ENV	KWLWYKIF	772	10	16	25		12593
ENV	KWLWYKIF	772	10	16	25		12594
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ENV	KWLWYKIF	772	10	16	25		12603
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ENV	KWLWYKIF	772	10	16	25		12606
ENV	KWLWYKIF	772	10	16	25		12607
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ENV	KWLWYKIF	772	10	16	25		12651
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ENV	KWLWYKIF	772	10	16	25		12661
ENV	KWLWYKIF	772	10	16	25		12662
ENV	KWLWYKIF	772	10	16	25		12663
ENV	KWLWYKIF	772	10	16	25		12664
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ENV	KWLWYKIF	772	10	16	25		12667
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ENV	KWLWYKIF	772	10	16	25		12673
ENV	KWLWYKIF	772	10	16	25		12674
ENV	KWLWYKIF	772	10	16	25		12675
ENV	KWLWYKIF	772	10	16	25		12676
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ENV	KWLWYKIF	772	10	16	25		12680
ENV	KWLWYKIF	772	10	16	25		12681
ENV	KWLWYKIF	772	10	16	25		12682
ENV	KWLWYKIF	772	10	16	25		12683
ENV	KWLWYKIF	772	10	16	25		12684
ENV	KWLWYKIF	772	10	16	25		12685
ENV	KWLWYKIF	772	10	16	25		12686
ENV	KWLWYKIF	772	10	16	25		12687
ENV	KWLWYKIF	772	10	16	25		12688
ENV	KWLWYKIF	772	10	16	25		12689
ENV	KWLWYKIF	772	10	16	25		12690
ENV	KWLWYKIF	772	10	16	25		12691
ENV	KWLWYKIF	772	10	16	25		12692
ENV	KWLWYKIF	772	10	16	25		12693
ENV	KWLWYKIF	772	10	16	25		12694
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ENV	KWLWYKIF	772	10	16	25		12697
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ENV	KWLWYKIF	772	10	16	25		12699
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ENV	KWLWYKIF	772	10	16	25		12701
ENV	KWLWYKIF	772	10	16	25		12702
ENV	KWLWYKIF	772	10	16	25		12703
ENV	KWLWYKIF	772	10	16	25		12704
ENV	KWLWYKIF	772	10	16	25		12705
ENV	KWLWYKIF	772	10	16	25		12706
ENV	KWLWYKIF	772	10	16	25		12707
ENV	KWLWYKIF	772	10	16	25		12708
ENV	KWLWYKIF	772	10	16	25		12709
ENV	KWLWYKIF	772	10	16	25		127

Table XVIII
HIV-A24 Peptide Sequences with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
ENV	VWKEATITL	55	9	22	34		12570
ENV	VWKEATITLF	55	10	22	34		12571
ENV	VWKEATITL	862	10	22	34	0.0300	12572
ENV	VWKEATITL	862	10	22	34	0.2700	12573
ENV	NWLWKYKI	772	8	25	39		12574
ENV	NWLWKYKIF	772	9	25	39		12575
ENV	KYKVVYKIF	563	10	25	39		12576
ENV	NWLWKYKIF	772	10	25	39		12577
ENV	GFLAWDDIL	848	10	25	39		12578
ENV	QVWYKQGLI	772	11	25	39		12579
ENV	KWASLWNV	760	8	26	41		12580
ENV	KWASLWNVF	760	9	26	41		12581
ENV	IYCAPAGF	262	8	27	42		12582
ENV	IYCAPAGFAI	262	10	27	42		12583
ENV	IYCAPAGFAIL	262	11	27	42		12584
ENV	QVWYKQGLI	772	10	25	39		12585
ENV	QVWYKQGLI	772	9	25	39	0.0200	12586
ENV	RYLKDQQL	671	9	29	45	0.7000	12587
ENV	QMIHEDISLW	116	10	29	45		12588
ENV	GYSPLSFQTL	806	10	29	45		12589
ENV	RYLKDQQL	671	8	30	47		12590
ENV	QVWYKQGLI	772	10	25	39		12591
ENV	QVWYKQGLI	772	10	25	39		12592
ENV	QVWYKQGLI	772	8	35	56		12593
ENV	QVWYKQGLI	772	9	35	55		12594
ENV	SPNCCGEFF	437	8	36	56		12595
ENV	DMRDVWRSFL	552	10	37	58		12596
ENV	TMGAASTL	615	10	37	58		12597
ENV	QVWYKQGLI	772	9	37	61		12598
ENV	QVWYKQGLI	772	9	37	61		12599
ENV	QVWYKQGLI	772	10	43	67		12600
ENV	QVWYKQGLI	772	8	48	75		12601
ENV	QVWYKQGLI	681	9	48	75		12602
ENV	QVWYKQGLI	772	8	49	77		12603
ENV	QVWYKQGLI	772	8	49	77		12604
GAG	LYPLASLKS	544	10	10	17		12605
GAG	LYPLASLKS	544	11	10	17		12606
GAG	KYKLVHIV	29	9	10	16		12607
GAG	GWMTSNPI	269	9	10	16		12608
GAG	IMWQSNF	408	8	11	17		12609
GAG	QVWYKQGLI	772	8	13	20		12610
GAG	QVWYKQGLI	772	10	13	20		12611
GAG	QVWYKQGLI	772	11	13	20		12612
GAG	QVWYKQGLI	772	8	14	22		12613
GAG	QVWYKQGLI	300	8	14	22		12614
GAG	QVWYKQGLI	299	9	14	22		12615
GAG	QVWYKQGLI	45	8	16	25		12616
GAG	QVWYKQGLI	270	8	16	25		12617
GAG	QVWYKQGLI	270	8	16	25		12618
GAG	QVWYKQGLI	339	8	16	25		12619

Table XVIII
HIV-2 gp120 gp120 peptides with binding information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
GAG	KYRLKILVW	29	9	16	25		12620
GAG	BEAVNGRL	45	8	16	25		12621
GAG	LYCVIQR	87	8	18	28	0.0100	12622
GAG	GWATNNPPI	269	8	18	28	0.0140	12623
GAG	RFALNIGL	45	8	20	31		12624
GAG	WATNNPPI	270	8	20	31		12625
GAG	RFALNIGL	270	8	20	31		12626
GAG	WATNNPPI	270	8	20	31		12627
GAG	AWKVEEKA	80	8	22	34		12628
GAG	AWKVEEKA	175	11	24	38		12629
GAG	AMOMLKEH	218	9	26	41		12630
GAG	IMMORGNF	408	8	27	42		12631
GAG	DYVDYDFKL	319	10	27	42		12632
GAG	CFNCKRGHII	425	10	27	42		12633
GAG	CFNCKRGHII	425	10	27	42		12634
GAG	AWKVEEKA	319	10	28	44	0.0010	12635
GAG	AWKVEEKA	175	11	28	44		12636
GAG	NYPIVQNI	152	8	31	48		12637
GAG	AMOMLKDTI	218	9	33	52		12638
GAG	PERDYDFRF	316	10	35	55		12639
GAG	NWMTETLL	339	8	38	59		12640
GAG	RYSPVSLDI	299	8	38	59		12641
GAG	RYSPVSLDI	299	8	40	63		12642
GAG	MYSPVSLDI	300	10	40	63		12643
GAG	MYSPVSLI	300	8	42	66		12644
GAG	QWREPRGSDI	248	10	44	70		12645
GAG	VWASRELERF	136	10	45	70		12646
GAG	ASPEVPMF	134	8	50	78	0.0078	12647
GAG	RYERWILGL	285	8	54	84	0.0140	12648
GAG	RYERWILGL	285	10	54	84		12649
GAG	RAVILGLNKI	288	10	56	88		12650
GAG	PRDYVDRE	316	8	63	98		12651
NEF	PMYKGF	105	8	12	19		12652
NEF	TYKGFADL	107	8	12	19		12653
NEF	TYKGFADL	107	10	12	19		12654
NEF	WVYVTEGF	192	8	13	20		12655
NEF	WVYVTEGF	192	9	13	20		12656
NEF	LWVYHTQGF	190	10	13	20		12657
NEF	NYTRGIRF	206	10	13	20		12658
NEF	VYHTQGFHD	192	11	13	20		12659
NEF	RPLTGWCF	216	9	18	27		12660
NEF	RYSKRGEL	175	9	18	29		12661
NEF	RYSKRGEL	175	10	18	29		12662
NEF	ADLSFEL	111	8	18	28		12663
NEF	DWQNYTGRG	203	11	18	28		12664
NEF	RPLTGW	216	8	20	32		12665
NEF	NYTRGRI	206	8	20	31		12666
NEF	KWSKSSNGW	4	10	20	31		12667
NEF	KYLITGWCF	216	10	21	33		12668
NEF	VYHTQGTG	192	8	21	33		12669

Table XVIII
IIIc. A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
NEF	LWVHTGGV ¹	180	10	21	33		12670
NEF	SLHGGKGD	192	10	21	33		12671
NEF	SFLKGGEL	115	10	22	34		12672
NEF	FLKKGGL	116	9	26	41		12673
NEF	RYPLTGW	216	8	27	43		12674
NEF	HLKKGGL	116	8	29	45		12675
NEF	TGWCFKL	222	8	48	75		12676
NEF	GIYRQVPL	7	10	10	16		12678
NEF	WVQVQVPL	7	10	10	16		12679
POL	NMLTGLGL	175	10	10	16		12680
POL	TWETWTDY	589	10	10	16		12681
POL	TWTDYWQA	592	11	10	16		12682
POL	CWAGIQEFL	882	10	11	17		12683
POL	WVQVQVPL	574	8	11	17		12684
POL	WVQVQVPL	574	8	11	17		12685
POL	WVQVQVPL	574	8	11	17		12686
POL	WVQVQVPL	574	8	11	17		12687
POL	WVQVQVPL	574	8	11	17		12688
POL	WVQVQVPL	574	8	11	17		12689
POL	WVQVQVPL	574	8	11	17		12690
POL	WVQVQVPL	574	8	11	17		12691
POL	WVQVQVPL	574	8	11	17		12692
POL	WVQVQVPL	574	8	11	17		12693
POL	WVQVQVPL	574	8	11	17		12694
POL	WVQVQVPL	574	8	11	17		12695
POL	WVQVQVPL	574	8	11	17		12696
POL	WVQVQVPL	574	8	11	17		12697
POL	WVQVQVPL	574	8	11	17		12698
POL	WVQVQVPL	574	8	11	17		12699
POL	WVQVQVPL	574	8	11	17		12700
POL	WVQVQVPL	574	8	11	17		12701
POL	WVQVQVPL	574	8	11	17		12702
POL	WVQVQVPL	574	8	11	17		12703
POL	WVQVQVPL	574	8	11	17		12704
POL	WVQVQVPL	574	8	11	17		12705
POL	WVQVQVPL	574	8	11	17		12706
POL	WVQVQVPL	574	8	11	17		12707
POL	WVQVQVPL	574	8	11	17		12708
POL	WVQVQVPL	574	8	11	17		12709
POL	WVQVQVPL	574	8	11	17		12710
POL	WVQVQVPL	574	8	11	17		12711
POL	WVQVQVPL	574	8	11	17		12712
POL	WVQVQVPL	574	8	11	17		12713
POL	WVQVQVPL	574	8	11	17		12714
POL	WVQVQVPL	574	8	11	17		12715
POL	WVQVQVPL	574	8	11	17		12716
POL	WVQVQVPL	574	8	11	17		12717
POL	WVQVQVPL	574	8	11	17		12718
POL	WVQVQVPL	574	8	11	17		12719

Table XVIII
 HIV-1 A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	DYQWATVI	596	8	20	31		12720
POL	KFLPQKEITW	580	11	20	31		12721
POL	CWAGIKQKEF	882	10	21	33		12722
POL	YVQVQVQV	882	9	21	33	0.0190	12723
POL	WWAGIKQKEF	883	9	21	33	0.0120	12724
POL	WWAGIKQKEF	883	11	21	33		12725
POL	NFTQTLW	86	8	22	34		12726
POL	AWYPAIKGI	726	9	22	34		12727
POL	SPQTLW	86	8	23	36		12728
POL	WYQVQVQV	593	10	23	36		12729
POL	WYQVQVQV	593	11	23	36		12730
POL	WYQVQVQV	593	11	23	36		12731
POL	WYQVQVQV	593	11	23	36		12732
POL	WYQVQVQV	593	11	23	36		12733
POL	WYQVQVQV	593	11	23	36		12734
POL	WYQVQVQV	593	11	23	36		12735
POL	WYQVQVQV	593	11	23	36		12736
POL	WYQVQVQV	593	11	23	36		12737
POL	WYQVQVQV	593	11	23	36		12738
POL	WYQVQVQV	593	11	23	36		12739
POL	WYQVQVQV	593	11	23	36		12740
POL	WYQVQVQV	593	11	23	36		12741
POL	WYQVQVQV	593	11	23	36		12742
POL	WYQVQVQV	593	11	23	36		12743
POL	WYQVQVQV	593	11	23	36		12744
POL	WYQVQVQV	593	11	23	36		12745
POL	WYQVQVQV	593	11	23	36		12746
POL	WYQVQVQV	593	11	23	36		12747
POL	WYQVQVQV	593	11	23	36		12748
POL	WYQVQVQV	593	11	23	36		12749
POL	WYQVQVQV	593	11	23	36		12750
POL	WYQVQVQV	593	11	23	36		12751
POL	WYQVQVQV	593	11	23	36		12752
POL	WYQVQVQV	593	11	23	36		12753
POL	WYQVQVQV	593	11	23	36		12754
POL	WYQVQVQV	593	11	23	36		12755
POL	WYQVQVQV	593	11	23	36		12756
POL	WYQVQVQV	593	11	23	36		12757
POL	WYQVQVQV	593	11	23	36		12758
POL	WYQVQVQV	593	11	23	36		12759
POL	WYQVQVQV	593	11	23	36		12760
POL	WYQVQVQV	593	11	23	36		12761
POL	WYQVQVQV	593	11	23	36		12762
POL	WYQVQVQV	593	11	23	36		12763
POL	WYQVQVQV	593	11	23	36		12764
POL	WYQVQVQV	593	11	23	36		12765
POL	WYQVQVQV	593	11	23	36		12766
POL	WYQVQVQV	593	11	23	36		12767
POL	WYQVQVQV	593	11	23	36		12768
POL	WYQVQVQV	593	11	23	36		12769

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	TYVQVQRF	530	9	42	66	0.3000	12770
POL	KMKPGGGI	120	10	42	66		12771
POL	DFKRYTAFTI	312	10	42	66		12772
POL	QNTYQVQEP	528	11	42	66		12773
POL	YYDPSKDL	510	8	43	67	0.0110	12774
POL	SMTKILEFF	352	9	43	67	0.0016	12775
POL	NWAKMAHSDF	770	9	43	67		12776
POL	YKQKQKQK	548	8	43	67		12777
POL	INGKIPKE	574	8	48	75		12778
POL	EWEFVNTPL	605	10	50	78		12779
POL	GMDGRVKQ	201	10	51	80		12780
POL	TWIPEWEF	601	8	52	81	0.0660	12781
POL	YWGATWIPE	597	10	52	81		12782
POL	SNKLLKTI	905	9	53	81		12783
POL	SNKLLKTI	905	9	53	81		12784
POL	EFVNTPL	607	8	54	84		12785
POL	GYHAELVI	834	8	54	84		12786
POL	SWTVNDIQKL	440	10	54	84		12787
POL	EFVNTPLVKL	607	11	54	84		12788
POL	QWPLITEKI	210	9	56	88		12789
POL	QWPLITEKI	210	9	56	88		12790
POL	FWELQGLI	275	8	57	89		12791
POL	FWELQGLI	275	8	57	89		12792
POL	GYSAGIERI	945	8	57	89		12793
POL	LYVGSQLEI	376	9	58	91		12794
POL	KWKRLVDF	259	8	59	92		12795
POL	GWKGSPIAI	341	8	59	92		12796
POL	GWKGSPIAI	341	8	59	92		12797
POL	HWQVLTIL	811	9	59	92	0.0095	12798
POL	LWKSGEAVVI	904	10	59	92		12799
POL	KWKRLVDFRE	259	11	59	92		12800
POL	NEFKRGGI	936	8	60	94	0.0001	12801
POL	GYELHPDKW	420	9	60	94	0.0190	12802
POL	QMAIHLNF	929	9	60	94		12803
POL	LYVGSQLEI	376	11	60	94		12804
POL	IVQYMDLI	369	8	61	95		12805
POL	YMDLIYVGS	372	11	61	95		12806
POL	KMGIGGCGF	132	9	62	97	0.0011	12807
POL	KMGIGGCGF	132	10	62	97	0.0001	12808
POL	QYNVLPQGW	334	9	63	98	0.0036	12809
POL	QYNVLPQGW	334	11	63	98		12810
POL	PTLWAGYEL	412	9	63	100		12811
REV	RWRKQRQRI	48	9	11	17		12812
REV	RWRKQRQRI	48	9	35	55		12813
TAT	CYCKKCCF	28	8	11	17		12814
TAT	CFHCQVCF	34	8	11	17		12815
TAT	CFHAKGLGI	40	9	14	22		12816
VIF	RYSTQVDPGL	98	10	16	16		12817
VIF	RYSTQVDPGL	98	10	16	16		12818
VIF	QYLALAKL	151	11	10	17		12819

Table XVIII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2001	SIC ID NO
VIF	QYLALAL	151	8	12	19		12820
VIF	RMKRTWNSL	15	10	12	19		12821
VIF	WVQVDRMD	119	11	12	19		12822
VIF	CFSSAIRNAI	119	11	12	19		12823
VIF	WVQVDRMKI	10	9	13	20		12824
VIF	IMIVFDCE	113	8	15	23		12825
VIF	RMKRTWNSL	15	10	15	23		12826
VIF	WVQVDRMD	119	11	15	23		12827
VIF	DMWQVDRSI	81	10	18	28		12828
VIF	WVQVDRMD	119	11	20	31		12829
VIF	WVQVDRMD	119	11	21	33		12830
VIF	DMWQVDRSI	81	10	21	33		12831
VIF	WVQVDRMD	119	11	22	34		12832
VIF	QYLALAL	151	9	28	44		12833
VIF	WVQVDRMD	119	10	28	44		12834
VIF	DMWQVDRSI	81	8	33	52		12835
VIF	WVQVDRMD	119	9	43	62		12836
VIF	WVQVDRMD	119	9	48	75		12837
VIF	WVQVDRMD	119	9	48	75		12838
VIF	WVQVDRMD	119	9	48	75		12839
VIF	WVQVDRMD	119	9	48	75		12840
VIF	WVQVDRMD	119	9	48	75		12841
VIF	WVQVDRMD	119	9	48	75		12842
VIF	WVQVDRMD	119	9	48	75		12843
VIF	WVQVDRMD	119	9	48	75		12844
VIF	WVQVDRMD	119	9	48	75		12845
VIF	WVQVDRMD	119	9	48	75		12846
VIF	WVQVDRMD	119	9	48	75		12847
VIF	WVQVDRMD	119	9	48	75		12848
VIF	WVQVDRMD	119	9	48	75		12849
VIF	WVQVDRMD	119	9	48	75		12850
VIF	WVQVDRMD	119	9	48	75		12851
VIF	WVQVDRMD	119	9	48	75		12852
VIF	WVQVDRMD	119	9	48	75		12853
VIF	WVQVDRMD	119	9	48	75		12854
VIF	WVQVDRMD	119	9	48	75		12855
VIF	WVQVDRMD	119	9	48	75		12856
VIF	WVQVDRMD	119	9	48	75		12857
VIF	WVQVDRMD	119	9	48	75		12858
VIF	WVQVDRMD	119	9	48	75		12859
VIF	WVQVDRMD	119	9	48	75		12860
VIF	WVQVDRMD	119	9	48	75		12861
VIF	WVQVDRMD	119	9	48	75		12862
VIF	WVQVDRMD	119	9	48	75		12863

655007-2992140

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO
ENV	VSTQLLNG	61	95	KPVVSTQLLNGSLA	299	29	45	12864
ENV	VSTQLLN	60	94	IKPVVSTQLLNGSL	298	29	45	12865
ENV	LTWQKQL	59	92	LLQLTWQKQLQAR	651	26	44	12866
ENV	LLSGVQVQ	58	91	AKLLSGVQVQSLN	79	26	34	12867
ENV	WATHACVPT	56	86	WATHACVPTSPQ	69	44	69	12868
ENV	VGVQSPSL	55	86	LGFLGAASTMGAS	605	36	56	12869
ENV	LLNLGSLAE	54	84	VNRVQSTSPISQI	800	36	57	12870
ENV	VKLTPLCVT	53	83	STQLLNGSLAEFEV	303	16	25	12871
ENV	LEAIEAQH	51	80	RPCVGLTFLCYLNC	130	29	45	12872
ENV	VSTVQTHG	51	80	NNLLKAIDAQILLQ	639	18	45	12873
ENV	LGWGSCKK	50	80	QVGLWGSCKKSLK	636	18	45	12874
ENV	LGFLGAAST	49	78	CGQLLWGSCKSLK	626	46	72	12875
ENV	LGFLGAAST	49	77	ISLWQSLAPCYAL	121	35	55	12876
ENV	WATHACVP	49	77	AVELFLGAASTMG	602	19	30	12877
ENV	WGRQLQAR	49	77	VHNVWATHACVPTD	78	34	53	12878
ENV	LWYKIRIM	43	67	LTWQKQLQAKVLA	654	39	61	12879
ENV	FCASDAKAY	42	66	THWQKQLKFNKSL	651	18	44	12880
ENV	HNWIGEL	41	64	THWQKQLKFNKSL	651	18	28	12881
ENV	VYGVGVVVK	41	64	FMVIGGLGVDFE	780	22	34	12882
ENV	IKFLQARVL	40	63	YKIFEMVIGGLQL	776	30	47	12883
ENV	MGAASTLT	39	61	WYGVVGVVVKREAT	46	22	34	12884
ENV	IKFLQARVL	39	61	VWGRQLQARVLAVE	656	31	49	12885
ENV	MGAASTLT	39	61	LWYKIRIMVIGGLI	774	31	49	12886
ENV	IKFLQARVL	37	58	GNWQKQLKFNKSL	613	21	44	12887
ENV	IKFLQARVL	37	58	WYGVVGVVVKREAT	46	22	34	12888
ENV	IKFLQARVL	36	56	SSNTGLLITROGGL	516	06	9	12889
ENV	IKFLQARVL	36	56	FMVIGGLGVDFE	779	21	33	12890
ENV	IKFLQARVL	35	55	IFMIVIGGLGVDFE	779	22	34	12891
ENV	IKFLQARVL	35	55	LTLYQARQLSGVQ	622	15	27	12892
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12893
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12894
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12895
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12896
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12897
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12898
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12899
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12900
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12901
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12902
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12903
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12904
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12905
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12906
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12907
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12908
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12909
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12910
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12911
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12912
ENV	IKFLQARVL	35	55	WQSLAPCYAL	121	35	55	12913

HIV DR Super-Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Contrastivity (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Contrastivity (%)	SEQ ID NO
ENV	LTKLCVTIN	29	45	CVKLPLCVLTINCTD	132	11	17	12914
ENV	LXXYXAVKI	29	45	RSELVYKVKVKEPL	558	0	36	12915
ENV	VPWNSWSN	29	45	TYNVWNSWSNSEL	691	0	8	12916
ENV	YRLNCSNT	28	44	YKRYLNCNCSNT	235	01	5	12917
ENV	IHYCAPAE	27	42	FRYLQDQLLHGGC	670	25	39	12918
ENV	LKDQQLGI	27	42	SELVYKVKVKEPL	559	24	38	12919
ENV	YKVKVKE	27	42	THGHPVSTOLLN	295	24	38	12920
ENV	IRPVYSTOL	26	41	LLADKWASLWNWFD	755	08	41	12921
ENV	LYKSLVSLN	26	41	LIGLRVIAVLSN	787	10	13	12922
ENV	LVKSLVSLN	26	41	OLLNGSLABEEVI	305	13	20	12923
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12924
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12925
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12926
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12927
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12928
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12929
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12930
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12931
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12932
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12933
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12934
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12935
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12936
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12937
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12938
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12939
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12940
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12941
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12942
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12943
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12944
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12945
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12946
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12947
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12948
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12949
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12950
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12951
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12952
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12953
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12954
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12955
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12956
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12957
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12958
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12959
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12960
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12961
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12962
ENV	LVKSLVSLN	26	41	LYKSLVSLN	305	13	20	12963

HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
ENV	LNATAIAY	15	23	AVSLNATAIAVEG	918	10	16	12864
ENV	LRIPIAAV	15	23	LIGLRIFAIVLSVN	787	11	17	12865
ENV	VYVAVKAY	15	23	NTSVITQCPKVSFE	241	08	11	12866
ENV	YVWNLQWY	15	23	VLKYVWNLQWYQSE	899	09	14	12867
ENV	FAILKNDK	14	22	PAGFALKNDKRN	790	09	14	12868
ENV	IFAVLSVN	14	22	YKLVNCTSAIQAC	235	13	22	12869
ENV	INCNTSAI	14	22	YKLVNCTSAIQAC	919	10	16	12870
ENV	LNATIAIAY	14	22	YKLVNCTSAIQAC	919	10	16	12871
ENV	WNSWNNKS	14	22	NVPWNSSWSNKLDE	693	03	5	12872
ENV	WNSWNNKS	14	22	NVPWNSSWSNKLDE	693	02	3	12873
ENV	IKCTTPWV	13	21	NVPWNSSWSNKLDE	693	06	20	12874
ENV	LLKLTWYGI	13	20	GKLCTTPWNASW	686	06	20	12875
ENV	LYKYVYVEI	13	20	QOHLIKTYVWGRQL	648	08	11	12876
ENV	MELFGLAA	13	20	RSELTKYKYVYVEI	460	07	11	12877
ENV	MHSFNCGE	13	20	YVWNSWNSGGEPIFY	430	13	10	12878
ENV	YWSQELKNS	13	20	LLOYWSQELKNSVS	906	10	16	12879
ENV	IGAVFLGFL	12	19	AVGGVAVFLGFLQAA	595	09	14	12880
ENV	LICTTPWV	12	19	DFLLAAARTVELLGH	870	04	9	12881
ENV	LYKSLGAE	12	19	SGKLCTTTPWNASW	685	03	5	12882
ENV	YVWQELKNS	12	19	TQLLINGSLAGGHH	906	03	3	12883
ENV	IAARTVELL	11	17	YVWQELKNSVLLNAT	871	03	5	12884
ENV	LFUGFLGAA	11	17	IGALFGLFGLAAGST	600	06	9	12885
ENV	LNKNSVLL	11	17	SGQELKNSVLLNAT	911	08	13	12886
ENV	YVSLNATAI	11	17	KRAYGGVAVFLGFLG	593	11	14	12887
ENV	YATGDIGD	11	17	NSAVSLNATAIAVAA	916	13	14	12888
ENV	IAIAYAGT	10	16	QTFYATGDIGDIHQ	925	04	6	12889
ENV	IHYCTPAGT	10	16	PHIYCTPAGTAIF	258	02	3	12890
ENV	ILGLVICS	10	16	GTLLGLVICSASH	714	03	13	12891
ENV	LNKNSVLL	10	16	VDIHNNMTWMEWER	19	03	5	12892
ENV	LRIPIAAV	10	16	TLILGLVICSASN	20	04	9	12893
ENV	LTPCLVLLD	10	16	YHLRLDFLLIARTY	865	03	5	12894
ENV	MLQLTWYGI	10	16	CVKLTPLCYTLDCIN	648	08	13	12895
ENV	VEINTNRN	10	16	QNSVWNTGNTNNNT	338	02	3	12896
ENV	VROLGSAV	10	15	TVQVROLGSAVQQQ	624	08	13	12897
ENV	LLGLVICS	10	15	WGTLILGLVICSAS	18	07	11	12898
ENV	LNKNSVLL	9	14	LNTVGGHQAAOMOLK	209	09	14	12899
ENV	LNKNSVLL	9	14	TETLLVQNANPDCKT	342	26	38	12900
ENV	VQANPDCK	9	14	TLIVQANANPDCKT	240	26	38	12901
ENV	LGANKVRM	8	13	WILGKNSVLLNAT	240	26	38	12902
ENV	LSGATPQD	8	13	YKRWILGKNSVLLN	193	55	86	12903
ENV	WILGLTACI	8	13	YKRWILGKNSVLLN	286	24	34	12904
ENV	LEEMTACI	8	13	QATLEEMTACQGVG	364	42	84	12905
ENV	YKRWILGL	8	13	GEYKRWILGLNKN	283	37	58	12906
ENV	YKRWILGL	8	13	VGGHYKRWILGLNKN	282	37	58	12907
ENV	VNSNTYIVQ	8	13	SSQYKRWILGLNKN	145	09	25	12908
ENV	WPKTRILPQ	50	78	LQKWERILPQGRK	13	13	13	12909
ENV	IAGTITLAP	46	72	GSDIAGTITLQGRK	234	45	70	12910

665001-2982160
Table XIXa
HIV DR Super Motif Peptides.

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
GAG	WASRELERF	46	72	HLVWASRELERFALN	34	17	27	13014
GAG	IMRSALRE	45	70	IMRSALRE	189	43	69	13015
GAG	IMRSALRE	45	70	VIMESALSSEGAATQ	189	43	67	13016
GAG	VIMESALS	45	70	SFEVIMESALSSEGA	186	40	63	13017
GAG	MTSPVSILQ	41	64	IVEMVSPVSILDRQ	297	23	36	13018
GAG	IVMVSIVS	40	63	LNKVIVMVSIVSILD	294	39	61	13019
GAG	VRMVSIVS	40	63	NKVIVMVSIVSILD	295	38	59	13020
GAG	YSPVSILDI	40	63	VRMVSIVSILDRQ	294	38	58	13021
GAG	MTSPVSLN	37	58	YSPVSIVSILDRQ	295	38	57	13022
GAG	WMTLLVQ	37	58	KNVWMTLLVQNS	337	34	53	13023
GAG	SPKTLNAV	36	56	HOASPKTLNAVYVQ	165	27	42	13024
GAG	VSNVMTL	36	56	TOEVSNVMTLLVQ	334	14	22	13025
GAG	IKPNCORE	34	53	QKRIKPCNGKEGHL	418	05	8	13026
GAG	IPVGEIYKR	34	53	NHPVPGEIYKRWII	377	02	51	13027
GAG	VTAYPMORG	32	51	KGVVTAYPMORG	379	02	50	13028
GAG	WDRLEHPVHA	29	47	YNTVATLYYVQIIE	81	07	11	13029
GAG	WDRLEHPVHA	29	45	AAEWDRLEHPVHAPI	230	22	34	13030
GAG	FLASSPEPT	28	44	PGNFLOSRPEPTAPP	483	27	43	13031
GAG	FKTLAEQA	27	42	DRFKTLRAEOATOE	322	16	25	13032
GAG	MYHOISRRT	27	42	QGMVHOISRRTLIN	160	16	25	13033
GAG	YHQAISRT	27	42	YHQAISRTLIN	161	16	24	13034
GAG	YHQAISRT	27	42	DRFYKTLBAEQASDE	322	12	19	13035
GAG	YHQAISRT	25	39	YSPVSVILDRQPKKE	301	24	38	13036
GAG	LAHAMSQVT	23	37	ARVLAHAMSQVNSA	384	08	13	13037
GAG	LOKWSHSK	23	36	ANTLGLKWSHSKGRF	467	22	34	13038
GAG	VKPCRCKE	23	36	KCTVKPCRCRGEHII	420	07	11	13039
GAG	YNTVATLYC	23	36	YNTVATLYC	81	07	11	13040
GAG	LYKTVATLY	22	34	WDRLYKTVATLYHAG	233	15	23	13041
GAG	MTDILLVQN	22	34	LESLNTVATLYCVH	77	13	20	13042
GAG	WMTDILLVQ	22	34	KNWMTDILLVQNP	338	16	25	13043
GAG	LEVYDKTEA	21	33	VKNWMTDILLVQNP	337	16	25	13044
GAG	LOQNVVHQA	21	33	HQREVKDTEKALDK	91	11	11	13045
GAG	WMTNTP	20	31	WDRVWMTNTP	248	16	25	13046
GAG	WMTNTP	20	31	LOQNVVHQA	248	16	25	13047
GAG	LAGQMERP	19	30	QIGWMTNTPPVGE	267	16	25	13048
GAG	VHAGPIAPG	19	30	ACTVHAGPIAPGPGS	241	19	30	13049
GAG	LPQATILEE	18	28	LHPVHAGPIAPQMR	226	14	22	13050
GAG	VHAGPIPG	18	28	LRLPQATILEEMAT	358	09	14	13051
GAG	LEPSTLN	17	27	VHPVHAGPIPTQKKE	248	16	25	13052
GAG	YRLSHLVYA	17	27	HOASLEPSTLN	165	10	16	13053
GAG	LGPAANTILE	16	25	KCKVYRLSHLVYASRE	27	13	20	13054
GAG	LKALGPAAT	16	25	LKALGPAATILEVMT	358	16	25	13055
GAG	LKQKEPPLA	01	25	QBLKQKEPPLASLR	355	16	25	13056
GAG	LSQGLDIAW	16	25	QBLKQKEPPLASLR	352	01	25	13057
GAG	VKNVMTDILL	16	25	IGWMTNTPPVGEHII	268	06	11	13058
GAG	VKNVMTDILL	16	25	TOEVKNVMTDILLVQ	334	11	7	13059
GAG	VSILDRQPKKE	16	25	YSPVSVILDRQPKKE	301	16	25	13060
GAG	WMTNTP	16	25	QIGWMTNTPPVGE	267	10	15	13061
GAG	WMTNTP	16	25	QIGWMTNTPPVGE	267	06	10	13062

66500759021400
Table XIXa
MIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Consistency (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Consistency (%)	SEQ ID NO.
GAG	FNVTATYC	15	33	KSLNVTATVGVVQ	78	07	11	13064
GAG	FNVTATYC	5	23	VPVMTALSEGAT	187	13	20	13065
GAG	FNVTATYC	15	23	LYPLASLSLFGNDP	544	06	11	13066
GAG	FNVTATYC	15	23	SRELREAVNPGLE	39	14	22	13067
GAG	FNVTATYC	15	23	LESLFNVTATVGVV	77	07	11	13068
GAG	FNVTATYC	15	23	VPVMTALSEGATQ	189	14	22	13069
GAG	FNVTATYC	15	23	AAEWKQVHPVIAHPI	250	12	19	13070
GAG	FNVTATYC	14	22	SEHLEFALNPGLE	294	12	20	13071
GAG	FNVTATYC	14	22	SEHLEFALNPGLE	39	14	22	13072
GAG	FNVTATYC	14	22	TSTLOQIAWMTGNP	261	05	8	13073
GAG	FNVTATYC	14	22	WDKVFVPIAGIPRG	233	11	17	13074
GAG	FNVTATYC	14	22	SPREVFMTALSEGA	186	13	20	13075
GAG	FNVTATYC	14	22	NKIVMAYSTILSDI	295	13	19	13076
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13077
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13078
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13079
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13080
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13081
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13082
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13083
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13084
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13085
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13086
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13087
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13088
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13089
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13090
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13091
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13092
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13093
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13094
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13095
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13096
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13097
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13098
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13099
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13100
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13101
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13102
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13103
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13104
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13105
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13106
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13107
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13108
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13109
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13110
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13111
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13112
GAG	FNVTATYC	13	20	LYPLASLSLFGNDP	544	06	11	13113

665007.2921400
Table XIXa
HIV DR Supert Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
NEF	WGFAIRER	10	17	SSVWGFAIRERMR	8	03	5	13114
NEF	WCFKLIVVE	11	17	IFWGCKLVVPEK	8	04	6	13115
NEF	FISRLAHIL	10	16	IFGCKLVVPEK	322	02	4	13116
NEF	WCFKLIVVE	10	16	GWCKLVVPEK	224	10	16	13117
POL	VPLERATK	63	98	RQVLEMTFKGAF	98	04	6	13118
POL	LLDTGADTD	63	98	KEALLDTGADDTYLE	107	37	58	13119
POL	WMGYLHDP	63	98	PELWMGYLHDPWT	415	60	94	13120
POL	YQVYNLPQG	63	98	GIRYQVYNLPQDWKG	330	32	16	13121
POL	FRKYTAFTI	61	97	IKSYNYNLPQDWKG	330	32	16	13122
POL	WYVYHQGL	61	97	KDSYNYNLPQDWKG	438	43	67	13123
POL	WYVYHQGL	61	95	IKWLDICTHLEGRIL	812	29	45	13124
POL	LDVGDVYFS	61	95	VTVLDVGDVYFSVFL	295	50	78	13125
POL	MDLLYAGSD	61	95	YQVMDLLYAGSDLEI	370	57	89	13126
POL	VIPAETQGE	61	95	EAETVIPAETQGTAY	837	57	89	13127
POL	WKGEGAVVI	61	95	ALLWKGEGAVVIQDN	810	32	80	13128
POL	WQDICTHLE	61	95	IKWLDICTHLEGRIL	810	32	80	13129
POL	WQDICTHLE	60	94	RKLVDPEIKAKITQD	261	57	89	13130
POL	WQDICTHLE	59	92	PKWKAPEKGGGCF	126	39	61	13131
POL	VAVHVASGY	59	92	SPQWQLDICTHLEGR	809	56	88	13132
POL	WKGSAIRQ	59	92	ILILVAVHVASGYTEA	824	26	41	13133
POL	IGGYSKIER	58	92	PQOWKGSYAPQSSIM	939	32	46	13134
POL	WQDICTHLE	58	91	IKWLDICTHLEGRIL	810	32	80	13135
POL	PKWVGLGP	57	89	DSQYALHIOGPDIX	690	39	59	13136
POL	IKKKDKSTKW	57	89	TDQFWFVQLGHPIFA	273	52	81	13137
POL	LQHQAPQD	57	89	VFAIKKKDKSTKWKL	249	36	56	13138
POL	LGHPIPAQL	56	89	QYALGHPIPAQPKSE	692	39	61	13139
POL	VNTHPLVKL	57	89	EVQLGHPIPAQKKKK	778	31	46	13140
POL	WQDICTHLE	57	89	IKWLDICTHLEGRIL	810	32	80	13141
POL	WQDICTHLE	56	88	KESVYLDVGDVYFS	292	49	77	13142
POL	ISPIETVPI	56	88	TLNFIPIETVPIVVK	183	52	83	13143
POL	FYNTHPLVK	54	86	EWEPFYNTHPLVKLWY	185	52	81	13144
POL	LNPISEPI	55	86	GCTLNPISEPIETVPI	605	50	78	13145
POL	WEPNTHPLVK	54	84	IKWLDICTHLEGRIL	810	32	80	13146
POL	LNPISEPI	54	84	IKWLDICTHLEGRIL	810	32	80	13147
POL	WQDICTHLE	54	84	IKWLDICTHLEGRIL	810	32	80	13148
POL	WQDICTHLE	54	84	IKWLDICTHLEGRIL	810	32	80	13149
POL	WQDICTHLE	54	84	IKWLDICTHLEGRIL	810	32	80	13150
POL	WQDICTHLE	53	83	IKWLDICTHLEGRIL	810	32	80	13151
POL	WQDICTHLE	53	83	IKWLDICTHLEGRIL	810	32	80	13152
POL	WQDICTHLE	53	83	IKWLDICTHLEGRIL	810	32	80	13153
POL	WQDICTHLE	53	83	IKWLDICTHLEGRIL	810	32	80	13154
POL	WQDICTHLE	53	83	IKWLDICTHLEGRIL	810	32	80	13155
POL	WQDICTHLE	53	83	IKWLDICTHLEGRIL	810	32	80	13156
POL	WQDICTHLE	53	83	IKWLDICTHLEGRIL	810	32	80	13157
POL	WQDICTHLE	52	81	IKWLDICTHLEGRIL	810	32	80	13158
POL	WQDICTHLE	52	81	IKWLDICTHLEGRIL	810	32	80	13159
POL	WQDICTHLE	52	81	IKWLDICTHLEGRIL	810	32	80	13160
POL	WQDICTHLE	52	81	IKWLDICTHLEGRIL	810	32	80	13161
POL	WQDICTHLE	52	81	IKWLDICTHLEGRIL	810	32	80	13162
POL	WQDICTHLE	52	81	IKWLDICTHLEGRIL	810	32	80	13163

65001-650110
Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
POL	VYQVMDLL	51	80	PEVYQVMDLLVYG	365	23	36	13164
POL	LKRSQSVTV	49	78	PAGLRSQSVTVLDY	386	46	32	13165
POL	YVNGKTRF	40	77	YVNGKTRFV	1040	41	64	13166
POL	VYNGKTRF	47	71	SESVNGKTRFRLP	84	09	14	13167
POL	YVDGAARE	46	72	ETVYVDGAARETKL	570	23	38	13168
POL	PNKLTGRY	45	70	QEFKNLTKGRYAKM	630	24	38	13169
POL	IQTKRLQK	45	70	ATDIQTKRLQKQTK	535	15	23	13170
POL	YGRQMAQDD	45	70	YGRQMAQDDQK	937	24	38	13171
POL	WVAGKQAN	47	67	WVAGKQANQK	1147	31	34	13172
POL	ISLGPBPR	42	66	ISLHSPASISLNP	768	21	48	13173
POL	LTQGTCLN	41	64	EGKSKLGPBPNFT	233	40	63	13174
POL	IQAQDPKS	40	63	RNLLTQGTCLNFT	174	21	33	13175
POL	LPKDSWTV	40	63	ALGIQAQDPKSESE	694	38	59	13176
POL	FQSSMTKL	38	59	IVLPKDSWTVNDI	432	13	20	13177
POL	FLPSINNE	38	59	PAFQSSMTKLEPT	346	32	56	13178
POL	IRKQKQK	38	59	PAFQSSMTKLEPT	346	32	56	13179
POL	IRKQKQK	37	58	SPAFQSSMTKLEP	345	33	52	13180
POL	LSWVPAHK	37	58	VQIEQLKKEKYY	710	19	30	13181
POL	YLSWVPAHK	37	58	KVYLSWVPAHKGG	722	23	37	13182
POL	YTAFTPSI	37	58	EKYYLSWVPAHKGG	721	15	24	13183
POL	IATDIQTK	35	55	FRKYTAFTPSINNE	113	37	52	13184
POL	IRKQKQK	35	55	IRKQKQKQK	92	27	34	13185
POL	LOKGLDTQ	35	55	RDWKGDTAKLWGG	983	34	53	13186
POL	LKGLDITQ	34	53	TKELORQTKIONFR	962	29	46	13187
POL	VYLSWVPAH	33	52	GGQLREALLDTGADD	103	31	48	13188
POL	FILKLAGRW	32	50	KEKYLSWVPAHKGT	720	15	23	13189
POL	LEKQITVA	31	48	TAYFLKLAGRWPK	849	27	42	13190
POL	YVNGKTRF	31	48	ETAYFLKLAGRWV	848	30	47	13191
POL	HLVAHVVA	30	47	EGKILVAHVAVSGY	821	30	47	13192
POL	HWGTPKFR	30	47	SVHWGTPKFRFLH	571	22	34	13193
POL	LAGRWPKV	30	47	LLKLAGRWPKVHIIT	853	19	30	13194
POL	VVAKEIVAS	30	47	LPVVAKEIVASCDK	780	21	33	13195
POL	IDUATDQ	29	45	EGKILVAHVAVSGY	821	30	47	13196
POL	IGRNMALQ	29	45	GRGDIAATDQIC	949	11	16	13197
POL	IKVQLCKL	29	45	PVNIIGRNMALQIC	168	21	36	13198
POL	VDKLVSSGI	29	45	YAGIKVQCKLLAG	460	18	28	13199
POL	YVGAETFY	28	44	NEQVQCKLLAG	737	26	41	13200
POL	LPVPAKEI	28	44	KEPVGAETFYDGA	623	16	25	13201
POL	YVQKQK	27	42	DPNLPVPAKEIVAS	777	16	25	13202
POL	FTSAVKAA	27	42	FTSAVKAAKVVW	425	13	20	13203
POL	FTSAVKAA	27	42	ASDFNPNVPAKEI	775	25	39	13204
POL	LALQDSGLE	27	42	GSNFTSAVKAAKVVW	870	25	39	13205
POL	LPVPAKEI	27	42	AHIALQDSGLEVNI	673	15	23	13206
POL	LQDSGLEVN	27	42	DPNLPVPAKEIVAS	777	20	31	13207
POL	FNLPVPAK	26	41	HLAQDSGLEVNVT	675	13	20	13208
POL	IQHRAKLE	26	41	EGKILVAHVAVSGY	821	30	47	13209
POL	LENNVTD	26	41	DEGQIRALKEIHL	381	21	36	13210
POL	LENNVTD	26	41	PVNIIGRNMALQIC	168	21	33	13211
POL	LENNVTD	26	41	DSGLEVNVTDSQVA	680	26	41	13212
POL	LENNVTD	26	41	DSGLEVNVTDSQVA	680	26	41	13213

665007-69821-60
Table XIXa
MIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
POL	LRGAKALTD	26	41	CKLRGAKALTDVTP	469	12	19	13214
POL	LVSSGRKRV	26	41	VDKLVSSGRKRVFL	740	15	39	13215
POL	FLKLAGRW	25	39	TAYFLKLAGRWVTK	663	19	30	13216
POL	LALQDSGE	25	39	ALALQDSGEVNT	675	08	13	13217
POL	LQDSGEVN	25	39	KALQDSGEVNT	859	08	13	13218
POL	VKVIHDNG	25	39	RMPVKVIHDNGSNF	859	21	33	13219
POL	WPKVLTDD	25	39	AGRWPKVLTDDINGS	857	20	31	13220
POL	LVKQKAGT	25	39	ETAYELLKLAGRWPV	848	24	38	13221
POL	LVKQKAGT	24	38	LJECGKKAIGTVLV	150	12	34	13222
POL	IVAKEWAS	24	38	LPVIVAKEWASCKR	780	12	34	13223
POL	LRWGFTPD	24	38	QILLARWGFTPDKHH	817	12	34	13224
POL	LEKVLVA	23	36	LEKVLVAHIVASGY	396	13	36	13225
POL	LVILVAIVA	23	36	LEKVLVAHIVASGY	821	21	33	13226
POL	LVILVAIVA	23	36	LEKVLVAHIVASGY	821	21	33	13227
POL	LVILVAIVA	22	34	VRQYDQLIEICCK	143	08	12	13228
POL	LVILVAIVA	22	34	VRQYDQLIEICCK	721	10	12	13229
POL	LVILVAIVA	22	34	VRQYDQLIEICCK	721	10	12	13230
POL	LVILVAIVA	22	34	VRQYDQLIEICCK	721	10	12	13231
POL	LVILVAIVA	22	34	VRQYDQLIEICCK	721	10	12	13232
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13233
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13234
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13235
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13236
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13237
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13238
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13239
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13240
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13241
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13242
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13243
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13244
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13245
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13246
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13247
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13248
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13249
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13250
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13251
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13252
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13253
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13254
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13255
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13256
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13257
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13258
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13259
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13260
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13261
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13262
POL	LVILVAIVA	21	33	VRQYDQLIEICCK	721	10	12	13263

[illegible]

	(c)	(d)	(e)	(f)	(g)	(h)	(i)	(j)	(k)	(l)	(m)	(n)	(o)	(p)	(q)	(r)	(s)	(t)	(u)	(v)	(w)	(x)	(y)	(z)
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Table XIXa

HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO
VIF	LQYLALTL	33	52	VGSLOYLALTLALPKP	147	14	22	13314
VIF	LGHGVSVW	31	48	DWHLQGVSVWRKR	81	11	17	13315
VIF	VDMRRTW	28	44	HLVYDQFSSGAINI	113	15	23	13316
VIF	YWGQITGR	28	44	ITTYWGLTIGERDWH	68	08	14	13317
VIF	IRTWNSLVK	27	42	RMRTWNSLVKJHM	15	12	22	13318
VIF	LGGGVSVW	26	41	DWHLQGVSVWRKK	81	07	19	13319
VIF	LVKHHMYVS	21	33	WNSLVKHHMYVSCKA	21	07	11	13320
VIF	PLGEGARLV	19	30	WNSLVKHHMYVSCKA	21	07	8	13321
VIF	YKTHMTIS	9	16	WNSLVKHHMYVSCKA	21	05	8	13322
VIF	YKTHMTIS	16	25	SLOYLALTLALPKPK	149	11	17	13323
VIF	IRTWNSLVK	15	23	RMRTWNSLVKJHM	15	14	22	13324
VIF	LADQLHLY	15	23	DPDLADQLHLYFD	104	07	11	13325
VIF	LADQLHLY	15	23	LQYLALTLALPKPK	150	08	13	13326
VIF	VDPLADQL	15	23	STQVDPLADQLHL	100	14	25	13327
VIF	YTFDFCRS	14	24	EPGSDSFAIRKALG	117	10	16	13328
VIF	YTFDFCRS	13	20	EPGSDSFAIRKALG	117	10	16	13329
VIF	LADQLHLY	13	20	EPGSDSFAIRKALG	117	10	16	13330
VIF	WQYDMRKIR	13	20	EPGSDSFAIRKALG	117	10	16	13331
VIF	FDSFAIRKA	12	19	LIVWQYDMRKIRTN	8	08	14	13332
VIF	FDSFAIRKA	12	19	PDGSDSFAIRKALG	117	05	8	13333
VIF	FDSFAIRKA	12	19	PDGSDSFAIRKALG	117	05	8	13334
VIF	IVSRCEVQ	12	19	PDGSDSFAIRKALG	117	06	9	13335
VIF	IVSRCEVQ	12	19	PDGSDSFAIRKALG	117	06	9	13336
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13337
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13338
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13339
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13340
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13341
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13342
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13343
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13344
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13345
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13346
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13347
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13348
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13349
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13350
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13351
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13352
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13353
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13354
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13355
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13356
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13357
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13358
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13359
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13360
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13361
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13362
VIF	YDMRRTW	12	19	VGSLOYLALTLALPK	147	04	6	13363

655001-09321130

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO
VP1	LRQRKIDL	17	27	RKLRQRKIDRLDR	44	11	17	13364
VP1	LRQRKIDL	15	23	IAIVVWTIVFIEYR	27	07	11	13365
VP1	VAVTIVFIE	14	22	IAIVVWTIVFIEYR	28	06	9	13366
VP1	IEYRKILIQ	13	21	IVFIEYRKILQRKI	26	07	11	13367
VP1	ILAVIALVY	11	17	SLYLAVIALVIAII	3	01	2	13368
VP1	WTIVFIEYR	10	16	IVFIEYRKILQRKI	30	05	8	13369
VP1	LAIALVVA	09	15	LQLAVIALVAGII	4	02	3	13370

[illegible]

665091-69021-420
Table XIX
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DRw19	DR7	DRw2	DR9	DRw3	SEQ ID NO.
VSTQLLNG	KPVVSTQLLNGSLA						12864
VVSTQLLN	IKPVVSTQLLNGSLA						12865
LTWVQQL	LQVTVKRLQQLNR		0.0180				12866
LVVQQL	LVVQQLNR						12867
WAHACVPT	HRWVAHACVPTDPN						12868
LGAAGSTAG	LQFLGAAGSTMGAA						12869
VRQGTSHLS	VNRVRQGTSTLSRQT		-0.0007				12870
LLNLGLAE	STQLLNGSLAEEV						12871
VKLTPLOY	KCVKLTPLOYLNC						12872
LVVQQL	LVVQQLNR						12873
VSTVQCTIG	CNVSTVQCTIGHK		0.0150				12874
LGWQCSKRG	QQLLGWQCSKRLIC						12875
LWQDSLKPC	ISLWDQSLKPCVKL		0.0012				12876
LGFLGAAGSTM	AVPLGFLGAAGSTM						12877
VWATHACVP	VHWATHACVPTDPN						12878
LVVQQL	LVVQQLNR						12879
LWYKGFIM	TNWLWYKGFIMVYG						12880
FCASDAKAY	TLFCASDAKAYDTE						12881
IVGGLIGLR	FMIVGGLIGLRVFE						12882
FMIVYGGI	YKIFIMYGGIIGL	-0.0004	0.0310	0.0049	0.4600		12883
VYVGVVWVK	WYVGVVWVKVAVT						12884
IKENMVG	VWVKGLQARVLAWE						12885
MGAASITLT	LVYKIFIMYGGI						12886
YKIFIMIV	GSTMGAASITLTVOA						12887
ITGLLTTRD	WLVYKIFIMYGGI						12888
FMVCAKAY	SSNTGLLTTRDGGK						12889
VOARGLLSG	FMVYGGIIGLRV						12890
FEPTPHVC	TLTVQARGLLSGVQ						12891
LRSLCLFSY	WDLRLSLCLFSYRL						12892
WKNNAVEQ	WKNNAKAVYQDHE						12893
WKNNAVEQA	WKNNAKAVYQDHE						12894
WKNNAVEQA	WKNNAKAVYQDHE						12895
YGVVYVWKE	FMVWKNNAVEQMHED						12896
LLQLTWGI	VTVYGVVYVWKEAT	0.0160		0.0210	0.5100		12897
IEPLGVAPT	QSHLLQLTWGKQL	0.3900					12898
LVVQQL	VYKREPLGVATKAR						12899
LVVQQL	VYKREPLGVATKAR						12900
WDLJSLCL	KOLQARVLAVERYL						12901
INHTHRE	ALAWDLJSLCLFSY						12902
ITOACPKVS	SRFINHTHREKR						12903
WQGSNLL	RPINHTHREKZA						12904
VSTHRE	TSVITQACPKVSFEP						12905
WVWGTLFLG	LSQVQGSNLL						12906
FAVLSVNR	INHTHREKZA						12907
LVNGLABE	ARPAVSTHREKKA						12908
	QNLVWAGTLFLGMLM						12909
	QNLVWAGTLFLGMLM						12910
	RIVFAVLSVNRVRO						12911
	TQLLNGSLAEEV						12912
	TQLLNGSLAEEV						12913

Core Sequence

Core Sequence	Exemplar Sequence	DRI	DR2w48l	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID No
LDPLVLTN	CYKLTPLVLTNCTD	0.0066	0.0320	0.0014		0.0011	0.0190	0.0042		12914
LYKYKVKI	RSELYKYKVKIEPL									12915
PWNSSWSN	TTNPWNSSWSNKS									12916
YRLNCSIT	YKEFRLNCSITAIT									12917
YHICAFAG	PPIHYCAPAGFAIL									12918
LKDQQLGI	ERYLKDQQLGIWGC									12919
LYKYKVKIE	SELKYKVKIEGLG									12920
YHICAFAG	YHICAFAGFAIL									12921
YHICAFAG	YHICAFAGFAIL									12922
YHICAFAG	YHICAFAGFAIL									12923
LYKYKVKI	LLADKXWASLNSTLL	12924								
LYKYKVKI	LIGLRIVFAVLSN	12925								
LYKYKVKI	QLLNGSLAIEEVI	12926								
LYKYKVKI	LYKYKVKIEPLGVA	12927								
LYKYKVKI	RSLKGLRLGWEGLK	12928								
LYKYKVKI	LCIFSYYRLADLI	12929								
LYKYKVKI	SVENCTRNPNTRK	12930								
LYKYKVKI	YHICAFAGFAIL	12931								
LYKYKVKI	YHICAFAGFAIL	12932								
LYKYKVKI	YHICAFAGFAIL	12933								
LYKYKVKI	GGEFYCNISGLNS	12934								
LYKYKVKI	RAAFGLGALFLGLG	12935								
LYKYKVKI	GGEFYCNISGLNST	12936								
LYKYKVKI	VGGJGLRIVFAVLS	12937								
LYKYKVKI	XKAVGLGALFLGLG	12938								
LYKYKVKI	YHICAFAGFAIL	12939								
LYKYKVKI	GGELICTTAVPNSSW	12940								
LYKYKVKI	GGELICTTAVPNSSW	12941								
LYKYKVKI	IEPLGVAPTKAKRRV	12942								
LYKYKVKI	SGKLICTTAVPNSSW	12943								
LYKYKVKI	ERYLRDQQLGIWGC	12944								
LYKYKVKI	LGAVFLGLOAAGST	12945								
LYKYKVKI	YHICAFAGFAIL	12946								
LYKYKVKI	YHICAFAGFAIL	12947								
LYKYKVKI	GLRIVFAVLSNVR	12948								
LYKYKVKI	GLRIVFAVLSNVR	12949								
LYKYKVKI	GLRIVFAVLSNVR	12950								
LYKYKVKI	TTAVPNSSWSNKS	12951								
LYKYKVKI	GGELIGLRIFAVALS	12952								
LYKYKVKI	IGBIHQIAHONSRK	12953								
LYKYKVKI	PLOWAPTKAKRRVQ	12954								
LYKYKVKI	YHICAFAGFAIL	12955								
LYKYKVKI	SYRIGRGDTAYAGD	12956								
LYKYKVKI	SYRIGRGDTAYAGD	12957								
LYKYKVKI	QTAIRYLALNQYEN	12958								
LYKYKVKI	YGGELIGLRIFAVALS	12959								
LYKYKVKI	WYNLLQYWSQELNS	12960								
LYKYKVKI	WYNLLQYWSQELNS	12961								
LYKYKVKI	IRLYSGHIALAWDD	12962								
LYKYKVKI	IRLYSGHIALAWDD	12963								
LYKYKVKI	IRLYSGHIALAWDD	12964								
LYKYKVKI	IRLYSGHIALAWDD	12965								
LYKYKVKI	IRLYSGHIALAWDD	12966								
LYKYKVKI	IRLYSGHIALAWDD	12967								
LYKYKVKI	IRLYSGHIALAWDD	12968								
LYKYKVKI	IRLYSGHIALAWDD	12969								
LYKYKVKI	IRLYSGHIALAWDD	12970								
LYKYKVKI	IRLYSGHIALAWDD	12971								
LYKYKVKI	IRLYSGHIALAWDD	12972								
LYKYKVKI	IRLYSGHIALAWDD	12973								
LYKYKVKI	IRLYSGHIALAWDD	12974								
LYKYKVKI	IRLYSGHIALAWDD	12975								
LYKYKVKI	IRLYSGHIALAWDD	12976								
LYKYKVKI	IRLYSGHIALAWDD	12977								
LYKYKVKI	IRLYSGHIALAWDD	12978								
LYKYKVKI	IRLYSGHIALAWDD	12979								
LYKYKVKI	IRLYSGHIALAWDD	12980								
LYKYKVKI	IRLYSGHIALAWDD	12981								
LYKYKVKI	IRLYSGHIALAWDD	12982								
LYKYKVKI	IRLYSGHIALAWDD	12983								
LYKYKVKI	IRLYSGHIALAWDD	12984								
LYKYKVKI	IRLYSGHIALAWDD	12985								
LYKYKVKI	IRLYSGHIALAWDD	12986								
LYKYKVKI	IRLYSGHIALAWDD	12987								
LYKYKVKI	IRLYSGHIALAWDD	12988								
LYKYKVKI	IRLYSGHIALAWDD	12989								
LYKYKVKI	IRLYSGHIALAWDD	12990								
LYKYKVKI	IRLYSGHIALAWDD	12991								
LYKYKVKI	IRLYSGHIALAWDD	12992								
LYKYKVKI	IRLYSGHIALAWDD	12993								
LYKYKVKI	IRLYSGHIALAWDD	12994								
LYKYKVKI	IRLYSGHIALAWDD	12995								
LYKYKVKI	IRLYSGHIALAWDD	12996								
LYKYKVKI	IRLYSGHIALAWDD	12997								
LYKYKVKI	IRLYSGHIALAWDD	12998								
LYKYKVKI	IRLYSGHIALAWDD	12999								
LYKYKVKI	IRLYSGHIALAWDD	13000								
LYKYKVKI	IRLYSGHIALAWDD	13001								
LYKYKVKI	IRLYSGHIALAWDD	13002								
LYKYKVKI	IRLYSGHIALAWDD	13003								
LYKYKVKI	IRLYSGHIALAWDD	13004								
LYKYKVKI	IRLYSGHIALAWDD	13005								
LYKYKVKI	IRLYSGHIALAWDD	13006								
LYKYKVKI	IRLYSGHIALAWDD	13007								
LYKYKVKI	IRLYSGHIALAWDD	13008								
LYKYKVKI	IRLYSGHIALAWDD	13009								
LYKYKVKI	IRLYSGHIALAWDD	13010								
LYKYKVKI	IRLYSGHIALAWDD	13011								
LYKYKVKI	IRLYSGHIALAWDD	13012								
LYKYKVKI	IRLYSGHIALAWDD	13013								
LYKYKVKI	IRLYSGHIALAWDD	13014								
LYKYKVKI	IRLYSGHIALAWDD	13015								
LYKYKVKI	IRLYSGHIALAWDD	13016								
LYKYKVKI	IRLYSGHIALAWDD	13017								

Sequence: 2921-2931-10
Table XIXb
HIV DR Super-Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w/19	DR7	DR8w/2	DR9	DRw/53	SEQ ID NO
LTPLEVTNLI	CVKLTILCYTLNCTD						12914
LVNNTNLS	LVNNTNLS						12915
VWNNSSNS	TNNWNNSSNSKST						12916
YRLNNTS	YKYEYRLNNTSAT						12917
HYCAPAGF	PIPHYCAPAGFAIL						12918
LKDQQLGI	ERYLKDQQLGIWGC						12919
YKYYKRIE	SELKYKYYKRIEPLG						12920
YKYYKRIE	SELKYKYYKRIEPLG						12921
LDKWSIWN	LLALDKWSIWNWFD						12922
LRVFAVLS	LIGLRVFAVLSVNI						12923
LNGLAEIE	QLLNGLAEIEVVI						12924
YKYYKRIE	LYKYYKYYKRIEPLVA						12925
LKGLRGWE	IKSLIKGLRGWELK						12926
YKYYKRIE	SELKYKYYKRIEPLG						12927
YKYYKRIE	SELKYKYYKRIEPLG						12928
YKYYKRIE	SELKYKYYKRIEPLG						12929
YKYYKRIE	SELKYKYYKRIEPLG						12930
YKYYKRIE	SELKYKYYKRIEPLG						12931
YKYYKRIE	SELKYKYYKRIEPLG						12932
YKYYKRIE	SELKYKYYKRIEPLG						12933
YKYYKRIE	SELKYKYYKRIEPLG						12934
YKYYKRIE	SELKYKYYKRIEPLG						12935
YKYYKRIE	SELKYKYYKRIEPLG						12936
YKYYKRIE	SELKYKYYKRIEPLG						12937
YKYYKRIE	SELKYKYYKRIEPLG						12938
YKYYKRIE	SELKYKYYKRIEPLG						12939
YKYYKRIE	SELKYKYYKRIEPLG						12940
YKYYKRIE	SELKYKYYKRIEPLG						12941
YKYYKRIE	SELKYKYYKRIEPLG						12942
YKYYKRIE	SELKYKYYKRIEPLG						12943
YKYYKRIE	SELKYKYYKRIEPLG						12944
YKYYKRIE	SELKYKYYKRIEPLG						12945
YKYYKRIE	SELKYKYYKRIEPLG						12946
YKYYKRIE	SELKYKYYKRIEPLG						12947
YKYYKRIE	SELKYKYYKRIEPLG						12948
YKYYKRIE	SELKYKYYKRIEPLG						12949
YKYYKRIE	SELKYKYYKRIEPLG						12950
YKYYKRIE	SELKYKYYKRIEPLG						12951
YKYYKRIE	SELKYKYYKRIEPLG						12952
YKYYKRIE	SELKYKYYKRIEPLG						12953
YKYYKRIE	SELKYKYYKRIEPLG						12954
YKYYKRIE	SELKYKYYKRIEPLG						12955
YKYYKRIE	SELKYKYYKRIEPLG						12956
YKYYKRIE	SELKYKYYKRIEPLG						12957
YKYYKRIE	SELKYKYYKRIEPLG						12958
YKYYKRIE	SELKYKYYKRIEPLG						12959
YKYYKRIE	SELKYKYYKRIEPLG						12960
YKYYKRIE	SELKYKYYKRIEPLG						12961
YKYYKRIE	SELKYKYYKRIEPLG						12962
YKYYKRIE	SELKYKYYKRIEPLG						12963

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2w61	DR2w282	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO
LLNATAIAV	AYSLNATAIAVAEG									12864
LEIFAIVLS	LGLAIFAIVLSYN									12865
VITQACPKV	NTSVITQACPKYSRE									12866
YWNLLQYV	YKTYWNLLQYVWSLE									12867
YKATKNSK	YKATKNSKNSKNSK									12868
FLVLSYN	LEIFAIVLSINVE									12869
INCKTSAT	YRLNGKTSATQAC									12870
LNATAIAV	VSLNATAIAVAEGT									12871
WNSSWSNKS	NYPWNSSWSNKSLE									12872
WNASWSNKS	NYPWNASWSNKSIED									12873
CTCTTTPVNN	GKLCICTTTPVNASV									12874
LLKLTWYGI	QQHLLKLTWYGIKQL									12875
LYKTKYVEI	RSBLLYKTKYVEI									12876
YKNSQKQ	YKNSQKQYKNSQKQ									12877
YKNSQKQ	EYVHNSQKQREFFY									12878
YWSOLENS	LLOYWSOLENSAVS									12879
IGAVFLOFL	AYGIGAVFLOFLGVA									12880
LAARTVEL	DPILAARTVELLGH									12881
LAARTVEL	SKLCICTTTPVNAS									12882
LCTCTTVPW	TQLLINGSLSAEGEI									12883
LLNGSLAEG	LYWYWGQELKNSNS									12884
YWGQELKNS	YWGQELKNSNS									12885
YKATKNSK	YKATKNSKNSKNSK									12886
YKATKNSK	YKATKNSKNSKNSK									12887
YKATKNSK	YKATKNSKNSKNSK									12888
YKATKNSK	YKATKNSKNSKNSK									12889
YKATKNSK	YKATKNSKNSKNSK									12890
YKATKNSK	YKATKNSKNSKNSK									12891
YKATKNSK	YKATKNSKNSKNSK									12892
YKATKNSK	YKATKNSKNSKNSK									12893
YKATKNSK	YKATKNSKNSKNSK									12894
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YKATKNSK	YKATKNSKNSKNSK									12901
YKATKNSK	YKATKNSKNSKNSK									12902
YKATKNSK	YKATKNSKNSKNSK									12903
YKATKNSK	YKATKNSKNSKNSK									12904
YKATKNSK	YKATKNSKNSKNSK									12905
YKATKNSK	YKATKNSKNSKNSK									12906
YKATKNSK	YKATKNSKNSKNSK									12907
YKATKNSK	YKATKNSKNSKNSK									12908
YKATKNSK	YKATKNSKNSKNSK									12909
YKATKNSK	YKATKNSKNSKNSK									12910
YKATKNSK	YKATKNSKNSKNSK									12911
YKATKNSK	YKATKNSKNSKNSK									12912
YKATKNSK	YKATKNSKNSKNSK									12913
YKATKNSK	YKATKNSKNSKNSK									12914
YKATKNSK	YKATKNSKNSKNSK									12915

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6/19	DR7	DR8/2	DR9	DR-s3	SEQ ID NO.
LNMTAAV	AYSLNMTAAVAG						12944
LNMTAAV	AYSLNMTAAVAG						12945
VTQACKV	NTSVTQACKVSE						12946
YVWNLLOTW	VLKYVWNLQYWSQE						12947
FAILKNDK	PAGFAILKCDKEN						12948
IFAVLSYN	LEIFIAVLSYNVR						12949
INQNTSAT	YINQNTSATQRC						12950
WNSWSKNS	YNSWSWSKNSLDE						12951
WNASWSKNS	NYPNASWSKNSYED						12952
ICITTPVNW	CKLICITTPVWNASW						12953
LLKLTYWGI	QQLKLTYWGHOL						12954
YFYRYVYDI	YFYRYVYDIL						12955
YFYRYVYDI	YFYRYVYDIL						12956
YFYRYVYDI	YFYRYVYDIL						12957
YFYRYVYDI	YFYRYVYDIL						12958
YFYRYVYDI	YFYRYVYDIL						12959
YFYRYVYDI	YFYRYVYDIL						12960
YFYRYVYDI	YFYRYVYDIL						12961
YFYRYVYDI	YFYRYVYDIL						12962
YFYRYVYDI	YFYRYVYDIL						12963
YFYRYVYDI	YFYRYVYDIL						12964
YFYRYVYDI	YFYRYVYDIL						12965
YFYRYVYDI	YFYRYVYDIL						12966
YFYRYVYDI	YFYRYVYDIL						12967
YFYRYVYDI	YFYRYVYDIL						12968
YFYRYVYDI	YFYRYVYDIL						12969
YFYRYVYDI	YFYRYVYDIL						12970
YFYRYVYDI	YFYRYVYDIL						12971
YFYRYVYDI	YFYRYVYDIL						12972
YFYRYVYDI	YFYRYVYDIL						12973
YFYRYVYDI	YFYRYVYDIL						12974
YFYRYVYDI	YFYRYVYDIL						12975
YFYRYVYDI	YFYRYVYDIL						12976
YFYRYVYDI	YFYRYVYDIL						12977
YFYRYVYDI	YFYRYVYDIL						12978
YFYRYVYDI	YFYRYVYDIL						12979
YFYRYVYDI	YFYRYVYDIL						12980
YFYRYVYDI	YFYRYVYDIL						12981
YFYRYVYDI	YFYRYVYDIL						12982
YFYRYVYDI	YFYRYVYDIL						12983
YFYRYVYDI	YFYRYVYDIL						12984
YFYRYVYDI	YFYRYVYDIL						12985
YFYRYVYDI	YFYRYVYDIL						12986
YFYRYVYDI	YFYRYVYDIL						12987
YFYRYVYDI	YFYRYVYDIL						12988
YFYRYVYDI	YFYRYVYDIL						12989
YFYRYVYDI	YFYRYVYDIL						12990
YFYRYVYDI	YFYRYVYDIL						12991
YFYRYVYDI	YFYRYVYDIL						12992
YFYRYVYDI	YFYRYVYDIL						12993
YFYRYVYDI	YFYRYVYDIL						12994
YFYRYVYDI	YFYRYVYDIL						12995
YFYRYVYDI	YFYRYVYDIL						12996
YFYRYVYDI	YFYRYVYDIL						12997
YFYRYVYDI	YFYRYVYDIL						12998
YFYRYVYDI	YFYRYVYDIL						12999
YFYRYVYDI	YFYRYVYDIL						13000
YFYRYVYDI	YFYRYVYDIL						13001
YFYRYVYDI	YFYRYVYDIL						13002
YFYRYVYDI	YFYRYVYDIL						13003
YFYRYVYDI	YFYRYVYDIL						13004
YFYRYVYDI	YFYRYVYDIL						13005
YFYRYVYDI	YFYRYVYDIL						13006
YFYRYVYDI	YFYRYVYDIL						13007
YFYRYVYDI	YFYRYVYDIL						13008
YFYRYVYDI	YFYRYVYDIL						13009
YFYRYVYDI	YFYRYVYDIL						13010
YFYRYVYDI	YFYRYVYDIL						13011
YFYRYVYDI	YFYRYVYDIL						13012
YFYRYVYDI	YFYRYVYDIL						13013

66501-9921450
Table XIXb
HIV DR Super-Motif Peptides with Binding Information

Cons-Sequence	Exemplary Sequence	DR6+19	DR7	DR3+2	DR9	DRw53	SEQ ID NO.
WASRELERF	HLVWASRELERFALN						13014
IPMFALSIE	PEVIMFALSISBOAT						13015
MRSLAEQA	STENMRSLAESIEA						13016
MTSPVSLD	IVKMTSPVSLDIHQ	0.0007	-0.0007	0.0130	0.0130		13018
IVKMTSPVSI	LAKIVKMTSPVSILD						13019
YPMYSPVSI	NKTYPMYSPVSLDI						13020
YPMYSPVSI	YPMYSPVSLDIHQ						13021
MTLTLNQ	YPMYSPVSLDIHQ						13022
WNTLTLNQ	YPMYSPVSLDIHQ						13023
ISPTLNW	YPMYSPVSLDIHQ	0.0012	0.0280	0.0008	0.0053		13024
VKNWMTL	YPMYSPVSLDIHQ						13025
IKCPNCKE	YPMYSPVSLDIHQ						13026
IPVQYRKR	YPMYSPVSLDIHQ						13027
YPMYSPVSI	YPMYSPVSLDIHQ						13028
WNTLTLNQ	YPMYSPVSLDIHQ						13029
WNTLTLNQ	YPMYSPVSLDIHQ						13030
WNTLTLNQ	YPMYSPVSLDIHQ						13031
WNTLTLNQ	YPMYSPVSLDIHQ						13032
WNTLTLNQ	YPMYSPVSLDIHQ						13033
WNTLTLNQ	YPMYSPVSLDIHQ						13034
WNTLTLNQ	YPMYSPVSLDIHQ						13035
WNTLTLNQ	YPMYSPVSLDIHQ						13036
WNTLTLNQ	YPMYSPVSLDIHQ						13037
WNTLTLNQ	YPMYSPVSLDIHQ						13038
WNTLTLNQ	YPMYSPVSLDIHQ						13039
WNTLTLNQ	YPMYSPVSLDIHQ						13040
WNTLTLNQ	YPMYSPVSLDIHQ						13041
WNTLTLNQ	YPMYSPVSLDIHQ						13042
WNTLTLNQ	YPMYSPVSLDIHQ						13043
WNTLTLNQ	YPMYSPVSLDIHQ						13044
WNTLTLNQ	YPMYSPVSLDIHQ						13045
WNTLTLNQ	YPMYSPVSLDIHQ						13046
WNTLTLNQ	YPMYSPVSLDIHQ						13047
WNTLTLNQ	YPMYSPVSLDIHQ						13048
WNTLTLNQ	YPMYSPVSLDIHQ						13049
WNTLTLNQ	YPMYSPVSLDIHQ						13050
WNTLTLNQ	YPMYSPVSLDIHQ						13051
WNTLTLNQ	YPMYSPVSLDIHQ						13052
WNTLTLNQ	YPMYSPVSLDIHQ						13053
WNTLTLNQ	YPMYSPVSLDIHQ						13054
WNTLTLNQ	YPMYSPVSLDIHQ						13055
WNTLTLNQ	YPMYSPVSLDIHQ						13056
WNTLTLNQ	YPMYSPVSLDIHQ						13057
WNTLTLNQ	YPMYSPVSLDIHQ						13058
WNTLTLNQ	YPMYSPVSLDIHQ						13059
WNTLTLNQ	YPMYSPVSLDIHQ						13060
WNTLTLNQ	YPMYSPVSLDIHQ						13061
WNTLTLNQ	YPMYSPVSLDIHQ						13062
WNTLTLNQ	YPMYSPVSLDIHQ						13063

Table XIXb

CRFMIYKQAFDLSFF
CFKLVVPYDPREVEEA

655007-29027-60
Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DRGw19	DR7	DRsw2	DR9	DRw53	SFQ ID NO.
INTVATLYC	KSLFNTVATLYCVHIQ						13064
IPMTALSE	PEVPIPTALSEGGAT						13065
LASLAKLPG	LSLAKLPG						13066
LENTVATLYC	LSLEFNTVATLYCVH						13067
MTALSEGA	LSLEFNTVATLYCVH						13068
WDVHPYHA	VIPMTALSEGAHQ						13069
IVMTSPTS	AAEWDVRVHPVHAQ						13070
LEREALNPG	LSLELEALNPGELLE						13071
IVMTSPTS	LSLELEALNPGELLE						13072
WDVHPYHA	WDVHPYHA						13073
VIPMTALS	WDVHPYHA						13074
VIPMTALS	WDVHPYHA						13075
VRMTSPTS	VRMTSPTS						13076
LGRWFSNK	ANFLGRWFSNKGRP						13077
LTSLSLPG	LYPLTSLSLFOND						13078
MTSPTSIL	LYPLTSLSLFOND						13079
YPLASLSL	KKXKLKHVWASRE						13080
YPLASLSL	VRMTSPTSILDRQG						13081
LTSLSLFG	LYPLTSLSLFOND						13082
MAALNTVUGH	DI-NMAALNTVUGHQA						13083
IDVKTKEA	HQRIDVKDTKEALDK						13084
IGWMTSNP	QFGQWMTSNP						13085
YPLASLSL	YPLASLSL						13086
YPLASLSL	DKELYPLASLSLFG						13087
VHOALSPT	GVHVAHQAALSRILMA						13088
YPLASLSL	REFAVNRGLLETSECC						13089
ELONPPEL	KELYPLASLSLPGN						13090
YPLASLSL	KONYPLASLSLPGN						13091
LAEMSQVQ	ANFLKQWFSNKGRP						13092
LGRWFSNK	ANFLKQWFSNKGRP						13093
LNFLGLETA	REFALNFGLETAEGC						13094
YPLASLSL	KELYPLASLSLPGN						13095
WQNTYTPG	QFGQWMTSNP						13096
YPLASLSL	GVHVAHQAALSRILMA						13097
YPLASLSL	REFAVNRGLLETSECC						13098
YPLASLSL	KONYPLASLSLPGN						13099
YPLASLSL	KONYPLASLSLPGN						13100
YPLASLSL	REFAVNRGLLETSECC						13101
YPLASLSL	KONYPLASLSLPGN						13102
YPLASLSL	KONYPLASLSLPGN						13103
YPLASLSL	KONYPLASLSLPGN						13104
YPLASLSL	KONYPLASLSLPGN						13105
YPLASLSL	KONYPLASLSLPGN						13106
YPLASLSL	KONYPLASLSLPGN						13107
YPLASLSL	KONYPLASLSLPGN						13108
YPLASLSL	KONYPLASLSLPGN						13109
YPLASLSL	KONYPLASLSLPGN						13110
YPLASLSL	KONYPLASLSLPGN						13111
YPLASLSL	KONYPLASLSLPGN						13112
YPLASLSL	KONYPLASLSLPGN						13113

Table XIX.b
HIV DR Super Motif Peptides with Binding Information

[illegible]

665007-20021460
Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VGWFAIRER	SSVGWFAIRERMR						13114
WCFLLVYIE	TWCFLLVYIEPK						13115
FKLAPMIR	FKSLAPMIRMR						13116
VPLRMITK	GVCEKLVPLRMIEVE						13117
LLQTGADDT	RVQVPLRMITKGF						13118
WMQGVLIPI	KEALLDTGADDTYLE						13119
YQYNVLQGS	PELWMQGVLIPIPKWT		-0.0003				13120
YQYNVLQGS	GRYQYNVLQGVKWK						13121
YQYNVLQGS	DKQPRKLTATITSL						13122
YQYNVLQGS	YQYNVLQGVKWK		-0.0005				13123
LDLTHLEK	INQLDLTHLEKUIL						13124
LDVGDAYS	VTVLVDVGDAYSFVPL						13125
MDLLYQSD	YQYMDLLYQSDLEI						13126
VIPAETQE	EAETVIPAETQETAY						13127
WKBEGAVVI	KLWKBEGAVVIQDN						13128
YQSDTHLE	YQSDTHLEKCTI	0.0450	0.2400	0.0450	0.2100		13129
WKBEGAVVI	KLWKBEGAVVIQDN						13130
WKBEGAVVI	WKBEGAVVIQDN						13131
WKBEGAVVI	WKBEGAVVIQDN						13132
WKBEGAVVI	WKBEGAVVIQDN						13133
WKBEGAVVI	WKBEGAVVIQDN						13134
WKBEGAVVI	WKBEGAVVIQDN						13135
WKBEGAVVI	WKBEGAVVIQDN						13136
WKBEGAVVI	WKBEGAVVIQDN						13137
WKBEGAVVI	WKBEGAVVIQDN						13138
WKBEGAVVI	WKBEGAVVIQDN						13139
WKBEGAVVI	WKBEGAVVIQDN						13140
WKBEGAVVI	WKBEGAVVIQDN						13141
WKBEGAVVI	WKBEGAVVIQDN						13142
WKBEGAVVI	WKBEGAVVIQDN						13143
WKBEGAVVI	WKBEGAVVIQDN						13144
WKBEGAVVI	WKBEGAVVIQDN						13145
WKBEGAVVI	WKBEGAVVIQDN						13146
WKBEGAVVI	WKBEGAVVIQDN						13147
WKBEGAVVI	WKBEGAVVIQDN						13148
WKBEGAVVI	WKBEGAVVIQDN						13149
WKBEGAVVI	WKBEGAVVIQDN						13150
WKBEGAVVI	WKBEGAVVIQDN						13151
WKBEGAVVI	WKBEGAVVIQDN						13152
WKBEGAVVI	WKBEGAVVIQDN						13153
WKBEGAVVI	WKBEGAVVIQDN						13154
WKBEGAVVI	WKBEGAVVIQDN						13155
WKBEGAVVI	WKBEGAVVIQDN						13156
WKBEGAVVI	WKBEGAVVIQDN						13157
WKBEGAVVI	WKBEGAVVIQDN						13158
WKBEGAVVI	WKBEGAVVIQDN						13159
WKBEGAVVI	WKBEGAVVIQDN						13160
WKBEGAVVI	WKBEGAVVIQDN						13161
WKBEGAVVI	WKBEGAVVIQDN						13162
WKBEGAVVI	WKBEGAVVIQDN						13163

Table XIXb

388

Table X1b
HIV DR Super Motif Peptides with Binding Information

Conc Sequence	Exemplary Sequence	DR6w19	DK7	DR3w2	DR9	DRw53	SEQ ID NO.
VIVYVMDLL	PEHVIYVMDLLTVG						13164
LKKKASVTV	PAGLKAKSVTVLDV	0.0140					13165
YPRKAKKII	IKVYPRKAKIURDY	0.0030					13166
FQITLWOR	SSSFQITLWQRLV	0.0006					13167
WVQKTPR	ESSWVQKTPRFLV						13168
YVQVQKTPR	YVQVQKTPRFLV						13169
FNKLGKGY	QEFENKLGKGYAKM						13170
YKQKQKQ	ATDIQKQKQKQK						13171
YKQKQAGDD	IRDYKQKQAGDDCVA	0.0530		0.0250	0.0860		13172
WRAMASDFN	HSWRAMASDFNPLV						13173
IKQGPENP	EKKSKQGPENPTPT						13174
YKQKQKQ	ALGQKQKQKQKQ	-0.0005					13175
IFQKQKQ	PAIFQKQKQKQKQ						13176
IFQKQKQ	PAIFQKQKQKQKQ						13177
FQSSMTKIL	PAIFQSSMTKILFP	0.1100	0.7390	0.0140	0.9100		13178
FUPSRNE	YTAFTFUSRNETG						13179
IFQSSMTKI	SPAIFQSSMTKILEP	0.2300	0.3700	0.0150	2.1000		13180
IEQKQKQ	QKQKQKQKQKQK						13181
YKQKQKQ	QKQKQKQKQKQK						13182
YKQKQKQ	QKQKQKQKQKQK						13183
YKQKQKQ	QKQKQKQKQKQK						13184
YKQKQKQ	QKQKQKQKQKQK						13185
YKQKQKQ	QKQKQKQKQKQK						13186
YKQKQKQ	QKQKQKQKQKQK						13187
YKQKQKQ	QKQKQKQKQKQK						13188
YKQKQKQ	QKQKQKQKQKQK						13189
YKQKQKQ	QKQKQKQKQKQK						13190
YKQKQKQ	QKQKQKQKQKQK						13191
YKQKQKQ	QKQKQKQKQKQK						13192
YKQKQKQ	QKQKQKQKQKQK						13193
YKQKQKQ	QKQKQKQKQKQK						13194
YKQKQKQ	QKQKQKQKQKQK						13195
YKQKQKQ	QKQKQKQKQKQK						13196
YKQKQKQ	QKQKQKQKQKQK						13197
YKQKQKQ	QKQKQKQKQKQK						13198
YKQKQKQ	QKQKQKQKQKQK						13199
YKQKQKQ	QKQKQKQKQKQK						13200
YKQKQKQ	QKQKQKQKQKQK						13201
YKQKQKQ	QKQKQKQKQKQK						13202
YKQKQKQ	QKQKQKQKQKQK						13203
YKQKQKQ	QKQKQKQKQKQK						13204
YKQKQKQ	QKQKQKQKQKQK						13205
YKQKQKQ	QKQKQKQKQKQK						13206
YKQKQKQ	QKQKQKQKQKQK						13207
YKQKQKQ	QKQKQKQKQKQK						13208
YKQKQKQ	QKQKQKQKQKQK						13209
YKQKQKQ	QKQKQKQKQKQK						13210
YKQKQKQ	QKQKQKQKQKQK						13211
YKQKQKQ	QKQKQKQKQKQK						13212
YKQKQKQ	QKQKQKQKQKQK						13213

HIV DR Super Motif Peptides with Binding Information

[illegible]

665007-232740 Table XIXb HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DRw19	DR7	DR8x2	DR9	DRw53	SEQ ID NO.
LRGAKALTD	CKLLRGAKALTDVP						1314
LVSSGRKV	VDKLVSSGRKVLEL						1315
FLKLAGRW	TAYELLKLAGRWPK						1316
LAUQGGSE	HAUQGGSESNAT						1317
LAUQGGSE	HAUQGGSESNAT						1318
VKVIHTD	RWPKVKHIDDSNF						1319
WPKVHTD	AGRWPKVHTDNGS						1320
YELKLAGR	ETA YELKLAGRWPK						1321
ICOKKAGT	LIEDOKKAGTYLV		0.0041				1322
YAKEIVAS	ALPIYAKEIVASCK						1323
LEKIVILVA	CHLEKIVILVAVH						1324
LKWGITPD	ELLKLGWGITPKKH						1325
VILVAHVA	EGLKLVAVHVRASGY						1326
LAWVPAHG	KYVLAWVPAHGIGG	0.0014	0.1400	0.2500	0.3000		1327
YDQILIEC	WQYDQILIECCKC	0.0010	1.4000	1.6000	0.5000		1328
YLAWPAHK	ELAYLAWPAHKEG						1329
IGNRLTQI	ELAYLAWPAHKEG						1330
IGNRLTQI	WNGIGNRLTQIQC		0.0012				1331
WQRLVLT	QTLWQRLVLTGKG						1332
VSLTETNQ	QKVVSLTETNQKTE						1333
VYLAWVPAH	KEKYVLAWVPAHGI						1334
IGNRLTQI	ELIGNRLTQIATVP						1335
LYNQIEQL	ESELVYNQIEQLKK						1336
LYNQIEQL	ESELVYNQIEQLKK		0.0040				1337
YFSVLDKQ	GDATFSVLDKDFRK						1338
IGRNALTOI	VNIGRNALTOIQC						1339
LYNQIEQL	ELYNQIEQLKK						1340
LYNQIEQL	ELYNQIEQLKK						1341
WQRLVLT	QTLWQRLVLTGKG						1342
WQRLVLT	QTLWQRLVLTGKG						1343
YAGIKVQL	SQTYAGIKVQLCKL						1344
YAGIKVQL	SQTYAGIKVQLCKL						1345
YAGIKVQL	SQTYAGIKVQLCKL						1346
YAGIKVQL	SQTYAGIKVQLCKL						1347
YAGIKVQL	SQTYAGIKVQLCKL						1348
YAGIKVQL	SQTYAGIKVQLCKL						1349
YAGIKVQL	SQTYAGIKVQLCKL						1350
YAGIKVQL	SQTYAGIKVQLCKL						1351
YAGIKVQL	SQTYAGIKVQLCKL						1352
YAGIKVQL	SQTYAGIKVQLCKL						1353
YAGIKVQL	SQTYAGIKVQLCKL						1354
YAGIKVQL	SQTYAGIKVQLCKL						1355
YAGIKVQL	SQTYAGIKVQLCKL						1356
YAGIKVQL	SQTYAGIKVQLCKL						1357
YAGIKVQL	SQTYAGIKVQLCKL						1358
YAGIKVQL	SQTYAGIKVQLCKL						1359
YAGIKVQL	SQTYAGIKVQLCKL						1360
YAGIKVQL	SQTYAGIKVQLCKL						1361
YAGIKVQL	SQTYAGIKVQLCKL						1362
YAGIKVQL	SQTYAGIKVQLCKL						1363

65001-5921160 Table XIXb

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6wt19	DR7	DR8wt2	DR9	DRwt53	SEQ ID NO.
FTDSTNNE	YTAETFTSTNNEGK						13244
LEDRLNPK	DTVLEDRLNPKWKPK						13245
LDIVNPLE	AKALDIDVNLPLETAE						13246
LVTHIGGQ	QVTHLVTHIGGQK						13267
MDGQVQVQV	YKMRGQVQVQVQKQL						13268
VKTHTDNG	KWPKVKTHTDNGSNF						13269
VQVPLPEK	KWTQVQVPLPEKDSW						13270
WPKVKTHTD	AGRWPKVKTHTDNGS						13271
WQRLVTVK	ITLWQRLVTVKDGK						13272
WTQVQLP	PKTQVQLPQVQVQVQK						13273
YKQVQVQVQ	PKYKQVQVQVQVQVQK						13274
LDIASDI	ERADIASDIQDTE						13275
IVDIADI	GERVDIADIQDTK						13276
LEENLPK	DTVLLEENLPKWKPK						13277
LOATLALQ	TELOATLALQVQVQVQK						13278
YKQVQVQVQ	TEYKQVQVQVQVQVQK						13279
VYHADIQ	ERVDIADIQDTE						13280
YDQVPEG	VRCYDQVPEGCRK						13281
FNFPQTLW	VPTFNFPQTLWQRP						13282
IGRNALTLQ	YNGIRNALTLQDCT						13283
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13284
LVNPLETE	TKALTEVNPLETAE						13285
MSIVGWK	KIAMESIVGWKTK						13286
VPRKVKII	IKVYVPRKVKIURDY						13287
VPSFQIT	QQTYSFSPQITLWQ						13288
WYQLETH	YKQVQVQVQVQVQVQK						13289
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13290
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13291
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13292
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13293
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13294
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13295
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13296
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13297
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13298
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13299
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13300
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13301
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13302
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13303
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13304
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13305
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13306
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13307
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13308
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13309
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13310
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13311
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13312
YKQVQVQVQ	YKQVQVQVQVQVQVQK						13313

66999769321160 HIV DR Super Motif Peptides with Binding Information

Comp Sequence	Exemplary Sequence	DR1	DR2w/DR2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LYLALAL	VGSLOYLALALPKK								13114
LYLALAL	VGSLOYLALALPKK								13115
LYLALAL	VGSLOYLALALPKK								13116
LYLALAL	VGSLOYLALALPKK								13117
LYLALAL	VGSLOYLALALPKK								13118
LYLALAL	VGSLOYLALALPKK								13119
LYLALAL	VGSLOYLALALPKK								13120
LYLALAL	VGSLOYLALALPKK								13121
LYLALAL	VGSLOYLALALPKK								13122
LYLALAL	VGSLOYLALALPKK								13123
LYLALAL	VGSLOYLALALPKK								13124
LYLALAL	VGSLOYLALALPKK								13125
LYLALAL	VGSLOYLALALPKK								13126
LYLALAL	VGSLOYLALALPKK								13127
LYLALAL	VGSLOYLALALPKK								13128
LYLALAL	VGSLOYLALALPKK								13129
LYLALAL	VGSLOYLALALPKK								13130
LYLALAL	VGSLOYLALALPKK								13131
LYLALAL	VGSLOYLALALPKK								13132
LYLALAL	VGSLOYLALALPKK								13133
LYLALAL	VGSLOYLALALPKK								13134
LYLALAL	VGSLOYLALALPKK								13135
LYLALAL	VGSLOYLALALPKK								13136
LYLALAL	VGSLOYLALALPKK								13137
LYLALAL	VGSLOYLALALPKK								13138
LYLALAL	VGSLOYLALALPKK								13139
LYLALAL	VGSLOYLALALPKK								13140
LYLALAL	VGSLOYLALALPKK								13141
LYLALAL	VGSLOYLALALPKK								13142
LYLALAL	VGSLOYLALALPKK								13143
LYLALAL	VGSLOYLALALPKK								13144
LYLALAL	VGSLOYLALALPKK								13145
LYLALAL	VGSLOYLALALPKK								13146
LYLALAL	VGSLOYLALALPKK								13147
LYLALAL	VGSLOYLALALPKK								13148
LYLALAL	VGSLOYLALALPKK								13149
LYLALAL	VGSLOYLALALPKK								13150
LYLALAL	VGSLOYLALALPKK								13151
LYLALAL	VGSLOYLALALPKK								13152
LYLALAL	VGSLOYLALALPKK								13153
LYLALAL	VGSLOYLALALPKK								13154
LYLALAL	VGSLOYLALALPKK								13155
LYLALAL	VGSLOYLALALPKK								13156
LYLALAL	VGSLOYLALALPKK								13157
LYLALAL	VGSLOYLALALPKK								13158
LYLALAL	VGSLOYLALALPKK								13159
LYLALAL	VGSLOYLALALPKK								13160
LYLALAL	VGSLOYLALALPKK								13161
LYLALAL	VGSLOYLALALPKK								13162
LYLALAL	VGSLOYLALALPKK								13163

0.0200

0.0054

Table XIXb

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w/9	DK7	DR6w/2	DR9	DRw/33	SEQ ID NO
LOYLALTAL	VGSLOYLALTALIKP						13114
LGHQYSVIEW	DWHLGHQYSIEWRLR						13115
WVWVWVWVWVWVWV	WVWVWVWVWVWVWV						13116
WVDFSSSA	HLTYDFDSSSAIN						13117
WVGLHTIGER	HTTYWGLHTIGERDWH						13118
IRKTVNSLVK	RMRIKTVNSLVKJHIM						13119
WVLOGQYSVIEW	DWHLGQQYSIEWRCK						13120
WVGHRTYS	WNSLVKGHRTYSKKA						13121
WVGLHARLV	EVHPIGLHARLVRET						13122
WVWVWVWVWVWVWV	WVWVWVWVWVWVWV						13123
WVGLHTIGER	SLQYGLHTIGERKPK						13124
WVGLHTIGER	SLQYGLHTIGERKPK						13125
WVGLHTIGER	SLQYGLHTIGERKPK						13126
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WVGLHTIGER	SLQYGLHTIGERKPK						13320
WVGLHTIGER	SLQYGLHTIGERKPK						13321
WVGLHTIGER	SLQYGLHTIGERKPK						

Table XIXB

HIV DR Super Motif Peptides with Binding Information

[illegible]

663001-2327160
 Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Cone Sequence	Exemplary Sequence	DGdw19	DR7	DR8w2	DR9	DRw33	SEQ ID NO
LPQRKIDRL	RKLQRKIDRLDR						13364
IVVWTVFI	IATVWTVFIETFR						13365
VVWTVFIE	IATVWTVFIETFR						13366
IVETFRGLGK	IVETFRGLGK						13367
SLGKGLGK	SLGKGLGK						13368
ILAVALV	IVPVTIVETFRKIL						13369
WTIVETFR	IQLAIVAVVAGII						13370
LAVALVA							

065001.29821460

Table XXa

HIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	VPTDINQOE	53	83	HACVPTDINQOEVL	85	12	19	13371
ENV	YLDQQLG	31	48	VERYLDQQLGHWG	669	18	28	13372
ENV	MIEDIISLW	29	45	VEQMIEDIISLWDS	114	17	28	13373
ENV	VSEFPIH	29	45	GRKVSSEFPIHYCA	230	8	28	13374
ENV	LAVERYLKD	26	41	AKVLAVERYLKDQQL	230	15	23	13375
ENV	VKLEIPLVA	26	41	GVVYVKEAETITLQK	564	15	23	13376
ENV	VWKEATITL	22	36	GVVYVKEAETITLQK	564	22	34	13377
ENV	LAWDDIASK	22	36	FLALAWDDIASKLQF	52	34	30	13378
ENV	LGWEGLYL	20	31	IVTLIEESONQQRN	849	19	30	13379
ENV	LDLQKWSL	18	28	GIURLGWEGLYLWNL	737	07	11	13380
ENV	YLDQQLG	18	28	QELLELDKWSLWNL	753	07	23	13381
ENV	MQVEGKAM	15	23	IVHWQVEGKAMTAP	669	11	11	13382
ENV	IBEEGGRD	13	20	VERYLDQQLGHWG	669	12	19	13383
ENV	MINNENQTN	13	20	NDNANNENQTNSTW	827	08	13	13384
ENV	IRSENLNN	10	16	NGSLAEEVIRSEN	827	02	3	13385
ENV	INEEAERWD	10	16	QDILLALDKWSLWNL	309	04	6	13386
ENV	LAVERYLKD	10	16	ARVLAVERYLKDQQL	753	05	8	13387
ENV	IRSENLNN	10	16	EHRSRBNLNNKTS	664	10	8	13388
ENV	LAVERYLKD	10	16	MTNNEEAERWDRLH	721	03	5	13389
ENV	LAVERYLKD	10	16	KEINNEEAERWDRLH	721	18	28	13390
ENV	LAVERYLKD	10	16	EKASFEVPMFSL	182	36	56	13391
ENV	LAVERYLKD	10	16	KARVLAELAMQSOVTHS	383	09	14	13392
ENV	LAVERYLKD	10	16	AMOMKDTTNEEAAL	218	30	47	13393
ENV	LAVERYLKD	10	16	WVVAVVEKAESFEVI	176	38	14	13394
ENV	LAVERYLKD	10	16	FKTLRAEQALQEVYK	325	10	16	13395
ENV	LAVERYLKD	10	16	WVVAVVEKAESFEVI	218	22	34	13396
ENV	LAVERYLKD	10	16	KARVLAELAMQSOVTHS	383	03	5	13397
ENV	LAVERYLKD	10	16	LKJIEEQNKSKKA	103	09	14	13398
ENV	LAVERYLKD	10	16	FKTLRAEQALQEVYK	325	10	16	13399
ENV	LAVERYLKD	10	16	FKTLRAEQALQEVYK	325	10	16	13400
ENV	LAVERYLKD	10	16	TKQTTPDQNTTPTP	192	15	22	13401
ENV	LAVERYLKD	10	16	LSFLEKGGELGGLI	114	14	22	13402
ENV	LAVERYLKD	10	16	TSQFFPDWQNTTPTP	192	17	27	13403
ENV	LAVERYLKD	10	16	VGA VSDRLKRGHAI	46	11	17	13404
ENV	LAVERYLKD	10	16	IVQYMDLLYVGSILE	369	59	92	13405
ENV	LAVERYLKD	10	16	ISKGPBPYNTPTF	236	28	45	13406
ENV	LAVERYLKD	10	16	GYELHPDKWTVQIQ	420	59	92	13407
ENV	LAVERYLKD	10	16	EYNNVTSQSQVQIQ	420	59	92	13408
ENV	LAVERYLKD	10	16	QWPLTEBKALTEL	838	55	86	13409
ENV	LAVERYLKD	10	16	QWPLTEBKALTEL	838	55	86	13410
ENV	LAVERYLKD	10	16	SGVIEAVIPAETQ	210	26	41	13411
ENV	LAVERYLKD	10	16	RCVLFDDIDKQOE	749	32	50	13412
ENV	LAVERYLKD	10	16	PPVVAKEIVASCKK	794	47	34	13413
ENV	LAVERYLKD	10	16	KCOLKGEAMIGQYDC	794	47	34	13414
ENV	LAVERYLKD	10	16	DLYVGSIDRLGQHA	794	47	34	13415
ENV	LAVERYLKD	10	16	KAKIRDYGGQMGAD	1017	36	56	13416
ENV	LAVERYLKD	10	16	KAKIRDYGGQMGAD	1017	36	56	13417
ENV	LAVERYLKD	10	16	KAKIRDYGGQMGAD	1017	36	56	13418
ENV	LAVERYLKD	10	16	KAKIRDYGGQMGAD	1017	36	56	13419
ENV	LAVERYLKD	10	16	KAKIRDYGGQMGAD	1017	36	56	13420

Table XXa
HIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Consistency (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Consistency (%)	SEQ ID NO.
POL	MASDFNLP	47	73	WRAMSDFNLPVVA	771	24	38	13401
POL	PYYDGAAR	43	67	AETTYDGAARETK	629	31	31	13402
POL	IHTDNGSNF	42	66	YAVYHTDNGSNFTSK	492	31	27	13403
POL	ILKEPVGV	41	65	YVAVILKEPVGV	409	36	56	13404
POL	YVQFKNL	39	61	TYVQFKNLKTG	530	39	61	13405
POL	YVIRGKQ	39	61	VIRGYVIRGKQDAE	506	26	41	13406
POL	YVIRGKQ	39	61	KAGYVIRGKQKVVVS	646	19	30	13407
POL	LYTEAELEI	37	58	IVPLYTEAELEIEN	481	12	19	13408
POL	VIQDSDIK	37	58	GAVYIQDSDIKVVP	999	37	58	13409
POL	IATDIQTE	35	55	IDIATDIQTELOK	953	21	38	13410
POL	INNETGIR	32	51	ISNNETGIRYQY	514	21	48	13411
POL	LYAEQKQD	30	47	LYAEQKQDQKQ	514	09	14	13412
POL	YVIRGKQ	28	44	LYVICTEYKSGIS	221	14	22	13413
POL	YVIRGKQ	28	44	EPVGAETVYDGA	624	20	31	13414
POL	IKQETWTV	27	42	RLIQETWTVWTD	582	09	14	13415
POL	IKQETWTV	26	41	WAGIKQETWTVNQ	884	21	33	13416
POL	MAGDDCVAG	25	39	QKQMGDDCVAGRD	1025	23	36	13417
POL	IKQETWTV	20	31	EQIKQETWTVWTD	1035	19	30	13418
POL	MAGDDCVAS	19	30	EQIKQETWTVWTD	1035	18	29	13419
POL	WLDQDPR	16	25	WLDQDPRKQ	304	11	17	13420
POL	YVIRGKQ	16	25	WYQLEKRVHGAET	618	16	25	13421
POL	YVIRGKQ	16	25	KLWYQLEKRVHGAET	616	16	25	13422
POL	IKQETWTV	15	23	KLPIQETWTVWVTE	592	05	6	13423
POL	IKQETWTV	14	22	AFESSEQTUANSIT	4	05	16	13424
POL	IKQETWTV	14	22	YVIRGKQ	85	09	14	13425
POL	IKQETWTV	14	22	YVIRGKQ	564	09	14	13426
POL	IKQETWTV	14	22	YVIRGKQ	564	11	17	13427
POL	IKQETWTV	14	22	YVIRGKQ	564	13	20	13428
POL	IKQETWTV	13	20	DDTVLEENLPGKWK	116	11	17	13429
POL	IKQETWTV	13	20	EQIKQETWTVWTD	715	07	11	13430
POL	IKQETWTV	13	20	DDTVLEENLPGKWK	116	13	20	13431
POL	IKQETWTV	12	19	QTVLPKQSDTVND	481	12	19	13432
POL	IKQETWTV	12	19	QTVLPKQSDTVND	481	12	19	13433
POL	IKQETWTV	11	17	KALIKQSDTVND	1017	06	9	13434
POL	IKQETWTV	11	17	KEKVERETIDPAVQ	95	01	2	13435
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13436
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13437
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13438
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13439
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13440
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13441
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13442
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13443
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13444
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13445
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13446
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13447
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13448
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13449
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13450
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13451
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13452
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13453
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13454
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13455
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13456
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13457
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13458
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13459
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13460
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13461
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13462
POL	IKQETWTV	11	17	VKALIKQSDTVND	1017	01	2	13463

CoreSequence

[illegible]

665007-09921460 Table XXb HIV DR 3a Motif Peptides with Binding Information

Conc Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VPTDPOE	HACVTPDNPQEVVL						13371
VLKQQLG	VERYLKDQQLGHWG						13372
MIEDISLW	VIQMHEDISLWDQS						13373
VSFETIH	OPKVSFETPHYCA						13374
LAVERYLD	AKHVAERYLDKQQL						13375
WVKEATIL	WVKEATILKQQL						13376
WVKEATIL	GVVYVKEATILFCA						13377
LAWDLRL	FLALAWDLRLSLCLF						13378
LIIESQNK	IVTLIIESQNKQEN						13379
LGWLEGLKYL	GLRLGWLEGLKYLWNL						13380
LELDKWSL	QLLELDKWSLWNL						13381
WVKEATIL	WVKEATILKQQL						13382
WVKEATIL	WVKEATILKQQL						13383
WVKEATIL	WVKEATILKQQL						13384
WVKEATIL	WVKEATILKQQL						13385
WVKEATIL	WVKEATILKQQL						13386
WVKEATIL	WVKEATILKQQL						13387
WVKEATIL	WVKEATILKQQL						13388
WVKEATIL	WVKEATILKQQL						13389
WVKEATIL	WVKEATILKQQL						13390
WVKEATIL	WVKEATILKQQL						13391
WVKEATIL	WVKEATILKQQL						13392
WVKEATIL	WVKEATILKQQL						13393
WVKEATIL	WVKEATILKQQL						13394
WVKEATIL	WVKEATILKQQL						13395
WVKEATIL	WVKEATILKQQL						13396
WVKEATIL	WVKEATILKQQL						13397
WVKEATIL	WVKEATILKQQL						13398
WVKEATIL	WVKEATILKQQL						13399
WVKEATIL	WVKEATILKQQL						13400
WVKEATIL	WVKEATILKQQL						13401
WVKEATIL	WVKEATILKQQL						13402
WVKEATIL	WVKEATILKQQL						13403
WVKEATIL	WVKEATILKQQL						13404
WVKEATIL	WVKEATILKQQL						13405
WVKEATIL	WVKEATILKQQL						13406
WVKEATIL	WVKEATILKQQL						13407
WVKEATIL	WVKEATILKQQL						13408
WVKEATIL	WVKEATILKQQL						13409
WVKEATIL	WVKEATILKQQL						13410
WVKEATIL	WVKEATILKQQL						13411
WVKEATIL	WVKEATILKQQL						13412
WVKEATIL	WVKEATILKQQL						13413
WVKEATIL	WVKEATILKQQL						13414
WVKEATIL	WVKEATILKQQL						13415
WVKEATIL	WVKEATILKQQL						13416
WVKEATIL	WVKEATILKQQL						13417
WVKEATIL	WVKEATILKQQL						13418
WVKEATIL	WVKEATILKQQL						13419
WVKEATIL	WVKEATILKQQL						13420

665007.29821460
Table XXb
HIV DR 3a Motif Peptides with Binding Information

ConSequence	Exemplar Sequence	DRI	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR3w12	SEQ ID NO
MASDFILRP	WRMAISPNLPYVYA	0.0021	-0.0005	0.0046	0.3900	0.0150	-0.0006		13421
MAKMR	AEITYDGAANBEIK								13422
HTIDNGNF	VKVVHTDNGNFTSA								13423
ILKEPHVGV	NRELKEPHGVYTD	0.3000	0.1500	-0.0014	0.1000	0.1900	-0.0007	0.0250	13424
HYQEPENL	TYQYQEPKNLKTG				-0.0017				13425
YVYDFSKDL	VHGVTYDYSKDLAE								13426
YVYDFRQK	KATVYDFRQK								13427
YVYDFRQK	KATVYDFRQK								13428
YVYDFRQK	KATVYDFRQK								13429
YVYDFRQK	KATVYDFRQK								13430
YVYDFRQK	KATVYDFRQK								13431
YVYDFRQK	KATVYDFRQK								13432
YVYDFRQK	KATVYDFRQK								13433
YVYDFRQK	KATVYDFRQK								13434
YVYDFRQK	KATVYDFRQK								13435
YVYDFRQK	KATVYDFRQK								13436
YVYDFRQK	KATVYDFRQK								13437
YVYDFRQK	KATVYDFRQK								13438
YVYDFRQK	KATVYDFRQK								13439
YVYDFRQK	KATVYDFRQK								13440
YVYDFRQK	KATVYDFRQK								13441
YVYDFRQK	KATVYDFRQK								13442
YVYDFRQK	KATVYDFRQK								13443
YVYDFRQK	KATVYDFRQK								13444
YVYDFRQK	KATVYDFRQK								13445
YVYDFRQK	KATVYDFRQK								13446
YVYDFRQK	KATVYDFRQK								13447
YVYDFRQK	KATVYDFRQK								13448
YVYDFRQK	KATVYDFRQK								13449
YVYDFRQK	KATVYDFRQK								13450
YVYDFRQK	KATVYDFRQK								13451
YVYDFRQK	KATVYDFRQK								13452
YVYDFRQK	KATVYDFRQK								13453
YVYDFRQK	KATVYDFRQK								13454
YVYDFRQK	KATVYDFRQK								13455
YVYDFRQK	KATVYDFRQK								13456
YVYDFRQK	KATVYDFRQK								13457
YVYDFRQK	KATVYDFRQK								13458
YVYDFRQK	KATVYDFRQK								13459
YVYDFRQK	KATVYDFRQK								13460
YVYDFRQK	KATVYDFRQK								13461
YVYDFRQK	KATVYDFRQK								13462
YVYDFRQK	KATVYDFRQK								13463

Table XXb
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	D86w19	DR7	D86w2	DR9	DRw53	SEQ ID NO.
MASDNLPP	WRA MASDNLPPVVA	-0.0002	-0.0014	0.0035			13421
FDGAKK	WRAVYVVAANRETK						13422
ILTEPSSE	VXVHTDNGSNTSA	0.0120	0.0033	0.0010	0.0210		13423
ILKEPVHGV	NREILKEPVHGVYTD						13424
IVQEPFKL	TVQIVQEPFKNLKTG						13425
VYVYDFSKDL	VGVYVYDFSKDLAE						13426
VYVYDFGRQK	KAGVYVYDFGRQKVS						13427
LTEAELEL	LVPLTEAELELAEIN						13428
WQDSDSK	WQVWQDSDSKVTP	0.0447	-0.0014	-0.0009			13429
INNETGR	INNETGRVYV						13430
LIABIKOG	SKDLIABIKOGQGOQ						13431
ICTEMEKSG	LVEICTEMEKSGKIS						13432
VGAETVVD	EPVGAETVYDGA						13433
IQKETWEIV	RLPIQKETWEIVTWD						13434
IKQREGIPY	WYQKQKQETQYVW	0.0123	-0.0014	-0.0009			13435
MACGDKVYAS	MACGDKVYASVW						13436
VLQDKFRK	ROLKQKQYVLAWV	-0.0003	-0.0005	-0.0015	0.0011		13437
YQLEKEPV	YQLEKEPVGAETV						13438
IKQETWEIV	WYQLEKEPVGAETV						13439
IKQETWEIV	WYQLEKEPVGAETV						13440
IKQETWEIV	WYQLEKEPVGAETV						13441
IKQETWEIV	WYQLEKEPVGAETV						13442
IKQETWEIV	WYQLEKEPVGAETV						13443
IKQETWEIV	WYQLEKEPVGAETV						13444
IKQETWEIV	WYQLEKEPVGAETV						13445
IKQETWEIV	WYQLEKEPVGAETV						13446
IKQETWEIV	WYQLEKEPVGAETV						13447
IKQETWEIV	WYQLEKEPVGAETV						13448
IKQETWEIV	WYQLEKEPVGAETV						13449
IKQETWEIV	WYQLEKEPVGAETV						13450
IKQETWEIV	WYQLEKEPVGAETV						13451
IKQETWEIV	WYQLEKEPVGAETV						13452
IKQETWEIV	WYQLEKEPVGAETV						13453
IKQETWEIV	WYQLEKEPVGAETV						13454
IKQETWEIV	WYQLEKEPVGAETV						13455
IKQETWEIV	WYQLEKEPVGAETV						13456
IKQETWEIV	WYQLEKEPVGAETV						13457
IKQETWEIV	WYQLEKEPVGAETV						13458
IKQETWEIV	WYQLEKEPVGAETV						13459
IKQETWEIV	WYQLEKEPVGAETV						13460
IKQETWEIV	WYQLEKEPVGAETV						13461
IKQETWEIV	WYQLEKEPVGAETV						13462
IKQETWEIV	WYQLEKEPVGAETV						13463

Table XXC
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Consistency (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Consistency (%)	SEQ ID NO.
ENV	MELDNWSEL	40	63	GQMDRNWSELYKY	550	37	58	13464
ENV	LYVQAKQLL	36	56	LYVQAKQLL	625	37	58	13465
ENV	IEAQILLQ	35	55	IEAQILLQ	642	42	62	13466
ENV	IEAQILLQ	27	44	IEAQILLQ	370	34	53	13467
ENV	VEREKRAH	23	37	TGEIHQAOHNI	370	07	11	13468
ENV	MYDEMEDI	23	36	RRVVEREKRAVIGGA	582	11	17	13469
ENV	AWDDLSLC	20	31	KNNMVEQMIEDISL	110	19	30	13470
ENV	LEITHSFN	20	31	LALA WDDLSLC LFS	850	18	28	13471
ENV	YDTEVINW	18	28	GDDLEITHSFNCG	426	15	23	13472
ENV	AGTDRIIE	17	27	AKATDTEVINWATH	571	15	23	13473
ENV	VQREKAVG	15	23	RYVQREKAVGICG	977	05	8	13474
ENV	IEAQILLQ	15	23	LAIEAQILLQVQ	927	07	11	13475
ENV	IEAQILLQ	12	19	LAIEAQOHLITV	642	08	13	13476
ENV	LKNDKAFN	12	19	FAILKNDKKNFTG	269	05	8	13477
GAG	ANPDCKIL	45	70	VQNAFDPCKITKAL	347	27	42	13478
GAG	PFKTLRAEQ	28	44	VDRFYKTLRAEQSQ	321	19	30	13479
GAG	AFQMRREF	27	42	VDRFYKTLRAEQSQ	321	19	30	13480
GAG	PFKTLRAEQ	27	35	VDRFYKTLRAEQSQ	321	19	30	13481
GAG	AFQMRREF	20	32	VDRFYKTLRAEQSQ	321	26	41	13482
GAG	IAKNCIAPR	18	29	EGHIAKNCIAPKKG	431	19	30	13483
GAG	ATQVKNWM	18	28	EGHIAKNCIAPKKG	431	10	16	13484
GAG	ATQVKNWM	15	23	AEQATQVKNWMTDT	330	14	22	13485
GAG	IAKNCIAPR	13	21	AEQATQVKNWMTDT	330	11	17	13486
GAG	IAKNCIAPR	13	21	EGHIAKNCIAPKKG	431	13	20	13487
GAG	ATQVKNWM	11	17	EGHIAKNCIAPKKG	431	13	20	13488
GAG	ATQVKNWM	11	17	VQNAFDPCKITKAL	347	06	9	13489
GAG	ATQVKNWM	10	16	AEQATQVKNWMTDT	330	11	17	13490
NEF	IPWSEKRP	18	28	LGKIPWSEKRPGRNF	470	14	16	13491
NEF	IPWSEKRP	11	17	LGKIPWSEKRPGRNF	470	11	17	13492
NEF	LYSKRQGE	18	28	LDGLYSKROEILD	171	10	16	13493
NEF	VPVDREVE	11	17	FKQVPVDREVEAN	312	06	9	13494
POL	MOTELHPDK	58	91	FMWQGLIRDKATVY	416	60	94	13495
POL	MYNLEKXII	56	89	MYNLEKXII	930	57	89	13496
POL	YISNVQDA	44	69	MYNLEKXII	930	45	80	13497
POL	YISNVQDA	39	61	VMSMFKELKICQV	903	43	67	13498
POL	MEKEGKSK	36	56	HEKYHISNVWRAMASDF	764	23	36	13499
POL	YTRDSRDL	34	53	LKXITQVQDQAHIL	910	23	36	13500
POL	ANRETKOP	30	50	CTBMEXGKGRSGIP	225	22	34	13501
POL	IQGQLLEAL	25	43	FRYTYRDSRDLWKG	975	22	34	13502
POL	YTRDSRDL	19	30	FRYTYRDSRDLWKG	975	22	34	13503
POL	YTRDSRDL	14	22	TKISGQLEKALIT	99	17	27	13504
POL	YTRDSRDL	13	20	SVPLDKQFKRYTFT	306	17	27	13505
POL	YTRDSRDL	10	16	FRYTYRDSRDLWKG	975	13	21	13506
REV	YHNNWRAMA	16	61	LKXITQVQDQAHIL	910	13	20	13507
REV	AEKRRERAR	39	59	HEKYHISNVWRAMASDF	764	06	9	13508
REV	AEKRRERAR	18	28	TROAKNRRRRWRAR	38	18	28	13509
REV	LLKTVRLIK	10	16	HEKYHISNVWRAMASDF	764	13	20	13510
VIF	VSIEVHIL	27	42	HPHSSEVHPLGDA	48	08	13	13511
VIF	VSIEVHIL	27	43	HPHSSEVHPLGDA	48	08	13	13512
VIF	VSIEVHIL	11	17	GKGVSVSEVHPLRYSY	85	05	8	13513

66500 Table XX6 B2 Table B3 HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VPR	LESNYDGG	01	50	IGLPSTNGRRRN	82	01	2	13514
VPR	LEELKSEA	17	27	TELELELKNEAVRH	19	12	19	13515
VPR	LEELKSEA	16	25	TELELELKSEAVRH	19	15	23	13516
VTU	AKVDYRVI	01	33	DLLAKVDYRVYAF	3	01	2	13517
VTU	AKVDYRLGV	01	33	NPLAKVDYRLGVGL	3	01	2	13518
VTU	ILKQKIDR	13	23	YKILKQKIDRLID	42	12	19	13519

IIIV DR 3b Motif Peptides with Binding Information

[illegible]

66509 Table Xxd 98821460
HIV DR 3b Motif Peptides with Binding Information

Cont Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
MDPVRSEL	GDMDVNRVSELVYK						13464
LTVDNQSL	STLTVDNQKLLSL						13465
IEAQCHLO	LEAAEQCHLOQLTV						13466
ICDROAH	TCEIGBIRQAHCNI						13467
VEREKRAVG	RRVVEREKRAVGIGA						13468
MVEQMIEDI	KNNMVEQMIEDISL						13469
AWDLRLSLC	LALAWDLRLSLCLFS						13470
LEITITIRN	GGLEITITIRNCKGL						13471
YEVYVYVW	YEVYVYVWVWVWV						13472
VEGRRIE	IAVAGRIDRIEIVQ						13473
VEREKRAVG	RRVVEREKRAVGIGA						13474
AEGRDVIE	IAVAGTRDVIEVVQ						13475
IEAQHILLK	LEAAEQHILLKLTIV						13476
LNQDKKFN	FAILKNQDKKFNQGT						13477
ANPCKTIL	VQNMNPCKTILKAL						13478
FYKTLRAGD	DKFTYKTLRAGDQ						13479
MDPVRSEL	GDMDVNRVSELVYK						13480
FKTLRAHQ	VDRFKTLRAHQATQ						13481
IPWFKGRP	LQKIPWFKGRGKGF						13482
LARNCRAFR	EGHLARNCRAFRKKG						13483
IAKNCRAFR	EGHIAKNCRAFRKKG						13484
ATQEVKNWM	AEQATQEVKNWMATET						13485
ATQDVKNWM	AEQATQDVKNWMATET						13486
IPWFKGRP	LQKIPWFKGRGKGF						13487
IPWFKGRP	LQKIPWFKGRGKGF						13488
ASQEVKNWM	VQNMNPCKSILAL						13489
IPWFKGRP	AEQASQEVKNWMATET						13490
LYSKARQEF	LQKLYTSKGRGKGF						13491
VPVDPREVE	LDGLYTSKGRQELD						13492
MAKELHPRK	FCLVPMMAKELHPRK						13493
MAKELHPRK	FLVAGVYELHPRKWTY						13494
PHNFKRAG	MAYPHNFKRAGGIG						13495
NNKELKII	YESNNKELKIIQGV						13496
IGQVVRDQA	LCKUIGQVVRDQAHL						13497
YHSNWRAMA	HEKYTHSNWRAMASDF						13498
MEKEGKSK	CTBMEGKSKSKKGF						13499
YHSNWRAMA	HEKYTHSNWRAMASDF						13500
ANPCKTIL	DEGANPCKTILKAGY						13501
IGQOLKEAL	TIKIGQOLKEALLDT						13502
LOKDFRKYT	SVPLDKDFRKYTAFT						13503
Y'YHDSRPL	FRVY'YHDSRPLWKG						13504
IGQVREQA	LCKUIGQVREQAHL						13505
YHNNWRAMA	HEKYHNNWRAMASDF						13506
ARKNRNRW	TRQARNNRNRWAK						13507
LSSEVHPL	TRPALSSEVHPLWAK						13508
LSSEVHPL	DEELLKTYLKLKTY						13509
YHSNWRAMA	HEKYTHSNWRAMASDF						13510
YHSNWRAMA	HEKYTHSNWRAMASDF						13511
YHSNWRAMA	HEKYTHSNWRAMASDF						13512
YHSNWRAMA	HEKYTHSNWRAMASDF						13513

0.0048

HIV DR 3b Motif Peptides with Binding Information

Cons-Sequence	Exemplar-Sequence	DR1	DR2a01	DR2a02	DR3	DR4a4	DR4a15	DR5w11	DR5w12	SEQ ID NO.
LFSNTRGRG	IGLENTFRGRGRN									13514
LFELKNEA	TLLEBELKSEAVRI									13515
LFELKSEA	TLLEBELKSEAVRI									13516
LFELKSEA	TLLEBELKSEAVRI									13517
LFELKSEA	TLLEBELKSEAVRI									13518
AKNDYRLGV	NFLAKVDYRLGVGL				13.0000	-0.0055		0.1500		13519
LFELKSIDR	YEKLRFQRKIDRID	0.0024	0.0740	0.0410						

Table XXd
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw33	SEQ ID NO.
LPSNTRRG	IGLPSNTRGRHN						13514
LLLEKSA	TLELLEKSAVRH						13515
LLLEKSA	TLELLEKSAVRH						13516
AKVDYRLV	DLAKVDYRLVAF						13517
AKVDYRLGV	NELAKVDYRLGVGL						13518
ILQRKDR	YRKILQRKIDRLID	0.0016	-0.0014	0.0270			13519

TABLE XXI. Population coverage with combined HLA Supertypes

HLA-SUPERTYPES	PHENOTYPIC FREQUENCY					
	Caucasian	North American Black	Japanese	Chinese	Hispanic	Average
<u>a. Individual Supertypes</u>						
A2	45.8	39.0	42.4	45.9	43.0	43.2
A3	37.5	42.1	45.8	52.7	43.1	44.2
B7	38.6	52.7	48.8	35.5	47.1	44.7
A1	47.1	16.1	21.8	14.7	26.3	25.2
A24	23.9	38.9	58.6	40.1	38.3	40.0
B44	43.0	21.2	42.9	39.1	39.0	37.0
B27	28.4	26.1	13.3	13.9	35.3	23.4
B62	12.6	4.8	36.5	25.4	11.1	18.1
B58	10.0	25.1	1.6	9.0	5.9	10.3
<u>b. Combined Supertypes</u>						
A2, A3, B7	83.0	86.1	87.5	88.4	86.3	86.2
A2, A3, B7, A24, B44, A1	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44, A1, B27, B62, B58	99.9	99.6	100.0	99.8	99.9	99.8

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Table XXIII: Immunogenicity of HIV peptides

	Peptide	Sequence	Protein	Immunogenicity	
				patients	transgenic
A2 Supermotif	1261.04	LTFGWCFKL	HIV nef 221	4/12	3/3
	1261.15	MASDFNLPPV	hiv pol 774	1/15	2/6
	1069.32	VLAEAMSQV	hiv gag 386	6/19	3/3
	1261.16	CTLNFPISPI	hiv pol 182	0/1	1/6
	1261.02	LLQLTVWGI	HIV env 651	2/8	1/6
	1261.13	KLVGKLNWA	HIV pol 448	3/15	3/3
	1211.04	KLTPLCVTL	HIV env 134	2/12	2/6
	1261.08	ALVEICTEM	HIV pol 220	0/2	1/6
	1261.11	AIIRILQQL	HIV vpr 59	5/9	0/6
	1261.09	LVGPTPVNI	HIV pol 163	1/9	1/6
	1261.12	RILQQLLFI	HIV vpr 62	6/20	2/6
	1261.05	TLNFPISPI	HIV pol 183	1/7	0/6
	1261.03	MTNNPPIPV	HIV gag 271	2/17	4/6
	1261.17	KMIGGIGGI	HIV pol 132	2/7	0/6
	941.03	ILKEPVHGV	HIV pol 498	8/19	3/6
	1261.10	RAMASDFNL	HIV pol 772	2/9	0/6
	1261.07	KAACWWAGI	HIV pol 879	1/8	0/6
A3 Supermotif	1211.32	KIQNFRVYYR	HIV pol 971	4/6	
	1193.03	AVFIHNFKR	HIV pol 931	3/6	
	1069.49	QMAVFIHNFK	HIV pol 929	3/6	
	1150.14	MAVFIHNFK	HIV pol 930	6/6	
	1069.42	KVYLAWVPAHK	HIV pol 722	6/6	
	966.01	AIFQSSMTK	HIV pol 347	5/6	1/6
	940.03	QVPLRPMTYK	HIV nef 100	0/6	6/10
	1273.07	TLFCASDAK	HIV env 61	3/6	
	1273.09	VTIKIGGQLK	HIV pol 98	6/6	
	1069.43	TVYYGVVPWK	HIV env 48		28/33
	1069.47	VTVYYGVVPWK	HIV env 47	6/6	
DR Supermotif	27.0313	KRWILGLNKIVRMY	HIV gag 298	3/13	
	27.0311	GEIYKRWILGLNKI	HIV gag 294	2/13	
	27.0354	WEFVNTPLVKLWYQ	HIV pol 596	2/13	
	27.0377	QKQITKIQNFRVYYR	HIV pol 956	3/13	
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712	3/13	
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711	1/13	
	27.0304	QGQMVHQAIAPRTLN	HIV gag 171	4/13	
	27.0344	SPAIFQSSMTKILEP	HIV pol 335	3/13	
	27.0341	FRKYTAFTIPSINNE	HIV pol 303	3/13	
	27.0364	HSNWRAMASDFNLPP	HIV pol 758	3/13	
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915	4/13	

Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays				Radiolabeled peptide	
Species	Antigen	Allele	Cell line	Source	Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVV
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0203		HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0206	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0207	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV
	A3		21.221 (transfects)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A3			non-natural (A3CON1)	KVFPYALINK
	A11		GM3107	non-natural (A3CON1)	KVFPYALINK
	A24	A*2402	BVR	non-natural (A24CON1)	AYIDNYNKF
	A31	A*3101	KAS116	non-natural (A3CON1)	KVFPYALINK
	A33	A*3301	SPACH	non-natural (A3CON1)	KVFPYALINK
	A28/68	A*6801	LWAGS	non-natural (A3CON1)	STLPETVYVRR
	A28/68	A*6802	CIR	HBVc 141-151 T7->Y	FTOAGYPAL
	B7	B*0702	AMAI	HBV pol 646-654 C4->A	APRTLVL
	B8	B*0801	GM3107	A2 signal seq. 5-13 (L7->Y)	FLKDYQLL
	B27	B*2705	Steinlin	IVgp 586-593 Y1->F, Q5->R 605	FRYNGLIHR
	B35	B*3501	LG2	non-natural (B35CON2)	PPEKYAAAF
	B35	B*3502	CIR, BVR	non-natural (B35CON2)	PPEKYAAAF
	B35	B*3503	TISI	non-natural (B35CON2)	PPEKYAAAF
	B44	B*4403	EHM	non-natural (B35CON2)	AEMGRYSFY
	B51	B*5301	PITOUT	EF-1 G6->Y	PPEKYAAAF
	B54	B*5401	KAS116	non-natural (B35CON2)	PPEKYAAAF
	Cw4	Cw*0401	AMAI	non-natural (B35CON2)	PPEKYAAAF
	Cw6	Cw*0602	KT3	non-natural (B35CON2)	PPEKYAAAF
	Cw7	Cw*0702	CIR	non-natural (C4CON1)	QYDDAVYKL
			21.221 transfects	non-natural (C6CON1)	YRHDGGNVL
			21.221 transfects	non-natural (C6CON1)	YRHDGGNVL
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI
	K ^b		EL4	VSV NP 52-59	RGYVFQGL
	D ^d		P815	HIV-IIIb ENV G4->Y	RGFYRAFTI
	K ^d		P815	non-natural (KdCON1)	KFNPMKTYI
	L ^d		P815	HBVs 28-39	IPQSLDSYWTSL

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHEFNIVTPRPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAFAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIADFEARR
	DR4w4	DRB1*0401	Priess	non-natural (717.01)	YARFOSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFORQTLKAAA
	DR4w14	DRB1*0404	BN 40	non-natural (717.01)	YARFOSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFOSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFGITE
	DR9	DRB1*0901	HHD	Tet. tox. 830-843	QYIKANSKFGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFGITE
	DR51	DRB3*0101	3M3107 or L416.	Tet. tox. 830-843	QYIKANAKFGITE
	DR51	DRB3*0201	L255.1	HA 307-319	PKYVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFOSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*0301	PF	non-natural (ROIV)	AHAHAHAHAHAHAA
Mouse	IA ^b		DB27.4	non-natural (ROIV)	AHAHAHAHAHAHAA
	IA ^d		A20	non-natural (ROIV)	AHAHAHAHAHAHAA
	IA ^k		CH-12	HEL 46-61	YNTDGDSTDYQILQNSR
	IA ^s		LS102.9	non-natural (ROIV)	AHAHAHAHAHAHAA
	IA ^u		91.7	non-natural (ROIV)	AHAHAHAHAHAHAA
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

Table XXV. Monoclonal antibodies used in MHC purification.

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	H-2 D ^b and L ^d
34-5-8S	H-2 D ^d
B8-24-3	H-2 K ^b
SF1-1.1.1	H-2 K ^d
Y-3	H-2 K ^b
10.3.6	H-2 IA ^k
14.4.4	H-2 IE ^d , IE ^K
MKD6	H-2 IA ^d
Y3JP	H-2 IA ^b , IA ^s , IA ^u

Table XXVI. The table lists the 64 fully represented aligned amino acid sequences that were identified for Motif analysis. Included are the aligned amino acid sequence ID number, the complete nucleotide sequence name it was derived from, the accession numbers for the sequence, the subtype, country and the total length of all nine sequences.

	ID Number	Name	Accession Numbers	Subtype	Country	Length
1	A.KE.Q23-CxC-CG	HIVQ2317	AF004885	A	KE	3584
2	A.SE.UGSE8891	AUGSE8891	AF069673	A	SE	3584
3	A.UG.92UG037	H92UG037	U51190	A	UG	3584
4	A.UG.U455	HIVU455A	M62320	A	UG	3584
5	AC.IN.21301	21301	AF067156	AC	IN	3584
6	AC.RW.92RW009	92RW009	U88823	AC	RW	3584
7	AC.ZM.ZAM184	ZAM184	U86780	AC	ZM	3584
8	ADI.ZR.MAL	HIVMALCG	K03456, X04415	ADI	ZR	3584
9	AE.CF.90CR402	HIV90CF402	U51188	AE	CF	3584
10	AE.TH.93TH253	H93TH253	U51189	AE	TH	3584
11	AE.TH.CM240	HIV1CM240	U54771	AE	TH	3584
12	AG.DJ.DJ263	DJ263	AF063223	AG	DJ	3584
13	AG.DJ.DJ264	HDJ264	AF063224	AG	DJ	3584
14	AG.NG.92NG003	92NG003	U88825	AG	NG	3584
15	AG.NG.92NG083	H92NG083	U88826	AG	NG	3584
16	AG.NG.IBNG	HIVIBNG	L39106	AG	NG	3584
17	AGI.CY.94CY0323	94CY032-3	AF049337	AGI	CY	3584
18	AGI.ZR.Z321	HIVU76035, Z321B	U76035	AGI	ZR	3584
19	AGJ.AU.BFP90	HIVBFP90	AF064699	AGJ	AU	3584
20	B.CN.RL42	HCHRL42CG	U71182	B	CN	3584
21	B.DE.D31	HIV1D31	U43096	B	DE	3584
22	B.DE.HAN	HIVHAN2	U43141	B	DE	3584
23	B.FR.HXB2R	HIVHXB2	AF033819, K03455, M38432	B	FR	3584
24	B.GA.OYI	HIVYOI	M26727	B	GA	3584
25	B.GB.CAM1	HIVCAM1	D00917, D10112	B	GB	3584
26	B.GB.MANC	HIV1MANC	U23487	B	GB	3584
27	B.NL.ACH32OA	HIV1ACH32OA	U34604	B	NL	3584
28	B.US.ADA	HIV1AD8	AF004394	B	US	3584
29	B.US.DH123	HIV1DH123	AF069140	B	US	3584
30	B.US.JRC5F	HIVJRC5F	M38429	B	US	3584
31	B.US.JRFL	HIVJRFL	U63632	B	US	3584
32	B.US.MN	HIVMN	M17449	B	US	3584
33	B.US.P896	HIV1896	M96155, U39362	B	US	3584
34	B.US.RF	HIVRF	M12508	B	US	3584
35	B.US.SF2	HIVSF2CG	K02007	B	US	3584
36	B.US.WEAU160	HIVWEAU160	U21135	B	US	3584
37	B.US.WR27	HIV1WR27	U26546	B	US	3584
38	B.US.YU2	HIVYU2	M93258	B	US	3584
39	BF.BR.93BR029.4	93BR029	AF005495	BF	BR	3584
40	C.BR.92BR025	H92BR025	U52953	C	BR	3584
41	C.BW.BW96BW0502	96BW0502	AF110967	C	BW	3584
42	C.ET.ETH2220	HIVETH2220	U46016	C	ET	3584
43	C.IN.11246	1N11246	AF067159	C	IN	3584
44	C.IN.21068	C1N21068	AF067155	C	IN	3584
45	C.IN.301904	301904	AF067157	C	IN	3584
46	C.IN.301905	CIN301905	AF067158	C	IN	3584
47	C.IN.301999	CIN301999	AF067154	C	IN	3584
48	D.UG.94UG1141	94UG114	U88824	D	UG	3584
49	D.ZR.84ZR085	84ZR085	U88822	D	ZR	3584
50	D.ZR.ELI	HIVELICG	K03454, X04414	D	ZR	3584
51	D.ZR.NDK	HIVNDK	M27323	D	ZR	3584
52	F.BR.93BR0201	93BR020	AF005494	F	BR	3584
53	F.FN.FIN9363	FIN9363	AF075703	F	FN	3584
54	G.BE.DRCBL	DRCBL	AF084936	G	BE	3584
55	G.FI.HH87931	HH8793	AF061640, AF061641	G	FI	3584
56	G.SE.SE6165	SE6165	AF061642	G	SE	3584
57	H.BE.VI991	VI991	VI991	H	BE	3584
58	H.BE.VI997	VI997	VI997	H	BE	3584

	ID Number	Name	Accession Numbers	Subtype	Country	Length
59	H.CF.90CF056	90CF056	AF005496	H	CF	3584
60	J.SE.SE91733	SE91733	AF082395	J	SE	3584
61	J.SE.SE92809	SE92809	AF082394	J	SE	3584
62	N.CM.YBF3O	NCMYBF3O	AJ006022	N	CM	3584
63	O.CM.ANT7OC	HIVANT7OC	L20587	O	CM	3584
64	O.CM.MVP518O	HIVMVP518O	L20571	O	CM	3584

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TABLE XXVII
in vitro binding of conserved HIV derived peptides to HLA-A2 supertype alleles

peptide	AA	protein	Position	sequence	Conservation (%) total	A2-supertype binding capacity (IC50 nM)					alleles bound
						A*0201	A*0202	A*0203	A*0206	A*6802	
1261.14	10	NEF	221	LTFGWCFKL	55	74	48.9	185.2	57.8	6.2	5
1261.04	9	NEF	221	LTFGWCFKL	61	74	35.7	33.1	4545.5	205.6	4
1261.06	9	POL	316	YTATFTSL	58	68	26.3	6.1	9.1	7	5
1261.15	10	POL	774	VLAEAMSPV	39	68	62.5	22.6	55.6	33.6	5
1069.32	9	GAG	386	CTLNFTPSI	52	74	66.6	82.7	15.2	8.4	5
1261.16	9	POL	182	LIQLTVWGI	94	100	147	23.9	30.3	24.7	4
1261.02	9	ENV	448	KLVLKLVTL	53	63	9.8	215	43.5	39.8	4
1261.13	9	ENV	448	KLVLKLVTL	95	95	59.5	12.6	66.7	185	20000
1261.11	9	POL	134	KLTPLCVTL	81	95	217.3	187	140.8	264.3	2857.1
1211.04	9	ENV	220	ALVEICTEM	23	79	33.3	22.6	41.7	38.5	547.9
1261.08	9	POL	163	RIQLQLLFI	61	74	100	454.5	19.2	2846.2	67.8
1261.09	9	VPR	59	LVGPTVNI	56	74	19.2	1535.7	125	1947.4	57.1
1261.12	9	VPR	183	TLNFTPSI	31	89	166.6	7166.7	33.3	1608.7	12.1
1261.05	9	GAG	271	MTNFTPSI	97	95	172.4	54.4	4.8	770.8	333.3
1261.17	10	POL	132	KMIGGIGFI	64	79	192.3	2388.9	6.7	37000	303.6
941.03	9	POL	498	ILKEPVGV	64	79	217.3	116.2	25000	52.1	3076.9
1260.10	9	POL	772	RAMASDFNL	49	79	277.7	1075	83.3	160.9	2666.7
1261.07	9	ENV	814	KACWVWGI	22	68	9.8	1303	238.1	28.5	5479.4
1211.09	10	ENV	608	FLGAAGSTM	86	100	73.5	3583.3	1.5	4111.1	66666.7
1211.05	9	VPR	66	QLLFHRI	69	89	94.3	21500	25000	1608.7	476.2
25.0053	9	GAG	270	WNTNFTPSV	31	89	98	3071.4	16.9	18500	2222.2
1069.33	10	POL	993	LLWKGEAVV	95	100	111.1	632.4	25	770.8	3636.4
25.0142	10	NEF	219	PLTFGWCFKL	61	74	142.8	741.4	4761.9	3700	47.6
1069.34	9	POL	993	LLWKGEAVV	42	84	100	10750	21.7	1608.7	2666.7
1211.082	10	POL	452	KLWASQIYA	34	58	217.3	3909.1	400	6166.7	3076.9
25.0037	9	GAG	486	SLYNTVATL	34	68	277.7	3583.3	32.3	18500	2857.1
25.0046	9	POL	91	FLQSRPEPT	44	68	454.5	10750	2500	18500	2857.1

TABLE XXVIII

in vitro binding of conserved HIV derived peptides to HLA-A3 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		A3 supertype binding capacity (IC50 nM)							alleles bound	
					total	B	A*0301	A*1101	A*3101	A*3301	A*6801				
1273.01	9	GAG	163	MVHQALSPR	42	58	61.1	89.6	18.0	13.8	9.5	5	5		
1193.0200	9	POL	572	IVTWGKTPK	75	79	129.4	16.2	18.2	96.7	242.4	5	5		
1193.03	9	POL	931	AVFHNFKR	97	100	64.7	3.3	5.1	107.4	4.2	5	5		
1193.01	9	POL	724	YLAWVPAHK	34	95	142.9	105.3	327.3	33.0	2.0	5	5		
1211.32	10	POL	971	KIONFRVYVR	81	95	343.8	28.6	2.7	341.2	210.5	5	5		
1069.49	10	POL	929	QMAVFNFKR	94	100	9.2	8.5	268.7	432.8	400.0	4	4		
1273.03	10	GAG	162	QMVHQALSPR	42	58	42.3	600.0	243.2	290.0	186.0	4	4		
1193.09	9	POL	353	MTKILSPR	67	84	13750.0	375.0	81.8	69.0	25.8	4	4		
966.01	9	POL	347	AIHQSSMTK	56	79	10.0	10.0	1200.0	96666.7	242.4	3	3		
940.03	10	NEF	100	QVPLRPMTYK	72	79	18.0	9.5	1836.7	2230.8	133.3	3	3		
1069.43	10	ENV	48	TVTYGVPPVWK	64	95	11.0	3.5	1636.4	10357.1	14.5	3	3		
1273.05	9	POL	931	AVFHNFKR	91	100	114.6	20.7	1125.0	5000.0	307.7	3	3		
1273.07	10	ENV	61	TKIGGQQLK	27	63	40.7	181.8	1800.0	36250.0	72.7	3	3		
1273.06	9	ENV	64	TLFCASDAK	81	84	118.3	11.3	10588.2	22307.7	190.5	3	3		
1273.07	10	ENV	878	RIVELLGRR	34	89	119.6	27.3	9473.7	14500.0	140.4	3	3		
1273.04	9	ENV	878	VTIKGGQQLK	27	63	297.3	28.6	10588.2	11600.0	125.0	3	3		
1273.09	10	POL	98	NTVPFAIKK	58	94.7	333.3	100.0	3000.0	48333.3	4.7	3	3		
1273.02	9	POL	246	MAVFNFKR	94	100	647.1	20.0	375.0	517.9	2.5	3	3		
1150.14	9	POL	930	VNMVWQVDR	69	95	3235.3	272.7	3.8	5.3	242.4	3	3		
1273.08	9	VIF	7	VMTYGVPPVWK	64	94	84.6	11.3	4615.4	36250.0	170.2	3	3		
1069.47	11	ENV	47	VTYYGVPPVWK	64	94	84.6	11.3	4615.4	36250.0	170.2	3	3		
1069.42	11	POL	722	KVYLAWVPAHK	32	89	3.5	7.6	163.6	3580.2	8000.0	3	3		
1069.44	0	POL	855	KLGRWPVK	78	68	8.5	133.3	500.0	72500.0	80000.0	3	3		

TABLE XXIX
in vitro binding of conserved HIV derived peptides to HLA-B7 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		B7 supertype binding capacity (IC50 nM)					alleles bound	
					total	B	B*0702	B*3501	B*5101	B*5301	B*5401		
1146.01	9	NEF	94	FPVRPQVPL	75	74	15.7	43.0	11.6	481.9	71.4	5	
1296.01	9	ENV	259	IPHYCAPA	56	42	42.3	34.3	153	-	3.7	4	
15.0268	10	GAG	545	YPLASLSLSLF	15	32	392.9	480.0	39.3	150.0	714.3	4	
1261.01	9	POL	186	FPFSPIETV	88	95	3437.5	1043.5	148.6	251.4	9.1	3	
1296.02	9	ENV	250	CPKVSFEPI	47	79	100.0	5142.9	161.8	2447.4	100.0	3	
1296.03	11	POL	893	IPYNPQSGVV	92	89	458.3	72000.0	119.6	46500.0	66.7	3	
29.0028	8	REV	75	VPLQLPPL	56	68	112.2	6000.0	0.8	46500.0	270.3	3	
1292.13	9	GAG	237	HPVHAGHA	30	74	50.0	11.6	13750.0	4428.6	4.3	3	

Table XXX: A1-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
1.0431	EVNIVTDSQY	HIV pol 1187	83	93	472
1.0014	FRDYVDRFY	HIV gag 298	51	96	278
2.0129	IYQYMDDL	HIV pol 359	78	87	391
1069.27	VIYQYMDDL	HIV pol 358	78	87	446
1069.26	VTVLDVGDAY	HIV pol 265	96	93	439

Table XXXI: A24-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
25.0113	IWGCSGKLI	HIV env 69	69	91	444
25.0127	IYETYGDTW	HIV vpr 92	92	100	207
1069.60	IYQEPFKNL	HIV pol 1036	74	87	444
25.0128	PYNEWTLEL	HIV vpr 56	56	71	86
25.0123	PYNTPVFAI	HIV pol 74	74	100	387
1069.57	RYLKDQQLL	HIV env 2778	40	53	43
1069.58	RYLRDQQLL	HIV env 2778	23	32	52
1069.59	TYQIQEPPF	HIV pol 1033	78	93	67
25.0115	VWKEATTTL	HIV env 47	47	85	400
25.0218	VWKEATTTLF	HIV env 47	47	85	44
25.0219	YWQATWIPEW	HIV pol 96	96	93	182

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Table XXXII: Immunogenicity of A2-supertype cross-reactive binding peptides

Peptide	Sequence	Protein	Conservancy		Immunogenicity	
			Total	Clade B	patients	transgenic
1261.14	LTFGWCFKLV	HIV nef221	55	74	5	0/1
1261.04	LTFGWCFKL	HIV nef221	61	74	4	4/12
1261.06	YTAFTPSI	HIV pol 316	58	68	5	0/1
1261.15	MASDFNLPPV	HIV pol 774	39	68	5	1/15
1069.32	VLAEMSQV	HIV gag 386	52	74	5	6/19
1261.16	CTLNFTPSI	HIV pol 182	94	100	5	0/1
1261.02	LLQLTVWGI	HIV env 651	53	63	4	2/8
1261.13	KLVGKLNWA	HIV pol 448	95	95	4	3/15
1211.04	KLTPLCVTL	HIV env 134	85	79	4	2/12
1261.08	ALVEICTEM	HIV pol 220	23	79	4	0/2
1261.11	AIRILQQQL	HIV vpr 59	61	74	4	5/9
1261.09	LVGPTPVNI	HIV pol 163	84	100	4	1/9
1261.12	RILQQLLF	HIV vpr 62	56	74	3	6/20
1261.05	TLNFTPSI	HIV pol 183	97	100	3	1/7
1261.03	MTNPPPIV	HIV gag 271	31	89	3	2/17
1261.17	KMIGGIGFI	HIV pol 132	97	95	3	2/7
941.03	ILKEPVHGV	HIV pol 498	64	79	3	8/19
1261.10	RAMASDFNL	HIV pol 772	64	79	3	2/9
1261.07	KAACWWAGI	HIV pol 879	49	79	3	1/8
1211.09	SLLNATDIIV	HIV env 814	22	68	3	

Table XXXIII: Immunogenicity of HIV-derived A3-supertype peptides

Peptide	Sequence	Protein	Conservancy		Immunogenicity	
			Total	Clade B	transgenic	patients
1211.32	KIQNRYYYR	HIV pol 971	81	95	5	4/6
1193.02	IVIWGKTPK	HIV pol 572	75	79	5	0/6
1193.03	AVFIHFKR	HIV pol 931	97	100	5	3/6
1069.49	QMAVFIHFK	HIV pol 929	94	100	4	3/6
1150.14	MAVFIHFK	HIV pol 930	94	100	3	6/6
1069.48	AVFIHFKRK	HIV pol 931	91	100	3	0/6
1273.01	MVHQAIKSPR	HIV gag 163	42	58	5	0/6
1273.03	QMVHQAIKSPR	HIV gag 162	42	58	4	0/6
1193.01	YLAWVPAHK	HIV pol 724	34	95	5	0/6
1069.42	KVYLAWVPAHK	HIV pol 722	32	89	3	6/6
1193.09	MTKLEPR	HIV pol 353	67	84	4	0/8
966.01	AIFQSSMTK	HIV pol 347	56	79	3	5/6
940.03	QVPLRPMYK	HIV nef 100	72	79	3	0/6
1069.44	KLGRWPVK	HIV pol 855	78	68	3	0/6
1273.02	NTPVFAIKK	HIV pol 246	58	95	3	0/6
1273.08	VMIWQVDR	HIV vif 7	69	95	3	0/6
1273.04	RIVELIGRR	HIV env 878	34	89	3	
1273.07	TLFCAADAK	HIV env 61	78	84	3	3/6
1273.06	TLFCAADAK	HIV env 62	81	84	3	0/6
1273.09	VTIKGGQALK	HIV pol 98	27	63	3	6/6
1273.05	TIKGGQALK	HIV pol 99	27	63	3	0/6
1069.43	TVYYGVPVK	HIV env 48	64	95	3	28/33
1069.47	VTYYGVPVK	HIV env 47	64	94	3	6/6

Table XXXIV. HLA-DR screening panels

Screening Panel	Antigen	Representative Assay		Phenotypic Frequencies						
		Alleles	Allele	Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.	
Primary	DR1	DRB1*0101-03	DRB1*0101 (DR1)	18.5	8.4	10.7	4.5	10.1	10.4	
	DR4	DRB1*0401-12	DRB1*0401 (DR4w4)	23.6	6.1	40.4	21.9	29.8	24.4	
	DR7	DRB1*0701-02	DRB1*0701 (DR7)	26.2	11.1	1.0	15.0	16.6	14.0	
	Panel total			59.6	24.5	49.3	38.7	51.1	44.6	
Secondary	DR2	DRB1*1501-03	DRB1*1501 (DR2w2 B1)	19.9	14.8	30.9	22.0	15.0	20.5	
	DR2	DRB5*0101	DRB5*0101 (DR2w2 B2)	-	-	-	-	-	-	
	DR9	DRB1*0901,09012	DRB1*0901 (DR9)	3.6	4.7	24.5	19.9	6.7	11.9	
	DR13	DRB1*1301-06	DRB1*1302 (DR6w19)	21.7	16.5	14.6	12.2	10.5	15.1	
Panel total			42.0	33.9	61.0	48.9	30.5	43.2		
Tertiary	DR4	DRB1*0405	DRB1*0405 (DR4w15)	-	-	-	-	-	-	
	DR8	DRB1*0801-5	DRB1*0802 (DR8w2)	5.5	10.9	25.0	10.7	23.3	15.1	
	DR11	DRB1*1101-05	DRB1*1101 (DR5w11)	17.0	18.0	4.9	19.4	18.1	15.5	
	Panel total			22.0	27.8	29.2	29.0	39.0	29.4	
Quaternary	DR3	DRB1*0301-2	DRB1*0301 (DR3w17)	17.7	19.5	0.4	7.3	14.4	11.9	
	DR12	DRB1*1201-02	DRB1*1201 (DR5w12)	2.8	5.5	13.1	17.6	5.7	8.9	
	Panel total			20.2	24.4	13.5	24.2	19.7	20.4	

Table XXXV: cross-reactive HLA-DR binding peptides

Peptide	Sequence	Protein	Binding capacity (IC50 nM)										DR Alleles bound	
			DR1	DR2w2h1	DR2w2h2	DR3	DR4w4	DR4w15	DR5w12	DR6w19	DR7	DR8w2	DR9	DR53
270313	KRWILGLINKIVMY	HIV gag 298	7.2	5.1	24	188	633	464	54	0.36	379	49	38	12
270354	WFEVNTPLVLYWYQ	HIV pol 596	7.2	222	2.1	13636	28	20	317	1355	15	350	39	10
270377	QRQTKIQNFRVYTR	HIV pol 596	7.2	3.4	80	-	357	49	53	124	25	185	577	11
128003	KVYLAWVPAHKGIG	HIV pol 712	8.3	25	24	-	156	165	71	12598	179	196	250	9
270311	GEYTKRWILGLINKI	HIV gag 294	8.2	138	225	-	1667	380	213	1656	192	63	536	9
270361	EKVYLAWVPAHKGIG	HIV pol 710	3.6	21	4.9	3226	9.3	27	37	6478	18	31	144	9
270297	QHLQLTWGIRQLQ	HIV env 719	6.1	21	690	-	1316	345	2128	1064	350	46	907	8
270304	QQQMVHOASPRITLN	HIV gag 171	72	65	13	17647	60	400	-	412	455	7313	117	8
270344	SPAFQSSMTKLEP	HIV pol 335	357	217	667	-	3571	109	741	-	68	350	3267	33
F991.15	IKQFINMWQEVGKAMY	HIV pol 566	128	217	206	-	417	271	4878	-	13	30	803	104
270341	FRKYTAFTIPSDNNE	HIV pol 303	185	70	4167	-	294	136	1818	-	30	472	1960	7
270364	HSNWRAMASDPNLPF	HIV pol 758	33	-	125	-	11	15	95	-	4375	472	872	7
270373	KTAQMAVTEHNEK	HIV pol 915	161	650	690	-	909	452	182	18625	125	1441	2586	7

A dash indicates IC50>20nM

Table XXXVI: DR3 binding peptides

Peptide	Sequence	Protein	DR3
35.0135	YRKILRQRKIDRLID	HIV vpu 31	23
35.0131	WAGIKQEFGIPYNPQ	HIV pol 874	300
35.0127	EVNIVTDSQYALGII	HIV pol 674	732
35.0125	AETFYVDGAANRETK	HIV pol 619	769
35.0133	GAVVIQDNSDIKVPV	HIV pol 989	1000

TABLE XXXVII
Immunogenicity of HIV-derived DR-supermotif peptides

Peptide	Sequence	Protein	conservation (%)		DR Alleles bound	Patient Immunogenicity
			total	Clade B		
27.0313	KRWILGLNKIVRMV	HIV gag 298	85 [89]	94 [95]	12	3/13
27.0311	GEYKRWILGLNKI	HIV gag 294	58 [86]	95 [95]	9	2/13
27.0354	WEFVNTPLVKLWYQ	HIV pol 596	79 [89]	84 [95]	10	2/13
27.0377	QKQTKQNFRRYR	HIV pol 956	56 [67]	95 [95]	11	3/13
1280.03	KVYLAWVPAHKGG	HIV pol 712	32 [34]	89 [95]	9	1/13
27.0361	ERYLLAWVPAHKGG	HIV pol 711	32 [34]	94 [95]	9	4/13
27.0304	QGQMVHQALSFRTLN	HIV gag 171	41 [42]	52 [58]	8	3/13
27.0344	SPAFQSSMTKLEP	HIV pol 335	52 [59]	79 [78]	8	3/13
27.0341	PRKYIAFTIFSNNE	HIV pol 303	59 [58]	68 [68]	7	3/13
27.0364	HSNWRAMASDFNLPP	HIV pol 758	48 [67]	68 [79]	7	4/13
27.0373	KTAYQMAVFIHNEKR	HIV pol 915	87 [95]	94 [100]	7	4/13

1: conservation of core region

Table XXXVIII. Candidate CTL Epitopes

Restriction	Peptide	Protein	Sequence
HLA-A2	1069.32	HIV gag 386	VLAAMSQV
"	1261.03	HIV gag 271	MTNNPPIPV
"	1261.15	HIV pol 774	MASDFNLPPV
"	1261.13	HIV pol 448	KLVGKLNWA
"	1261.09	HIV pol 163	LVGPTPVNI
"	941.03	HIV pol 498	ILKEPVHGV
"	1261.07	HIV pol 879	KAACWWAGI
"	1261.17	HIV pol 132	KMIGGIGGFI
"	1261.10	HIV pol 772	RAMASDFNL
"	1261.05	HIV pol 183	TLNFPISPI
"	1211.04	HIV env 134	KLTPLCVTL
"	1261.02	HIV env 651	LLQLTVWGI
"	1211.09	HIV env 163	SLLNATDIAV
"	1261.04	HIV nef 221	LTFGWCFKL
"	1261.11	HIV vpr 59	AIIRLQQL
"	1261.12	HIV vpr 62	RILQQLLI
HLA-A3	1069.49	HIV pol 929	QMAVFIHNFK
"	1069.42	HIV pol 722	KVYLAWVPAHK
"	1211.32	HIV pol 971	KIONFRVYYR
"	1193.09	HIV pol 353	MTKILEPFR
"	966.01	HIV pol 347	AIQSSMTK
"	1273.09	HIV pol 98	VTIKIGGQLK
"	1273.07	HIV env 61	TTLFCASDAK
"	1069.47	HIV env 47	VTVYYGVVPVK
"	940.03	HIV nef 100	QVLRPMTYK
"	1273.08	HIV vif 7	VMIVWQVDR
"	1273.03	HIV gag 162	QMVHQAI SPR
HLA-B7	15.0268	HIV gag 545	YPLASLRSLF
"	1292.13	HIV gag 237	HPVHAGPIA
"	1261.01	HIV pol 186	FPISPIETV
"	1296.03	HIV pol 893	IPYNPQSGVV
"	1296.01	HIV env 259	IFIHYCAPA
"	1296.02	HIV env 250	CPKVSFEPI
"	1146.01	HIV nef 94	FPVRPQVPL
"	29.0028	HIV rev 75	VPLQLPPL
HLA-A1	1.0431	HIV pol 684	EVNIVTDSQY
"	1.0014	HIV gag 317	FRDYVDRFY
"	1069.27	HIV pol 368	VIIQYVMDL Y
"	1069.26	HIV pol 295	VTVLDVGDAY
HLA-A24	1069.60	HIV pol 533	IYQEPFKNL
"	25.0123	HIV pol 244	PYNTPVFAI
"	1069.59	HIV pol 530	TYQIYQEPF
"	25.0219	HIV pol 597	YWQATWIPEW
"	25.0113	HIV env 681	IWGCSGKLI
"	1069.57	HIV env 671	RYLKDQQLL
"	25.0115	HIV env 55	VWKEATTILF
"	25.0127	HIV vpr 46	IYETYGDTW
"	25.0128	HIV vpr 14	PYNEWLEL

Table XXXIX: HTL Candidate Epitopes

Selection Criteria	Peptide	Sequence	Protein
DR	27.0313	KRWIILGLNKIVRMV	HIV gag 298
	27.0354	WEFVNTPLVKLWYQ	HIV pol 596
	27.0377	QKQITKIQNFRVYYR	HIV pol 956
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712
	27.0311	GEIYKRWIILGLNKI	HIV gag 294
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711
	27.0297	QHLLQLTVWGKQLQ	HIV env 729
	27.0304	QGQMVHQAI SPRTL N	HIV gag 171
	27.0344	SPAIFQSSMTKILEP	HIV pol 335
	F091.15	IKQFINMWQEVGKAMY	HIV env 566
	27.0341	FRKYTAFTIPSINNE	HIV pol 303
	27.0364	HSNWRAMASDFNLPP	HIV pol 758
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915
	35.0135	YRKILRQRKIDRLID	HIV vpu 31
DR3	35.0131	WAGIKQEFGIPYNPQ	HIV pol 874
	35.0127	EVNIVTDSQYALGII	HIV pol 674
	35.0125	AETFYVDGAANRETK	HIV pol 619
	35.0133	GAVVIQDNSDIKVP	HIV pol 989

TABLE XL
Estimated population coverage by a panel of HIV derived HTL epitopes

Antigen	Alleles	Representative assay	No. of epitopes	Population coverage (phenotypic frequency)				
				Cauc.	Blk.	Jpn.	Chn.	Hisp. Avg.
DR1	DRB1*0101-03	DR1	13	18.5	8.4	10.7	4.5	10.1
DR2	DRB1*1501-03	DR2w2.81	12	19.9	14.8	30.9	22.0	15.0
DR2	DRB5*0101	DR2w2.82	12	-	-	-	-	-
DR3	DRB1*0301-2	DR3	5	17.7	19.5	0.40	7.3	14.4
DR4	DRB1*0401-12	DR4w4	10	23.6	6.1	40.4	21.9	29.8
DR4	DRB1*0401-12	DR4w15	13	-	-	-	-	-
DR7	DRB1*0701-02	DR7	11	26.2	11.1	1.0	15.0	16.6
DR8	DRB1*0801-5	DR8w2	9	5.5	10.9	25.0	10.7	23.3
DR9	DRB1*09011,09012	DR9	11	3.6	4.7	24.5	19.9	6.7
DR11	DRB1*1101-05	DR5w11	9	17.0	18.0	4.9	19.4	18.1
DR13	DRB1*1301-06	DR6w19	8	21.7	16.5	14.6	12.2	10.5
Total				98.5	95.1	97.1	91.3	94.3
								95.1

1. Total population coverage has been adjusted to account for the presence of DRX in many ethnic populations. It has been assumed that the range of specificities represented by DRX alleles will mirror those of previously characterized HLA-DR alleles. The proportion of DRX incorporated under each motif is representative of the frequency of the motif in the remainder of the population. Total coverage has not been adjusted to account for unknown gene types.
2. Number of epitopes represents a minimal estimate, considering only the epitopes shown in Table 13. Additional alleles possibly bound by nested epitopes have not been accounted.

WHAT IS CLAIMED IS

1. A peptide composition of less than 250 amino acid residues comprising a peptide epitope useful for inducing an immune response against human immunodeficiency virus-1 (HIV-1) said epitope (a) having an amino acid sequence of about 8 to about 13 amino acid residues that have at least 65% identity with a native amino acid sequence of HIV-1 and, (b) binding to at least one HLA class I HLA allele with an IC_{50} of less than about 500 nM.
2. The composition of claim 1, further wherein said peptide has at least 77% identity with a native HIV-1 amino acid sequence.
3. The composition of claim 1, further wherein said peptide has 100% identity with a native HIV-1 amino acid sequence.
4. A pharmaceutical composition comprising a peptide and a pharmaceutical carrier, wherein the peptide is a peptide of Table VII (A1 supermotif), Table VIII (A2 supermotif/A*0201 motif), Table IX (A3 supermotif), Table X (A24 supermotif), Table XI (B7 supermotif), Table XII (B27 supermotif), Table XIII (B58 supermotif), Table XIV (B62 supermotif), Table XV (A1 motif), Table XVI (A3 motif), Table XVII (A11 motif), or Table XVIII (A24 motif) comprising an IC_{50} of less than about 500 nM for at least one HLA class I molecule.
5. The pharmaceutical composition of claim 4 wherein the composition comprises the peptide in a form of nucleic acids that encode the peptide.
6. The pharmaceutical composition of claim 5 wherein the composition comprises the peptide in a form of nucleic acids that encode the epitope and one or more additional peptide(s).
7. The composition of claim 4, wherein the peptide is comprised by a longer peptide, with a *proviso* that the longer peptide is not an entire native antigen.
8. The pharmaceutical composition of claim 4 wherein the peptide is in a human dose form, and the carrier is in a human unit dose.

9. A peptide composition of claim 1 comprising an analog of a peptide epitope, wherein the peptide epitope is an epitope of Table VII (A1 supermotif), Table VIII (A2 supermotif/A2.1 motif), Table IX (A3 supermotif), Table X (A24 supermotif), Table XI (B7 supermotif), Table XII (B27 supermotif), Table XIII (B58 supermotif), Table XIV (B62 supermotif), Table XV (A1 motif), Table XVI (A3 motif), Table XVII (A11 motif), or Table XVIII (A24 motif), said analog comprising a preferred or less preferred amino acid of Table II substituted in for a starting residue, or having a deleterious residue of Table II substituted out of the starting sequence and replaced by a non-deleterious residue.

10. A method for inducing a cytotoxic T lymphocyte response, said method comprising steps of:

providing a peptide that comprises an IC_{50} of less than about 500 nM for an HLA class I molecule, wherein the peptide is a peptide of Table VII (A1 supermotif), Table VIII (A2 supermotif/A2.1 motif), Table IX (A3 supermotif), Table X (A24 supermotif), Table XI (B7 supermotif), Table XII (B27 supermotif), Table XIII (B58 supermotif), Table XIV (B62 supermotif), Table XV (A1 motif), Table XVI (A3 motif), Table XVII (A11 motif), or Table XVIII (A24 motif); and,

administering said peptide to a human.

11. The method of claim 10, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide.

12. The method of claim 10, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide and at least one additional peptide, with a *proviso* that an additional peptide is not an entire native antigen.

13. The method of claim 10, wherein the providing step provides the peptide comprised by a longer peptide, with a *proviso* that the longer peptide is not an entire native antigen.

14. A method for inducing a cytotoxic T lymphocyte response, said method comprising steps of:

providing a pharmaceutical composition comprising a peptide and a pharmaceutical carrier, wherein the peptide induces a cytotoxic T cell response *in vitro* and/or *in vivo*, and further wherein the peptide is a peptide of Table VII (A1 supermotif), Table VIII (A2 supermotif/A2.1 motif), Table IX (A3 supermotif), Table X (A24 supermotif), Table XI (B7 supermotif), Table XII (B27 supermotif), Table XIII (B58 supermotif), Table XIV (B62 supermotif), Table XV (A1 motif), Table XVI (A3 motif), Table XVII (A11 motif), Table XVIII (A24 motif) or Table XXIII; and,

administering said pharmaceutical composition to a human.

15. The method of claim 14, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide.

16. The method of claim 15, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide and at least one additional peptide, with a *proviso* that an additional peptide is not an entire native antigen.

17. The method of claim 14, wherein the providing step provides the peptide comprised by a longer peptide, with a *proviso* that the longer peptide is not an entire native antigen.

18. The method of claim 14, wherein the providing step comprises a peptide that induces a cytotoxic T cell response when complexed with an HLA class I molecule and is presented to an HLA class I-restricted cytotoxic T cell.

19. A peptide composition of less than 250 amino acid residues comprising a peptide epitope useful for inducing an immune response against human immunodeficiency virus-1 (HIV-1) said epitope (a) having an amino acid sequence of about 6 to about 25 amino acid residues that have at least 65% identity with a native amino acid sequence of HIV-1 and, (b) binding to at least one HLA class II HLA allele with an IC₅₀ of less than about 1000 nM.

20. The peptide composition of claim 19, further wherein said peptide has at least 77% identity with a native HIV-1 amino acid sequence.

22. A pharmaceutical composition comprising:

a human dose of a pharmaceutically acceptable carrier.

23. The pharmaceutical composition of claim 22 wherein the composition comprises the peptide in a form of nucleic acids that encode the peptide.

24. The pharmaceutical composition of claim 23 wherein the composition comprises the peptide in a form of nucleic acids that encode the peptide and at least one additional peptide, with a *proviso* that an additional peptide is not an entire native antigen.

25. The pharmaceutical composition of claim 24, wherein the peptide is comprised by a longer peptide, with a *proviso* that the longer peptide is not an entire native antigen.

26. A peptide composition of claim 19 comprising an analog of a peptide epitope of Table XIX or Table XX, said analog comprising a preferred or less preferred amino acid of Table III substituted in for a starting residue, and/or having a deleterious residue of Table III substituted out of the starting sequence and replaced by a non-deleterious residue.

27. A method for inducing a helper T lymphocyte response, said method comprising steps of:

providing a pharmaceutical composition comprising a human dose of a peptide that comprises an IC_{50} of less than about 1,000 nM for an HLA class II molecule and a human dose of a pharmaceutical carrier, wherein the peptide is a peptide of Table XIX or Table XX; and,

administering said peptide to a human.

28. The method of claim 27, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide.

29. The method of claim 28, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide and at least one additional peptide, with a *proviso* that an additional peptide is not an entire native antigen.

30. The method of claim 29, wherein the providing step provides the peptide comprised by a longer peptide, with a *proviso* that the longer peptide is not an entire native antigen.

31. A method for inducing a helper T lymphocyte response, said method comprising steps of:

providing a pharmaceutical composition comprising a human dose of a peptide that induces a helper T cell response *in vitro* and/or *in vivo* and a pharmaceutically acceptable carrier, wherein the peptide is a peptide of Table XIX or Table XX; and,

administering said pharmaceutical composition to a human.

32. The method of claim 31, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide.

33. The method of claim 32, wherein the providing step provides the peptide in a form of nucleic acids that encode the peptide and at least one additional peptide, with a *proviso* that an additional peptide is not an entire native antigen.

34. The method of claim 30, wherein the providing step provides the peptide comprised by a longer peptide, with a *proviso* that the longer peptide is not an entire native antigen.

35. The method of claim 31, wherein the providing step comprises a peptide that induces a helper T cell response when complexed with an HLA class II molecule and is presented to an HLA class II-restricted helper T cell.

36. A vaccine for preventing or treating HIV-1 infection that induces a protective or therapeutic immune response, wherein said vaccine comprises:
at least one peptide selected from Table(s) VII-XX; and,
a pharmaceutically acceptable carrier.

37. A kit for a vaccine that induces a protective or therapeutic immune response to HIV-1, said vaccine comprising:
at least one peptide selected from Table(s) VII-XX;
a pharmaceutically acceptable carrier; and,
instructions for administration to a patient.

38. A method for monitoring or evaluating an immune response to HIV-1 or an epitope thereof in a patient having a known HLA type, the method comprising:

incubating a T lymphocyte sample from the patient with a peptide selected from Table(s) VII-XX, wherein that peptide bears a motif corresponding to at least one HLA allele present in said patient; and,
detecting the presence of a T lymphocyte that recognizes the peptide.

39. The method of claim 38, wherein the peptide is selected from Tables VII-XVIII and is further comprised by a tetrameric complex.

ABSTRACT OF THE DISCLOSURE

This invention uses our knowledge of the mechanisms by which antigen is recognized by T cells to identify and prepare human immunodeficiency virus (HIV)

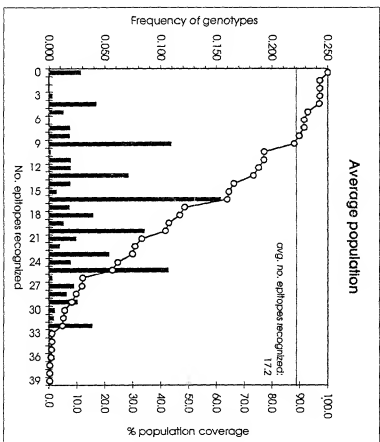
- 5 epitopes, and to develop epitope-based vaccines directed towards HIV. More specifically, this application communicates our discovery of pharmaceutical compositions and methods of use in the prevention and treatment of HIV infection.

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Figure 1



Plot of total frequency of genotypes as a function of the number of candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hit population cluster in proportion to the relative frequency of the cluster within the HLA specified population.

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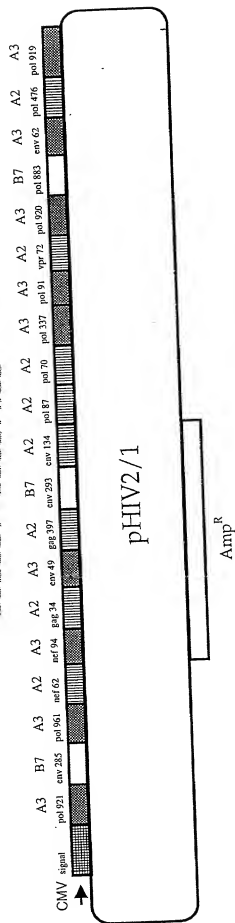


FIGURE 2

DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I declare that:

My residence, post office address and citizenship are as stated below next to my name; I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: **INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS** the specification of which _____ is attached hereto or _____ was filed on _____ as Application No. _____ and was amended on _____ (if applicable).

I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56. I claim foreign priority benefits under Title 35, United States Code, Section 119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)

Country	Application No.	Date of Filing	Priority Claimed Under 35 USC 119

I hereby claim the benefit under Title 35, United States Code § 119(e) of any United States provisional application(s) listed below:

Application No.	Filing Date

I claim the benefit under Title 35, United States Code, Section 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, Section 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, Section 1.56 which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

Application No.	Date of Filing	Status
09/189,702	11/10/98	Pending
08/205,713	3/4/94	Pending
08/159,184	11/29/93	Abandoned
08/073,205	6/4/93	Abandoned
08/027,146	3/5/93	Abandoned

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

Hector A. Alcega, Reg. No. 40,891
Randolph T. Apple, Reg. No. 36,429
Kevin L. Bastian, Reg. No. 34,774
Guy Chambers, Reg. No. 30,617
Karen B. Dow, Reg. No. 29,684
Gregory P. Einhorn, Reg. No. 38,440
M. Henry Heines, Reg. No. 28,219
Laurence J. Hyman, Reg. No. 35,551
Jeffrey J. King, Reg. No. 38,515

Joe Liebeschuetz, Reg. No. 37,505
Jeffrey S. Mann, Reg. No. 42,837
Annette S. Parent, Reg. No. 42,058
Steven W. Parmelee, Reg. No. 31,990
Brian W. Poor, Reg. No. 32,928
Margaret A. Powers, Reg. No. 39,804
Timothy L. Smith, Reg. No. 35,367
William M. Smith, Reg. No. 30,223
Joseph P. Snyder, Reg. No. 39,381
John R. Storella, Reg. No. 32,944
Eugenia Garrett-Wackowski, Reg. No. 37,330
Ellen Lauver Weber, Reg. No. 32,762
Kenneth A. Weber, Reg. No. 31,667
P. Ben Wang, Reg. No. 41,420
Kathleen Choi, Reg. No. 43,433
Jean M. Lockyer, Reg. No. P-44,879

Epimmune Inc.
Timothy J. Lithgow, M.D., J.D.
Reg. No. 36,856

Send Correspondence to: Jean M. Lockyer TOWNSEND and TOWNSEND and CREW LLP Two Embarcadero Center, 8th Floor San Francisco, California 94111-3834	Direct Telephone Calls to: (Name, Reg. No., Telephone No.) Name: Jean M. Lockyer Reg. No.: P-44,879 Telephone: 415-576-0200
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Full Name of Inventor 1:	Last Name: SETTE	First Name: ALESSANDRO	Middle Name or Initial:	
Residence & Citizenship:	City: La Jolla	State/Foreign Country: California	Country of Citizenship: Italy	
Post Office Address:	Post Office Address: 5551 Linda Rosa Avenue	City: La Jolla	State/Country: California	Postal Code: 92037
Full Name of Inventor 2:	Last Name: SIDNEY	First Name: JOHN	Middle Name or Initial:	
Residence & Citizenship:	City: San Diego	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 4218 Corte de la Siena	City: San Diego	State/Country: California	Postal Code: 92130
Full Name of Inventor 3:	Last Name: SOUTHWOOD	First Name: SCOTT	Middle Name or Initial:	
Residence & Citizenship:	City: Santee	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 10679 Strathmore Drive	City: Santee	State/Country: California	Postal Code: 92071
Full Name of Inventor 4:	Last Name: LIVINGSTON	First Name: BRIAN	Middle Name or Initial: D.	
Residence & Citizenship:	City: San Diego	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 13555 Chaco Court	City: San Diego	State/Country: California	Postal Code: 92129

Full Name of Inventor 5:	Last Name: CHESNUT	First Name: ROBERT	Middle Name or Initial:	
Residence & Citizenship:	City: Cardiff-by-the-Sea	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 1473 Kings Cross Drive	City: Cardiff-by-the-Sea	State/Country: California	Postal Code: 92007
Full Name of Inventor 6:	Last Name: BAKER	First Name: DENISE	Middle Name or Initial: MARIE	
Residence & Citizenship:	City: San Diego	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 11575 Caminito LaBar #21	City: San Diego	State/Country: California	Postal Code: 92126
Full Name of Inventor 7:	Last Name: CELIS	First Name: ESTEBAN	Middle Name or Initial:	
Residence & Citizenship:	City: Rochester	State/Foreign Country: Minnesota	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 3683 Wright Road S.W.	City: Rochester	State/Country: Minnesota	Postal Code: 55902
Full Name of Inventor 8:	Last Name: KUBO	First Name: RALPH	Middle Name or Initial: T.	
Residence & Citizenship:	City: Carlsbad	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 6921 Pear Tree Drive	City: Carlsbad	State/Country: California	Postal Code: 92009
Full Name of Inventor 9:	Last Name: GREY	First Name: HOWARD	Middle Name or Initial: M.	
Residence & Citizenship:	City: La Jolla	State/Foreign Country: California	Country of Citizenship: United States	
Post Office Address:	Post Office Address: 1461 Caminito Batea	City: La Jolla	State/Country: California	Postal Code: 92037

I further declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Signature of Inventor 1	Signature of Inventor 2	Signature of Inventor 3
<u>ALESSANDRO SETTE</u>	<u>JOHN SIDNEY</u>	<u>SCOTT SOUTHWOOD</u>
Date	Date	Date
Signature of Inventor 4	Signature of Inventor 5	Signature of Inventor 6
<u>BRIAN D. LIVINGSTON</u>	<u>ROBERT CHESNUT</u>	<u>DENISE MARIE BAKER</u>
Date	Date	Date

Signature of Inventor 7	Signature of Inventor 8	Signature of Inventor 9
<hr/>	<hr/>	<hr/>
ESTEBAN CELIS	RALPH T. KUBO	HOWARD M. GREY
Date	Date	Date

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